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(54) Title: 5' ESTs FOR SECRETED PROTEINS EXPRESSED IN TESTIS AND OTHER TISSUES

(57) Abstract

The sequences of 5' ESTs derived from mRNAs encoding secreted proteins are disclosed. The 5' ESTs may be to obtain cDNAs and genomic DNAs corresponding to the 5' ESTs. The 5' ESTs may also be used in diganostic, forensic, gene therapy, and chromosome mapping procedures. Upstream regulatory sequences may also be obtained using the 5' ESTs. The 5' ESTs may also be used to design expression vectors and secretion vectors.

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5' ESTs FOR SECRETED PROTEINS EXPRESSED IN TESTIS AND OTHER TISSUES

Background of the Invention

The estimated 50,000-100,000 genes scattered along the human chromosomes offer tremendous promise for the understanding, diagnosis, and treatment of human diseases. In addition, probes capable of specifically hybridizing to loci distributed throughout the human genome find applications in the construction of high resolution chromosome maps and in the identification of individuals.

In the past, the characterization of even a single human gene was a painstaking process, requiring years of effort. Recent developments in the areas of cloning vectors, DNA sequencing, and computer technology have merged to greatly accelerate the rate at which human genes can be isolated, sequenced, mapped, and characterized. Cloning vectors such as yeast artificial chromosomes (YACs) and bacterial artificial chromosomes (BACs) are able to accept DNA inserts ranging from 300 to 1000 kilobases (kb) or 100-400 kb in length respectively, thereby facilitating the manipulation and ordering of DNA sequences distributed over great distances on the human chromosomes. Automated DNA sequencing machines permit the rapid sequencing of human genes. Bioinformatics software enables the comparison of nucleic acid and protein sequences, thereby assisting in the characterization of human gene products.

Currently, two different approaches are being pursued for identifying and characterizing the genes distributed along the human genome. In one approach, large fragments of genomic DNA are isolated, cloned, and sequenced. Potential open reading frames in these genomic sequences are identified using bioinformatics software. However, this approach entails sequencing large stretches of human DNA which do not encode proteins in order to find the protein encoding sequences scattered throughout the genome. In addition to requiring extensive sequencing, the bioinformatics software may mischaracterize the genomic sequences obtained. Thus, the software may produce false positives in which non-coding DNA is mischaracterized as coding DNA or false negatives in which coding DNA is mislabeled as non-coding DNA.

An alternative approach takes a more direct route to identifying and characterizing human genes. In this approach, complementary DNAs (cDNAs) are synthesized from

isolated messenger RNAs (mRNAs) which encode human proteins. Using this approach, sequencing is only performed on DNA which is derived from protein coding portions of the genome. Often, only short stretches of the cDNAs are sequenced to obtain sequences called expressed sequence tags (ESTs). The ESTs may then be used to isolate or purify extended cDNAs which include sequences adjacent to the EST sequences. The extended cDNAs may contain all of the sequence of the EST which was used to obtain them or only a portion of the sequence of the EST which was used to obtain them. In addition, the extended cDNAs may contain the full coding sequence of the gene from which the EST was derived or, alternatively, the extended cDNAs may include portions of the coding sequence of the gene from which the EST was derived. It will be appreciated that there may be several extended cDNAs which include the EST sequence as a result of alternate splicing or the activity of alternative promoters.

In the past, these short EST sequences were often obtained from oligo-dT primed cDNA libraries. Accordingly, they mainly corresponded to the 3′ untranslated region of the mRNA. In part, the prevalence of EST sequences derived from the 3′ end of the mRNA is a result of the fact that typical techniques for obtaining cDNAs are not well suited for isolating cDNA sequences derived from the 5′ ends of mRNAs. (Adams *et al., Nature* 377:3-174, 1996; Hillier *et al., Genome Res.* 6:807-828, 1996).

In addition, in those reported instances where longer cDNA sequences have been obtained, the reported sequences typically correspond to coding sequences and do not include the full 5′ untranslated region of the mRNA from which the cDNA is derived. Such incomplete sequences may not include the first exon of the mRNA, particularly in situations where the first exon is short. Furthermore, they may not include some exons, often short ones, which are located upstream of splicing sites. Thus, there is a need to obtain sequences derived from the 5′ ends of mRNAs.

While many sequences derived from human chromosomes have practical applications, approaches based on the identification and characterization of those chromosomal sequences which encode a protein product are particularly relevant to diagnostic and therapeutic uses. Of the 50,000-100,000 protein coding genes, those genes encoding proteins which are secreted from the cell in which they are synthesized, as well as the secreted proteins themselves, are particularly valuable as potential therapeutic agents. Such proteins are often

involved in cell to cell communication and may be responsible for producing a clinically relevant response in their target cells.

In fact, several secretory proteins, including tissue plasminogen activator, G-CSF, GM-CSF, erythropoietin, human growth hormone, insulin, interferon-α, interferon-β, interferon-γ, and interleukin-2, are currently in clinical use. These proteins are used to treat a wide range of conditions, including acute myocardial infarction, acute ischemic stroke, anemia, diabetes, growth hormone deficiency, hepatitis, kidney carcinoma, chemotherapy induced neutropenia and multiple sclerosis. For these reasons, extended cDNAs encoding secreted proteins or portions thereof represent a particularly valuable source of therapeutic agents. Thus, there is a need for the identification and characterization of secreted proteins and the nucleic acids encoding them.

In addition to being therapeutically useful themselves, secretory proteins include short peptides, called signal peptides, at their amino termini which direct their secretion. These signal peptides are encoded by the signal sequences located at the 5′ ends of the coding sequences of genes encoding secreted proteins. Because these signal peptides will direct the extracellular secretion of any protein to which they are operably linked, the signal sequences may be exploited to direct the efficient secretion of any protein by operably linking the signal sequences to a gene encoding the protein for which secretion is desired. In addition, portions of signal sequences may also be used to direct the intracellular import of a peptide or protein of interest. This may prove beneficial in gene therapy strategies in which it is desired to deliver a particular gene product to cells other than the cell in which it is produced. Signal sequences encoding signal peptides also find application in simplifying protein purification techniques. In such applications, the extracellular secretion of the desired protein greatly facilitates purification by reducing the number of undesired proteins from which the desired protein must be selected. Thus, there exists a need to identify and characterize the 5′ portions of the genes for secretory proteins which encode signal peptides.

Public information on the number of human genes for which the promoters and upstream regulatory regions have been identified and characterized is quite limited. In part, this may be due to the difficulty of isolating such regulatory sequences. Upstream regulatory sequences such as transcription factor binding sites are typically too short to be utilized as probes for isolating promoters from human genomic libraries. Recently, some approaches

have been developed to isolate human promoters. One of them consists of making a CpG island library (Cross, *et al.*, *Nature Genetics* 6: 236-244, 1994). The second consists of isolating human genomic DNA sequences containing SpeI binding sites by the use of SpeI binding protein. (Mortlock *et al.*, *Genome Res.* 6:327-335, 1996). Both of these approaches have their limits due to a lack of specificity or of comprehensiveness.

The present 5′ ESTs may be used to efficiently identify and isolate upstream regulatory regions which control the location, developmental stage, rate, and quantity of protein synthesis, as well as the stability of the mRNA. (Theil, *BioFactors* 4:87-93, 1993). Once identified and characterized, these regulatory regions may be utilized in gene therapy or protein purification schemes to obtain the desired amount and locations of protein synthesis or to inhibit, reduce, or prevent the synthesis of undesirable gene products.

In addition, ESTs containing the 5′ ends of secretory protein genes may include sequences useful as probes for chromosome mapping and the identification of individuals. Thus, there is a need to identify and characterize the sequences upstream of the 5′ coding sequences of genes encoding secretory proteins.

Summary of the Invention

The present invention relates to purified, isolated, or recombinant ESTs which include sequences derived from the authentic 5′ ends of their corresponding mRNAs. The term "corresponding mRNA" refers to the mRNA which was the template for the cDNA synthesis which produced the 5′ EST. These sequences will be referred to hereinafter as "5′ ESTs." As used herein, the term "purified" does not require absolute purity; rather, it is intended as a relative definition. Individual 5′ EST clones isolated from a cDNA library have been conventionally purified to electrophoretic homogeneity. The sequences obtained from these clones could not be obtained directly either from the library or from total human DNA. The cDNA clones are not naturally occurring as such, but rather are obtained via manipulation of a partially purified naturally occurring substance (messenger RNA). The conversion of mRNA into a cDNA library involves the creation of a synthetic substance (cDNA) and pure individual cDNA clones can be isolated from the synthetic library by clonal selection. Thus, creating a cDNA library from messenger RNA and subsequently isolating individual clones from that library results in an approximately 10^4-10^6 fold purification of the native message.

Purification of starting material or natural material to at least one order of magnitude, preferably two or three orders, and more preferably four or five orders of magnitude is expressly contemplated.

As used herein, the term "isolated" requires that the material be removed from its original environment (e.g., the natural environment if it is naturally occurring). For example, a naturally-occurring polynucleotide present in a living animal is not isolated, but the same polynucleotide, separated from some or all of the coexisting materials in the natural system, is isolated.

As used herein, the term "recombinant" means that the 5′ EST is adjacent to "backbone" nucleic acid to which it is not adjacent in its natural environment. Additionally, to be "enriched" the 5′ ESTs will represent 5% or more of the number of nucleic acid inserts in a population of nucleic acid backbone molecules. Backbone molecules according to the present invention include nucleic acids such as expression vectors, self-replicating nucleic acids, viruses, integrating nucleic acids, and other vectors or nucleic acids used to maintain or manipulate a nucleic acid insert of interest. Preferably, the enriched 5′ ESTs represent 15% or more of the number of nucleic acid inserts in the population of recombinant backbone molecules. More preferably, the enriched 5′ ESTs represent 50% or more of the number of nucleic acid inserts in the population of recombinant backbone molecules. In a highly preferred embodiment, the enriched 5′ ESTs represent 90% or more of the number of nucleic acid inserts in the population of recombinant backbone molecules.

"Stringent", moderate," and "low" hybridization conditions are as defined in Example 29.

Unless otherwise indicated, a "complementary" sequence is fully complementary.

Thus, 5′ ESTs in cDNA libraries in which one or more 5′ ESTs make up 5% or more of the number of nucleic acid inserts in the backbone molecules are "enriched recombinant 5′ ESTs" as defined herein. Likewise, 5′ ESTs in a population of plasmids in which one or more 5′ EST of the present invention have been inserted such that they represent 5% or more of the number of inserts in the plasmid backbone are " enriched recombinant 5′ ESTs" as defined herein. However, 5′ ESTs in cDNA libraries in which 5′ ESTs constitute less than 5% of the number of nucleic acid inserts in the population of backbone molecules, such as libraries in

which backbone molecules having a 5′ EST insert are extremely rare, are not "enriched recombinant 5′ ESTs".

In particular, the present invention relates to 5′ ESTs which are derived from genes encoding secreted proteins. As used herein, a "secreted" protein is one which, when expressed in a suitable host cell, is transported across or through a membrane, including transport as a result of signal peptides in its amino acid sequence. "Secreted" proteins include without limitation proteins secreted wholly (e.g. soluble proteins), or partially (e.g. receptors) from the cell in which they are expressed. "Secreted" proteins also include without limitation proteins which are transported across the membrane of the endoplasmic reticulum.

Such 5′ ESTs include nucleic acid sequences, called signal sequences, which encode signal peptides which direct the extracellular secretion of the proteins encoded by the genes from which the 5′ ESTs are derived. Generally, the signal peptides are located at the amino termini of secreted proteins.

Secreted proteins are translated by ribosomes associated with the "rough" endoplasmic reticulum. Generally, secreted proteins are co-translationally transferred to the membrane of the endoplasmic reticulum. Association of the ribosome with the endoplasmic reticulum during translation of secreted proteins is mediated by the signal peptide. The signal peptide is typically cleaved following its co-translational entry into the endoplasmic reticulum. After delivery to the endoplasmic reticulum, secreted proteins may proceed through the Golgi apparatus. In the Golgi apparatus, the proteins may undergo post-translational modification before entering secretory vesicles which transport them across the cell membrane.

The 5′ ESTs of the present invention have several important applications. For example, they may be used to obtain and express cDNA clones which include the full protein coding sequences of the corresponding gene products, including the authentic translation start sites derived from the 5′ ends of the coding sequences of the mRNAs from which the 5′ ESTs are derived. These cDNAs will be referred to hereinafter as "full length cDNAs." These cDNAs may also include DNA derived from mRNA sequences upstream of the translation start site. The full length cDNA sequences may be used to express the proteins corresponding to the 5′ ESTs. As discussed above, secreted proteins are therapeutically important. Thus, the proteins expressed from the cDNAs may be useful in treating or

controlling a variety of human conditions. The 5′ ESTs may also be used to obtain the corresponding genomic DNA. The term "corresponding genomic DNA" refers to the genomic DNA which encodes the mRNA from which the 5′ EST was derived.

Alternatively, the 5′ ESTs may be used to obtain and express extended cDNAs encoding portions of the secreted protein. The portions may comprise the signal peptides of the secreted proteins or the mature proteins generated when the signal peptide is cleaved off. The portions may also comprise polypeptides having at least 10 consecutive amino acids encoded by the extended cDNAs or full length cDNAs. Alternatively, the portions may comprise at least 15 consecutive amino acids encoded by the extended cDNAs or full length cDNAs. In some embodiments, the portions may comprise at least 25 consecutive amino acids encoded by the extended cDNAs or full length cDNAs. In other embodiments, the portions may comprise at least 40 amino acids encoded by the extended cDNAs or full length cDNAs.

Antibodies which specifically recognize the entire secreted proteins encoded by the extended cDNAs, full length cDNAs, or fragments thereof having at least 10 consecutive amino acids, at least 15 consecutive amino acids, at least 25 consecutive amino acids, or at least 40 consecutive amino acids may also be obtained as described below. Antibodies which specifically recognize the mature protein generated when the signal peptide is cleaved may also be obtained as described below. Similarly, antibodies which specifically recognize the signal peptides encoded by the extended cDNAs or full length cDNAs may also be obtained.

In some embodiments, the extended cDNAs obtained using the 5′ ESTs include the signal sequence. In other embodiments, the extended cDNAs obtained using the 5′ ESTs may include the full coding sequence for the mature protein (*i.e.* the protein generated when the signal polypeptide is cleaved off). In addition, the extended cDNAs obtained using the 5′ ESTs may include regulatory regions upstream of the translation start site or downstream of the stop codon which control the amount, location, or developmental stage of gene expression.

As discussed above, secreted proteins are therapeutically important. Thus, the proteins expressed from the extended cDNAs or full length cDNAs obtained using the 5′ ESTs may be useful in treating or controlling a variety of human conditions.

The 5′ ESTs (or cDNAs or genomic DNAs obtained therefrom) may be used in forensic procedures to identify individuals or in diagnostic procedures to identify individuals having genetic diseases resulting from abnormal expression of the genes corresponding to the 5′ ESTs. In addition, the present invention is useful for constructing a high resolution map of the human chromosomes.

The present invention also relates to secretion vectors capable of directing the secretion of a protein of interest. Such vectors may be used in gene therapy strategies in which it is desired to produce a gene product in one cell which is to be delivered to another location in the body. Secretion vectors may also facilitate the purification of desired proteins.

The present invention also relates to expression vectors capable of directing the expression of an inserted gene in a desired spatial or temporal manner or at a desired level. Such vectors may include sequences upstream of the 5′ ESTs, such as promoters or upstream regulatory sequences.

Finally, the present invention may also be used for gene therapy to control or treat genetic diseases. Signal peptides may also be fused to heterologous proteins to direct their extracellular secretion.

Bacterial clones containing Bluescript plasmids having inserts containing the 5′ ESTs of the present invention (SEQ ID NOs: 38-270 are presently stored at 80°C in 4% (v/v) glycerol in the inventor's laboratories under the designations listed next to the SEQ ID NOs in II). The inserts may be recovered from the deposited materials by growing the appropriate clones on a suitable medium. The Bluescript DNA can then be isolated using plasmid isolation procedures familiar to those skilled in the art such as alkaline lysis minipreps or large scale alkaline lysis plasmid isolation procedures. If desired the plasmid DNA may be further enriched by centrifugation on a cesium chloride gradient, size exclusion chromatography, or anion exchange chromatography. The plasmid DNA obtained using these procedures may then be manipulated using standard cloning techniques familiar to those skilled in the art. Alternatively, a PCR can be done with primers designed at both ends of the EST insertion. The PCR product which corresponds to the 5′ EST can then be manipulated using standard cloning techniques familiar to those skilled in the art.

One aspect of the present invention is a purified or isolated nucleic acid having the sequence of one of SEQ ID NOs: 38-270 or having a sequence complementary thereto. In one embodiment, the nucleic acid is recombinant.

Another aspect of the present invention is a purified or isolated nucleic acid comprising at least 10 consecutive bases of the sequence of one of SEQ ID NOs: 38-270 or one of the sequences complementary thereto.

Yet another aspect of the present invention is a purified or isolated nucleic acid comprising at least 15 consecutive bases of one of the sequences of SEQ ID NOs: 38-270 or one of the sequences complementary thereto. In one embodiment, the nucleic acid is recombinant.

A further aspect of the present invention is a purified or isolated nucleic acid of at least 15 bases capable of hybridizing under stringent conditions to the sequence of one of SEQ ID NOs: 38-270 or one of the sequences complementary to the sequences of SEQ ID NOs: 38-270. In one embodiment, the nucleic acid is recombinant.

Another aspect of the present invention is a purified or isolated nucleic acid encoding a human gene product, said human gene product having a sequence partially encoded by one of the sequences of SEQ ID NO: 38-270.

Still another aspect of the present invention is a method of making a cDNA encoding a human secretory protein, said human secretory protein being partially encoded by one of SEQ ID NOs 38-270, comprising the steps of contacting a collection of mRNA molecules from human cells with a primer comprising at least 15 consecutive nucleotides of a sequence complementary to one of SEQ ID NOs: 38-270; hybridizing said primer to an mRNA in said collection that encodes said protein; reverse transcribing said hybridized primer to make a first cDNA strand from said mRNA; making a second cDNA strand complementary to said first cDNA strand; and isolating the resulting cDNA encoding said protein comprising said first cDNA strand and said second cDNA strand.

Another aspect of the invention is an isolated or purified cDNA encoding a human secretory protein, said human secretory protein comprising the protein encoded by one of SEQ ID NOs 38-270 or a fragment thereof of at least 10 amino acids, said cDNA being obtainable by the method described in the preceding paragraph. In one embodiment, the

cDNA comprises the full protein coding sequence of said protein which sequence is partially included in one of the sequences of SEQ ID NOs: 38-270.

Another aspect of the present invention is a method of making a cDNA encoding a human secretory protein that is partially encoded by one of SEQ ID NOs 38-270, comprising the steps of obtaining a cDNA comprising one of the sequences of SEQ ID NOs: 38-270; contacting said cDNA with a detectable probe comprising at least 15 consecutive nucleotides of said sequence of SEQ ID NO: 38-270 or a sequence complementary thereto under conditions which permit said probe to hybridize to said cDNA; identifying a cDNA which hybridizes to said detectable probe; and isolating said cDNA which hybridizes to said probe.

Another aspect of the present invention is an isolated or purified cDNA encoding a human secretory protein, said human secretory protein comprising the protein encoded by one of SEQ ID NOs 38-270 or a fragment thereof of at least 10 amino acids, said cDNA being obtainable by the method described in the preceding paragraph. In one embodiment, the cDNA comprises the full protein coding sequence partially included in one of the sequences of SEQ ID NOs: 38-270.

Another aspect of the present invention is a method of making a cDNA comprising one of the sequence of SEQ ID NOs: 38-270, comprising the steps of contacting a collection of mRNA molecules from human cells with a first primer capable of hybridizing to the polyA tail of said mRNA; hybridizing said first primer to said polyA tail; reverse transcribing said mRNA to make a first cDNA strand; making a second cDNA strand complementary to said first cDNA strand using at least one primer comprising at least 15 nucleotides of one of the sequences of SEQ ID NOs 38-270; and isolating the resulting cDNA comprising said first cDNA strand and said second cDNA strand.

Another aspect of the present invention is an isolated or purified cDNA encoding a human secretory protein, said human secretory protein comprising the protein encoded by one of SEQ ID NOs 38-270 or a fragment thereof of at least 10 amino acids, said cDNA being obtainable by the method described in the preceding paragraph. In one embodiment, the cDNA comprises the full protein coding sequence partially included in one of the sequences of SEQ ID NOs: 38-270.

In one embodiment of the method described in the two paragraphs above, the second cDNA strand is made by contacting said first cDNA strand with a first pair of primers, said

first pair of primers comprising a second primer comprising at least 15 consecutive nucleotides of one of the sequences of SEQ ID NOs 38-270 and a third primer having a sequence therein which is included within the sequence of said first primer; performing a first polymerase chain reaction with said first pair of nested primers to generate a first PCR product; contacting said first PCR product with a second pair of primers, said second pair of primers comprising a fourth primer, said fourth primer comprising at least 15 consecutive nucleotides of said sequence of one of SEQ ID NOs: 38-270 , and a fifth primer, said fourth and fifth primers being capable of hybridizing to sequences within said first PCR product; and performing a second polymerase chain reaction, thereby generating a second PCR product.

One aspect of the present invention is an isolated or purified cDNA encoding a human secretory protein, said human secretory protein comprising the protein encoded by one of SEQ ID NOs 38-270, or a fragment thereof of at least 10 amino acids, said cDNA being obtainable by the method of the preceding paragraph. In one embodiment, the cDNA comprises the full protein coding sequence partially included in one of the sequences of SEQ ID NOs: 38-270.

Another aspect of the present invention is the method described four paragraphs above in which the second cDNA strand is made by contacting said first cDNA strand with a second primer comprising at least 15 consecutive nucleotides of the sequences of SEQ ID NOs: 38-270; hybridizing said second primer to said first strand cDNA; and extending said hybridized second primer to generate said second cDNA strand.

Another aspect of the present invention is an isolated or purified cDNA encoding a human secretory protein, said human secretory protein comprising the protein partially encoded by one of SEQ ID NOs 38-270 or comprising a fragment thereof of at least 10 amino acids, said cDNA being obtainable by the method described in the preceding paragraph. In one embodiment, the cDNA comprises the full protein coding sequence partially included in of one of the sequences of SEQ ID NOs: 38-270.

Another aspect of the present invention is a method of making a protein comprising one of the sequences of SEQ ID NOs: 271-503, comprising the steps of obtaining a cDNA encoding the full protein sequence partially included in one of the sequences of sequence of SEQ ID NOs: 38-270; inserting said cDNA in an expression vector such that said cDNA is

operably linked to a promoter; introducing said expression vector into a host cell whereby said host cell produces the protein encoded by said cDNA; and isolating said protein.

Another aspect of the present invention is an isolated protein obtainable by the method described in the preceding paragraph.

Another aspect of the present invention is a method of obtaining a promoter DNA comprising the steps of obtaining DNAs located upstream of the nucleic acids of SEQ ID NOs: 38-270 or the sequences complementary thereto; screening said upstream DNAs to identify a promoter capable of directing transcription initiation; and isolating said DNA comprising said identified promoter. In one embodiment, the obtaining step comprises chromosome walking from said nucleic acids of SEQ ID NOs: 38-270 or sequences complementary thereto. In another embodiment, the screening step comprises inserting said upstream sequences into a promoter reporter vector. In another embodiment, the screening step comprises identifying motifs in said upstream DNAs which are transcription factor binding sites or transcription start sites.

Another aspect of the present invention is an isolated promoter obtainable by the method described above.

Another aspect of the present invention is an isolated or purified protein comprising one of the sequences of SEQ ID NOs: 271-503.

Another aspect of the present invention is the inclusion of at least one of the sequences of SEQ ID NOs: 38-270, or one of the sequences complementary to the sequences of SEQ ID NOs: 38-270, or a fragment thereof of at least 15 consecutive nucleotides in an array of discrete ESTs or fragments thereof of at least 15 nucleotides in length. In one embodiment, the array includes at least two of the sequences of SEQ ID NOs: 38-270, the sequences complementary to the sequences of SEQ ID NOs: 38-270, or fragments thereof of at least 15 consecutive nucleotides. In another embodiment, the array includes at least five of the sequences of SEQ ID NOs: 38-270, the sequences complementary to the sequences of SEQ ID NOs: 38-270, or fragments thereof of at least 15 consecutive nucleotides.

Another aspect of the present invention is a promoter having a sequence selected from the group consisting of SEQ ID NOs: 31, 34, and 37.

Brief Description of the Drawings

Figure 1 is a summary of a procedure for obtaining cDNAs which have been selected to include the 5′ ends of the mRNAs from which they derived.

Figure 2 shows the distribution of Von Heijne scores for 5′ ESTs in each of the categories described herein and the probability that these 5′ ESTs encode a signal peptide.

Figure 3 summarizes a general method used to clone and sequence extended cDNAs containing sequences adjacent to 5' ESTs.

Figure 4 (description of promoters structure isolated from SignalTag 5' ESTs) provides a schematic description of promoters isolated and the way they are assembled with the corresponding 5′ tags.

Detailed Description of the Preferred Embodiment

Table IV is an analysis of the 43 amino acids located at the N terminus of all human SwissProt proteins to determine the frequency of false positives and false negatives using the techniques for signal peptide identification described herein.

Table V shows the distribution of 5′ ESTs in each category described herein and the number of 5′ ESTs in each category having a given minimum Von Heijne's score.

Table VI shows the distribution of 5′ ESTs in each category described herein with respect to the tissue from which the 5' ESTs of the corresponding mRNA were obtained.

Table VII describes the transcription factor binding sites present in each of these promoters.

I. General Methods for Obtaining 5′ ESTs derived from mRNAs with intact 5' ends

In order to obtain the 5' ESTs of the present invention, mRNAs with intact 5' ends must be obtained. Currently, there are two approaches for obtaining such mRNAs with intact 5' ends as described below: either chemical (1) or enzymatic (2).

1. Chemical Methods for Obtaining mRNAs having Intact 5′ Ends

One of these approaches is a chemical modification method involving derivatization of the 5′ ends of the mRNAs and selection of the derivatized mRNAs. The 5′ ends of eukaryotic mRNAs possess a structure referred to as a "cap" which comprises a guanosine

methylated at the 7 position. The cap is joined to the first transcribed base of the mRNA by a 5′, 5′-triphosphate bond. In some instances, the 5′ guanosine is methylated in both the 2 and 7 positions. Rarely, the 5′ guanosine is trimethylated at the 2, 7 and 7 positions. In the chemical method for obtaining mRNAs having intact 5′ ends, the 5′ cap is specifically derivatized and coupled to a reactive group on an immobilizing substrate. This specific derivatization is based on the fact that only the ribose linked to the methylated guanosine at the 5′ end of the mRNA and the ribose linked to the base at the 3′ terminus of the mRNA, possess 2′, 3′-cis diols.

Optionally, the 2′, 3′-cis diol of the 3′ terminal ribose may be chemically modified, substituted, converted, or eliminated, leaving only the ribose linked to the methylated guanosine at the 5′ end of the mRNA with a 2′, 3′-cis diol. A variety of techniques are available for eliminating the 2′, 3′-cis diol on the 3′ terminal ribose. For example, controlled alkaline hydrolysis may be used to generate mRNA fragments in which the 3′ terminal ribose is a 3′-phosphate, 2′-phosphate or (2′, 3′)-cyclophosphate. Thereafter, the fragment which includes the original 3′ ribose may be eliminated from the mixture through chromatography on an oligodT column. Alternatively, a base which lacks the 2′, 3′-cis diol may be added to the 3′ end of the mRNA using an RNA ligase such as T4 RNA ligase. Example 1 below describes a method for ligation of a nucleoside diphosphate to the 3′ end of messenger RNA.

EXAMPLE 1

Ligation of the Nucleoside Diphosphate pCp to the 3' End of mRNA.

One µg of RNA was incubated in a final reaction medium of 10 µl in the presence of 5 U of T_4 phage RNA ligase in the buffer provided by the manufacturer (Gibco - BRL), 40 U of the RNase inhibitor RNasin (Promega) and, 2 µl of ^{32}pCp (Amersham #PB 10208). The incubation was performed at 37°C for 2 hours or overnight at 7-8°C.

Following modification or elimination of the 2′, 3′-cis diol at the 3′ ribose, the 2′, 3′-cis diol present at the 5′ end of the mRNA may be oxidized using reagents such as $NaBH_4$, $NaBH_3CN$, or sodium periodate, thereby converting the 2′, 3′-cis diol to a

dialdehyde. Example 2 describes the oxidation of the 2′, 3′-cis diol at the 5′ end of the mRNA with sodium periodate.

EXAMPLE 2

Oxidation of 2′, 3′-cis diol at the 5′ End of the mRNA with Sodium Periodate

0.1 OD unit of either a capped oligoribonucleotide of 47 nucleotides (including the cap) or an uncapped oligoribonucleotide of 46 nucleotides were treated as follows. The oligoribonucleotides were produced by *in vitro* transcription using the transcription kit "AmpliScribe T7" (Epicentre Technologies). As indicated below, the DNA template for the RNA transcript contained a single cytosine. To synthesize the uncapped RNA, all four NTPs were included in the *in vitro* transcription reaction. To obtain the capped RNA, GTP was replaced by an analogue of the cap, m7G(5′)ppp(5′)G. This compound, recognized by the polymerase, was incorporated into the 5′ end of the nascent transcript during the initiation of transcription but was not incorporated during the extension step. Consequently, the resulting RNA contained a cap at its 5′ end. The sequences of the oligoribonucleotides produced by the *in vitro* transcription reaction were:

+Cap:

5′m7GpppGCAUCCUACUCCCAUCCAAUUCCACCCUAACUCCUCCCAUCUCCAC-3′ (SEQ ID NO:1)

-Cap:

5′-pppGCAUCCUACUCCCAUCCAAUUCCACCCUAACUCCUCCCAUCUCCAC-3′ (SEQ ID NO:2)

The oligoribonucleotides were dissolved in 9 μl of acetate buffer (0.1 M sodium acetate, pH 5.2) and 3 μl of freshly prepared 0.1 M sodium periodate solution. The mixture was incubated for 1 hour in the dark at 4°C or room temperature. Thereafter, the reaction was stopped by adding 4 μl of 10% ethylene glycol. The product was ethanol precipitated, resuspended in at least 10 μl of water or appropriate buffer and dialyzed against water.

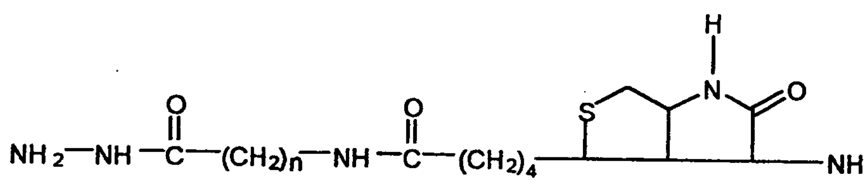
The resulting aldehyde groups may then be coupled to molecules having a reactive amine group, such as hydrazine, carbazide, thiocarbazide or semicarbazide groups, in order to facilitate enrichment of the 5′ ends of the mRNAs. Molecules having reactive amine groups

which are suitable for use in selecting mRNAs having intact 5′ ends include avidin, proteins, antibodies, vitamins, ligands capable of specifically binding to receptor molecules, or oligonucleotides. Example 3 below describes the coupling of the resulting dialdehyde to biotin.

EXAMPLE 3

Coupling of the Dialdehyde at the 5' End of Transcripts with Biotin

The oxidation product obtained in Example 2 was dissolved in 50 μl of sodium acetate at a pH between 5 and 5.2 and 50 μl of freshly prepared 0.02 M solution of biotin hydrazide in a methoxyethanol/water mixture (1:1) of formula:



In the compound used in these experiments, n=5. However, it will be appreciated that other commercially available hydrazides may also be used, such as molecules of the above formula in which n varies from 0 to 5. The mixture was then incubated for 2 hours at 37°C, precipitated with ethanol and dialyzed against distilled water. Example 4 demonstrates the specificity of the biotinylation reaction.

EXAMPLE 4

Specificity of Biotinylation of Capped Transcripts

The specificity of the biotinylation for capped mRNAs was evaluated by gel electrophoresis of the following samples:

Sample 1. The 46 nucleotide uncapped *in vitro* transcript prepared as in Example 2 and labeled with ^{32}pCp as described in Example 1.

Sample 2. The 46 nucleotide uncapped *in vitro* transcript prepared as in Example 2, labeled with ^{32}pCp as described in Example 1, treated with the oxidation reaction of Example 2, and subjected to the biotinylation conditions of Example 3.

Sample 3. The 47 nucleotide capped *in vitro* transcript prepared as in Example 2 and labeled with ^{32}pCp as described in Example 1.

Sample 4. The 47 nucleotide capped *in vitro* transcript prepared as in Example 2, labeled with ^{32}pCp as described in Example 1, treated with the oxidation reaction of Example 2, and subjected to the biotinylation conditions of Example 3.

Samples 1 and 2 had identical migration rates, demonstrating that the uncapped RNAs were not oxidized and biotinylated. Sample 3 migrated more slowly than Samples 1 and 2, while Sample 4 exhibited the slowest migration. The difference in migration of the RNAs in Samples 3 and 4 demonstrates that the capped RNAs were specifically biotinylated.

In some cases, mRNAs having intact 5′ ends may be enriched by binding the molecule containing a reactive amine group to a suitable solid phase substrate such as the inside of the vessel containing the mRNAs, magnetic beads, chromatography matrices, or nylon or nitrocellulose membranes. For example, where the molecule having a reactive amine group is biotin, the solid phase substrate may be coupled to avidin or streptavidin. Alternatively, where the molecule having the reactive amine group is an antibody or receptor ligand, the solid phase substrate may be coupled to the cognate antigen or receptor. Finally, where the molecule having a reactive amine group comprises an oligonucleotide, the solid phase substrate may comprise a complementary oligonucleotide.

The mRNAs having intact 5′ ends may be released from the solid phase following the enrichment procedure. For example, where the dialdehyde is coupled to biotin hydrazide and the solid phase comprises streptavidin, the mRNAs may be released from the solid phase by simply heating to 95 degrees Celsius in 2% SDS. In some methods, the molecule having a reactive amine group may also be cleaved from the mRNAs having intact 5′ ends following enrichment. Example 5 describes the capture of biotinylated mRNAs with streptavidin coated beads and the release of the biotinylated mRNAs from the beads following enrichment.

EXAMPLE 5

Capture and Release of Biotinylated mRNAs Using Streptavidin Coated Beads

The streptavidin coated magnetic beads were prepared according to the manufacturer's instructions (CPG Inc., USA). The biotinylated mRNAs were added to a

hybridization buffer (1.5 M NaCl, pH 5 - 6). After incubating for 30 minutes, the unbound and nonbiotinylated material was removed. The beads were then washed several times in water with 1% SDS. The beads thus obtained were incubated for 15 minutes at 95°C in water containing 2% SDS.

Example 6 demonstrates the efficiency with which biotinylated mRNAs were recovered from the streptavidin coated beads.

EXAMPLE 6

Efficiency of Recovery of Biotinylated mRNAs

The efficiency of the recovery procedure was evaluated as follows. Capped RNAs were labeled with ^{32}pCp, oxidized, biotinylated and bound to streptavidin coated beads as described above. Subsequently, the bound RNAs were incubated for 5, 15 or 30 minutes at 95°C in the presence of 2% SDS.

The products of the reaction were analyzed by electrophoresis on 12% polyacrylamide gels under denaturing conditions (7 M urea). The gels were subjected to autoradiography. During this manipulation, the hydrazone bonds were not reduced.

Increasing amounts of nucleic acids were recovered as incubation times in 2% SDS increased, demonstrating that biotinylated mRNAs were efficiently recovered.

In an alternative method for obtaining mRNAs having intact 5′ ends, an oligonucleotide which has been derivatized to contain a reactive amine group is specifically coupled to mRNAs having an intact cap. Preferably, the 3′ end of the mRNA is blocked prior to the step in which the aldehyde groups are joined to the derivatized oligonucleotide, as described above, so as to prevent the derivatized oligonucleotide from being joined to the 3′ end of the mRNA. For example, pCp may be attached to the 3′ end of the mRNA using T4 RNA ligase as described in example 1. However, as discussed above, blocking the 3′ end of the mRNA is an optional step. Derivatized oligonucleotides may be prepared as described in Example 7.

EXAMPLE 7

Derivatization of Oligonucleotides

An oligonucleotide phosphorylated at its 3′ end was converted to a 3′ hydrazide in 3′ by treatment with an aqueous solution of hydrazine or of dihydrazide of the formula $H_2N(R1)NH_2$ at about 1 to 3 M, and at pH 4.5 at a temperature of 8°C overnight. This incubation was performed in the presence of a carbodiimide type agent soluble in water such as 1-ethyl-3-(3-dimethylaminopropyl)carbodiimide at a final concentration of 0.3 M.

The derivatized oligonucleotide was then separated from the other agents and products using a standard technique for isolating oligonucleotides.

As discussed above, the mRNAs to be enriched may be treated to eliminate the 3′ OH groups which may be present thereon. This may be accomplished by enzymatic ligation of sequences lacking a 3′ OH, such as pCp, as described in Example 1. Alternatively, the 3′ OH groups may be eliminated by alkaline hydrolysis as described in Example 8 below.

EXAMPLE 8

Elimination of 3' OH Groups of mRNA Using Alkaline Hydrolysis

In a total volume of 100 μl of 0.1 N sodium hydroxide, 1.5 μg mRNA is incubated for 40 to 60 minutes at 4°C. The solution is neutralized with acetic acid and precipitated with ethanol. .

Following the optional elimination of the 3′ OH groups, the diol groups at the 5′ ends of the mRNAs are oxidized as described below in Example 9.

EXAMPLE 9

Oxidation of Diols of mRNA

Up to 1 OD unit of RNA was dissolved in 9 μl of buffer (0.1 M sodium acetate, pH 6-7) or water and 3 μl of freshly prepared 0.1 M sodium periodate solution. The reaction was incubated for 1 h in the dark at 4°C or room temperature. Following the incubation, the reaction was stopped by adding 4 μl of 10% ethylene glycol. Thereafter the mixture was incubated at room temperature for 15 minutes. After ethanol precipitation, the product was resuspended in at least 10 μl of water or appropriate buffer and dialyzed against water.

Following oxidation of the diol groups at the 5′ ends of the mRNAs, the derivatized oligonucleotide was joined to the resulting aldehydes as described in Example 10.

EXAMPLE 10

Ligature of Aldehydes of mRNA to Derivatized Oligonucleotides

The oxidized mRNA was dissolved in an acidic medium such as 50 μl of sodium acetate pH 4-6. Fifty μl of a solution of the derivatized oligonucleotide were added in order to obtain an mRNA:derivatized oligonucleotide ratio of 1:20. The mixture was reduced with a borohydride and incubated for 2 h at 37°C or overnight (14 h) at 10°C. The mixture was then ethanol precipitated, resuspended in 10 μl or more of water or appropriate buffer and dialyzed against distilled water. If desired, the resulting product may be analyzed using acrylamide gel electrophoresis, HPLC analysis, or other conventional techniques.

Following the attachment of the derivatized oligonucleotide to the mRNAs, a reverse transcription reaction may be performed as described in Example 11 below.

EXAMPLE 11

Reverse Transcription of mRNAs Ligatured to Derivatized Oligonucleotides

An oligodeoxyribonucleotide was derivatized as follows. Three OD units of an oligodeoxyribonucleotide of sequence 5'ATCAAGAATTCGCACGAGACCATTA3' (SEQ ID NO:3) having 5′-OH and 3′-P ends were dissolved in 70 μl of a 1.5 M hydroxybenzotriazole solution, pH 5.3, prepared in dimethylformamide/water (75:25) containing 2 μg of 1-ethyl-3-(3-dimethylaminopropyl)carbodiimide. The mixture was incubated for 2 h 30 min at 22°C and then precipitated twice in $LiClO_4$/acetone. The pellet was resuspended in 200 μl of 0.25 M hydrazine and incubated at 8°C from 3 to 14 h. Following the hydrazine reaction, the mixture was precipitated twice in $LiClO_4$/acetone.

The messenger RNAs to be reverse transcribed were extracted from blocks of placenta having sides of 2 cm which had been stored at -80°C. The total RNA was extracted using conventional acidic phenol techniques. Oligo-dT chromatography was used to purify the mRNAs. The integrity of the mRNAs was checked by Northern-blotting.

The diol groups on 7 μg of the placental mRNAs were oxidized as described above in Example 9. The derivatized oligonucleotide was joined to the mRNAs as described in Example 10 above except that the precipitation step was replaced by an exclusion chromatography step to remove derivatized oligodeoxyribonucleotides which were not joined to mRNAs. Exclusion chromatography was performed as follows:

Ten ml of Ultrogel AcA34 (BioSepra#230151) gel, a mix of agarose and acrylamide, were equilibrated in 50 ml of a solution of 10 mM Tris pH 8.0, 300 mM NaCl, 1 mM EDTA, and 0.05% SDS. The mixture was allowed to sediment. The supernatant was eliminated and the gel was resuspended in 50 ml of buffer. This procedure was repeated 2 or 3 times.

A glass bead (diameter 3 mm) was introduced into a 2 ml disposable pipette (length 25 cm). The pipette was filled with the gel suspension until the height of the gel stabilized at 1 cm from the top of the pipette. The column was then equilibrated with 20 ml of equilibration buffer (10 mM Tris HCl pH 7.4, 20 mM NaCl).

Ten μl of the mRNA which had reacted with the derivatized oligonucleotide were mixed in 39 μl of 10 mM urea and 2 μl of blue-glycerol buffer, which had been prepared by dissolving 5 mg of bromophenol blue in 60% glycerol (v/v), and passing the mixture through a 0.45 μm diameter filter.

The column was then loaded with the mRNAs coupled to the oligonucleotide. As soon as the sample had penetrated, equilibration buffer was added. Hundred μl fractions were then collected. Derivatized oligonucleotide which had not been attached to mRNA appeared in fraction 16 and later fractions. Thus, fractions 3 to 15 were combined and precipitated with ethanol.

To determine whether the derivatized oligonucleotide was actually linked to mRNA, one tenth of the combined fractions were spotted twice on a nylon membrane and hybridized to a radioactive probe using conventional techniques. The ^{32}P labeled probe used in these hybridizations was an oligodeoxyribonucleotide of sequence 5'TAATGGTCTCGTGCGAATTCTTGAT3' (SEQ ID NO:4) anticomplementary to the derivatized oligonucleotide. A signal observed after autoradiography, indicated that the derivatized oligonucleotide had been truly joined to the mRNA.

The remaining nine tenth of the mRNAs which had reacted with the derivatized oligonucleotide was reverse transcribed as follows. A reverse transcription reaction was

carried out with reverse transcriptase following the manufacturer's instructions and 50 pmol of nonamers with random sequence as primers.

To ensure that reverse transcription had been carried out through the cap structure, two types of experiments were performed.

In the first approach, after elimination of RNA of the cDNA:RNA heteroduplexes obtained from the reverse transcription reaction by an alkaline hydrolysis, a portion of the resulting single stranded cDNAs was spotted on a positively charged membrane and hybridized, using conventional methods, to a ^{32}P labeled probe having a sequence identical to that of the derivatized oligonucleotide. Control spots containing, 1 pmol, 100 fmol, 50 fmol, 10 fmol and 1 fmol of a control oligodeoxyribonucleotide of sequence identical to that of the derivatized oligonucleotide were included. The signal observed in the spots containing the cDNA indicated that approximately 15 fmol of the derivatized oligonucleotide had been reverse transcribed. These results demonstrate that the reverse transcription can be performed through the cap and, in particular, that reverse transcriptase crosses the 5'-P-P-P-5' bond of the cap of eukaryotic messenger RNAs.

In the second type of experiment, the single stranded cDNAs obtained from the above first strand synthesis were used as template for PCR reactions. Two types of reactions were carried out. First, specific amplification of the mRNAs for alpha globin, dehydrogenase, pp15 and elongation factor E4 were carried out using the following pairs of oligodeoxyribonucleotide primers.

alpha-globin

GLO-S: 5'CCG ACA AGA CCA ACG TCA AGG CCG C3' (SEQ ID NO:5)

GLO-As: 5'TCA CCA GCA GGC AGT GGC TTA GGA G 3' (SEQ ID NO:6)

dehydrogenase

3 DH-S: 5'AGT GAT TCC TGC TAC TTT GGA TGG C3' (SEQ ID NO:7)

3 DH-As: 5'GCT TGG TCT TGT TCT GGA GTT TAG A3' (SEQ ID NO:8)

pp15

PP15-S: 5'TCC AGA ATG GGA GAC AAG CCA ATT T3' (SEQ ID NO:9)

PP15-As: 5'AGG GAG GAG GAA ACA GCG TGA GTC C3' (SEQ ID NO:10)

Elongation factor E4

EFA1-S: 5'ATG GGA AAG GAA AAG ACT CAT ATC A3' (SEQ ID NO:11)

EF1A-As: 5'AGC AGC AAC AAT CAG GAC AGC ACA G3' (SEQ ID NO:12)

Second, non specific amplifications were also carried out with the antisense oligodeoxyribonucleotides of the pairs described above and with a primer derived from the sequence of the derivatized oligodeoxyribonucleotide (5'ATCAAGAATTCGCACGAGACCATTA3') (SEQ ID NO:13).

One twentieth of the following RT-PCR product samples were run on a 1.5% agarose gel and stained with ethidium bromide.

Sample 1: The products of a PCR reaction using the globin primers of SEQ ID NOs 5 and 6 in the presence of cDNA.

Sample 2: The products of a PCR reaction using the globin primers of SEQ ID NOs 5 and 6 in the absence of added cDNA.

Sample 3: The products of a PCR reaction using the dehydrogenase primers of SEQ ID NOs 7 and 8 in the presence of cDNA.

Sample 4: The products of a PCR reaction using the dehydrogenase primers of SEQ ID NOs 7 and 8 in the absence of added cDNA.

Sample 5: The products of a PCR reaction using the pp15 primers of SEQ ID NOs 9 and 10 in the presence of cDNA.

Sample 6: The products of a PCR reaction using the pp15 primers of SEQ ID NOs 9 and 10 in the absence of added cDNA.

Sample 7: The products of a PCR reaction using the EIF4 primers of SEQ ID NOs 11 and 12 in the presence of added cDNA.

Sample 8: The products of a PCR reaction using the EIF4 primers of SEQ ID NOs 11 and 12 in the absence of added cDNA.

A band of the size expected for the PCR product was observed only in samples 1, 3, 5 and 7, thus indicating the presence of the corresponding sequence in the cDNA population.

PCR reactions were also carried out with the antisense oligonucleotides of the globin and dehydrogenase primers (SEQ ID NOs 6 and 8) and an oligonucleotide whose sequence corresponds to that of the derivatized oligonucleotide. The presence of PCR products of the expected size in the samples equivalent to above samples 1 and 3 indicated that the derivatized oligonucleotide had been linked to mRNA.

The above examples summarize the chemical procedure for enriching mRNAs for those having intact 5′ ends as illustrated in Figure 1. Further detail regarding the chemical approaches for obtaining such mRNAs are disclosed in International Application No. WO96/34981, published November 7, 1996, which is incorporated herein by reference. Strategies based on the above chemical modifications to the 5′ cap structure may be utilized to generate cDNAs selected to include the 5′ ends of the mRNAs from which they derived. In one version of such procedures, the 5′ ends of the mRNAs are modified as described above. Thereafter, a reverse transcription reaction is conducted to extend a primer complementary to the 5′ end of the mRNA. Single stranded RNAs are eliminated to obtain a population of cDNA/mRNA heteroduplexes in which the mRNA includes an intact 5′ end. The resulting heteroduplexes may be captured on a solid phase coated with a molecule capable of interacting with the molecule used to derivatize the 5′ end of the mRNA. Thereafter, the strands of the heteroduplexes are separated to recover single stranded first cDNA strands which include the 5′ end of the mRNA. Second strand cDNA synthesis may then proceed using conventional techniques. For example, the procedures disclosed in WO 96/34981 or in Carninci. *et al.*, *Genomics* 37:327-336, 1996, the disclosures of which are incorporated herein by reference, may be employed to select cDNAs which include the sequence derived from the 5′ end of the coding sequence of the mRNA.

Following ligation of the oligonucleotide tag to the 5′ cap of the mRNA, a reverse transcription reaction is conducted to extend a primer complementary to the mRNA to the 5′ end of the mRNA. Following elimination of the RNA component of the resulting heteroduplex using standard techniques, second strand cDNA synthesis is conducted with a primer complementary to the oligonucleotide tag.

2. Enzymatic Methods for Obtaining mRNAs having Intact 5′ Ends

Other techniques for selecting cDNAs extending to the 5′ end of the mRNA from which they are derived are fully enzymatic. Some versions of these techniques are disclosed in Dumas Milne Edwards J.B. (Doctoral Thesis of Paris VI University, Le clonage des ADNc complets: difficultes et perspectives nouvelles. Apports pour l'etude de la regulation de l'expression de la tryptophane hydroxylase de rat, 20 Dec. 1993), EP0 625572 and Kato *et al., Gene* **150**:243-250, 1994, the disclosures of which are incorporated herein by reference.

Briefly, in such approaches, isolated mRNA is treated with alkaline phosphatase to remove the phosphate groups present on the 5′ ends of uncapped incomplete mRNAs. Following this procedure, the cap present on full length mRNAs is enzymatically removed with a decapping enzyme such as T4 polynucleotide kinase or tobacco acid pyrophosphatase. An oligonucleotide, which may be either a DNA oligonucleotide or a DNA-RNA hybrid oligonucleotide having RNA at its 3′ end, is then ligated to the phosphate present at the 5′ end of the decapped mRNA using T4 RNA ligase. The oligonucleotide may include a restriction site to facilitate cloning of the cDNAs following their synthesis. Example 12 below describes one enzymatic method based on the doctoral thesis of Dumas.

EXAMPLE 12

Enzymatic Approach for Obtaining 5′ ESTs

Twenty micrograms of PolyA+ RNA were dephosphorylated using Calf Intestinal Phosphatase (Biolabs). After a phenol chloroform extraction, the cap structure of mRNA was hydrolysed using the Tobacco Acid Pyrophosphatase (purified as described by Shinshi *et al., Biochemistry* 15: 2185-2190, 1976) and a hemi 5′DNA/RNA-3′ oligonucleotide having an unphosphorylated 5′ end, a stretch of adenosine ribophosphate at the 3′ end, and an EcoRI site near the 5′ end was ligated to the 5′P ends of mRNA using the T4 RNA ligase (Biolabs). Oligonucleotides suitable for use in this procedure are preferably 30 to 50 bases in length. Oligonucleotides having an unphosphorylated 5′ end may be synthesized by adding a fluorochrome at the 5′ end. The inclusion of a stretch of adenosine ribophosphates at the 3′ end of the oligonucleotide increases ligation efficiency. It will be appreciated that the oligonucleotide may contain cloning sites other than EcoRI.

Following ligation of the oligonucleotide to the phosphate present at the 5′ end of the decapped mRNA, first and second strand cDNA synthesis is carried out using conventional methods or those specified in EP0 625,572 and Kato *et al. supra*, and Dumas Milne Edwards, *supra*, the disclosures of which are incorporated herein by reference. The resulting cDNA may then be ligated into vectors such as those disclosed in Kato *et al.*, *supra* or other nucleic acid vectors known to those skilled in the art using techniques such as those described in Sambrook *et al.*, Molecular Cloning: A Laboratory Manual 2d Ed., Cold Spring Harbor Laboratory Press, 1989, the disclosure of which is incorporated herein by reference.

II. Obtention and Characterization of the 5′ ESTs of the Present Invention

The 5' ESTs of the present invention were obtained using the aforementioned chemical and enzymatic approaches for enriching mRNAs for those having intact 5′ ends as decribed below.

1. Obtention of 5' ESTS Using mRNAs with Intact 5' Ends

First, mRNAs were prepared as described in Example 13 below.

EXAMPLE 13

Preparation of mRNA With Intact 5' Ends

Total human RNAs or polyA$^+$ RNAs derived from 29 different tissues were respectively purchased from LABIMO and CLONTECH and used to generate 44 cDNA libraries as follows. The purchased RNA had been isolated from cells or tissues using acid guanidium thiocyanate-phenol-chloroform extraction (Chomczyniski and Sacchi, *Analytical Biochemistry* 162:156-159, 1987). PolyA$^+$ RNA was isolated from total RNA (LABIMO) by two passes of oligo dT chromatography, as described by Aviv and Leder, *Proc. Natl. Acad. Sci. USA* 69:1408-1412, 1972 in order to eliminate ribosomal RNA.

The quality and the integrity of the polyA+ RNAs were checked. Northern blots hybridized with a globin probe were used to confirm that the mRNAs were not degraded. Contamination of the polyA$^+$ mRNAs by ribosomal sequences was checked using Northern blots and a probe derived from the sequence of the 28S rRNA. Preparations of mRNAs with

less than 5% of rRNAs were used in library construction. To avoid constructing libraries with RNAs contaminated by exogenous sequences (prokaryotic or fungal), the presence of bacterial 16S ribosomal sequences or of two highly expressed fungal mRNAs was examined using PCR.

Following preparation of the mRNAs, the above described chemical and/or the enzymatic procedures for enriching mRNAs for thoses having intact 5′ ends were employed to obtain 5′ ESTs from various tissues. In both approaches, an oligonucleotide tag was attached to the 5′ ends of the mRNAs. The oligonucleotide tag had an EcoRI site therein to facilitate later cloning procedures. To facilitate the processing of single stranded and double stranded cDNA obtained in the construction of the librairies, the same nucleotidic sequence was used to design the ligated oligonucleotide in both chemical and enzymatic approaches. Nevertheless, in the chemical procedure, the tag used was an oligodeoxyribonucleotide which was linked to the cap of the mRNA whereas in the enzymatic ligation, the tag was a chimeric hemi 5'DNA/RNA3' oligonucleotide which was ligated to the 5' end of decapped mRNA as described in example 12.

Following attachment of the oligonucleotide tag to the mRNA by either the chemical or enzymatic methods, the integrity of the mRNA was examined by performing a Northern blot with 200 to 500 ng of mRNA using a probe complementary to the oligonucleotide tag before performing the first strand synthesis as described in example 14.

EXAMPLE 14

cDNA Synthesis Using mRNA Templates Having Intact 5′ Ends

For the mRNAs joined to oligonucleotide tags using both the chemical and enzymatic methods, first strand cDNA synthesis was performed using the Superscript II (Gibco BRL) or the Rnase H Minus M-MLV (Promega) reverse transcriptase with random nonamers as primers. In order to protect internal EcoRI sites in the cDNA from digestion at later steps in the procedure, methylated dCTP was used for first strand synthesis. After removal of RNA by an alkaline hydrolysis, the first strand of cDNA was precipitated using isopropanol in order to eliminate residual primers.

For both the chemical and the enzymatic methods, the second strand of the cDNA was synthesized with a Klenow fragment using a primer corresponding to the 5′ end of the

ligated oligonucleotide described in Example 12. Preferably, the primer is 20-25 bases in length. Methylated dCTP was also used for second strand synthesis in order to protect internal EcoRI sites in the cDNA from digestion during the cloning process.

Following cDNA synthesis, the cDNAs were cloned into pBlueScript as described in Example 15 below.

EXAMPLE 15

Cloning of cDNAsderived from mRNA with intact 5' ends into BlueScript

Following second strand synthesis, the ends of the cDNA were blunted with T4 DNA polymerase (Biolabs) and the cDNA was digested with EcoRI. Since methylated dCTP was used during cDNA synthesis, the EcoRI site present in the tag was the only hemi-methylated site, hence the only site susceptible to EcoRI digestion. The cDNA was then size fractionated using exclusion chromatography (AcA, Biosepra) and fractions corresponding to cDNAs of more than 150 bp were pooled and ethanol precipitated. The cDNA was directionally cloned into the SmaI and EcoRI ends of the phagemid pBlueScript vector (Stratagene). The ligation mixture was electroporated into bacteria and propagated under appropriate antibiotic selection.

Clones containing the oligonucleotide tag attached were then selected as described in Example 16 below.

EXAMPLE 16

Selection of Clones Having the Oligonucleotide Tag Attached Thereto

The plasmid DNAs containing 5' EST libraries made as described above were purified (Qiagen). A positive selection of the tagged clones was performed as follows. Briefly, in this selection procedure, the plasmid DNA was converted to single stranded DNA using gene II endonuclease of the phage F1 in combination with an exonuclease (Chang *et al.*, *Gene* 127:95-8, 1993) such as exonuclease III or T7 gene 6 exonuclease. The resulting single stranded DNA was then purified using paramagnetic beads as described by Fry *et al.*, *Biotechniques*, 13: 124-131, 1992. In this procedure, the single stranded DNA was hybridized with a biotinylated oligonucleotide having a sequence corresponding to the 3' end of the oligonucleotide described in Example 13. Preferably, the primer has a length of 20-25

bases. Clones including a sequence complementary to the biotinylated oligonucleotide were captured by incubation with streptavidin coated magnetic beads followed by magnetic selection. After capture of the positive clones, the plasmid DNA was released from the magnetic beads and converted into double stranded DNA using a DNA polymerase such as the ThermoSequenase obtained from Amersham Pharmacia Biotech. Alternatively, protocoles such as the one described in the Gene Trapper kit available from Gibco BRL may be used. The double stranded DNA was then electroporated into bacteria. The percentage of positive clones having the 5′ tag oligonucleotide was estimated to typically rank between 90 and 98% using dot blot analysis.

Following electroporation, the libraries were ordered in 384-microtiter plates (MTP). A copy of the MTP was stored for future needs. Then the libraries were transferred into 96 MTP and sequenced as described below.

EXAMPLE 17

Sequencing of Inserts in Selected Clones

Plasmid inserts were first amplified by PCR on PE 9600 thermocyclers (Perkin-Elmer, Applied Biosystems Division, Foster City, CA), using standard SETA-A and SETA-B primers (Genset SA), AmpliTaqGold (Perkin-Elmer), dNTPs (Boehringer), buffer and cycling conditions as recommended by the Perkin-Elmer Corporation.

PCR products were then sequenced using automatic ABI Prism 377 sequencers (Perkin Elmer). Sequencing reactions were performed using PE 9600 thermocyclers with standard dye-primer chemistry and ThermoSequenase (Amersham Pharmacia Biotech). The primers used were either T7 or 21M13 (available from Genset SA) as appropriate. The primers were labeled with the JOE, FAM, ROX and TAMRA dyes. The dNTPs and ddNTPs used in the sequencing reactions were purchased from Boehringer. Sequencing buffer, reagent concentrations and cycling conditions were as recommended by Amersham.

Following the sequencing reaction, the samples were precipitated with ethanol, resuspended in formamide loading buffer, and loaded on a standard 4% acrylamide gel. Electrophoresis was performed for 2.5 hours at 3000V on an ABI 377 sequencer, and the sequence data were collected and analyzed using the ABI Prism DNA Sequencing Analysis Software, version 2.1.2.

2. Computer analysis of the Obtained 5' ESTs: Construction of NetGene and SignalTag databases

The sequence data from the 44 cDNA libraries made as described above were transferred to a proprietary database, where quality control and validation steps were performed. A proprietary base-caller, working using a Unix system, automatically flagged suspect peaks, taking into account the shape of the peaks, the inter-peak resolution, and the noise level. The proprietary base-caller also performed an automatic trimming. Any stretch of 25 or fewer bases having more than 4 suspect peaks was considered unreliable and was discarded. Sequences corresponding to cloning vector or ligation oligonucleotides were automatically removed from the EST sequences. However, the resulting EST sequences may contain 1 to 5 bases belonging to the above mentioned sequences at their 5′ end. If needed, these can easily be removed on a case to case basis.

Following sequencing as described above, the sequences of the 5′ ESTs were entered in NetGene™, a proprietary database called for storage and manipulation as described below. It will be appreciated by those skilled in the art that the data could be stored and manipulated on any medium which can be read and accessed by a computer. Computer readable media include magnetically, optically, or electronically readable media. For example, the computer readable media may be a hard disc, a floppy disc, a magnetic tape, CD-ROM, RAM, or ROM as well as other types of other media known to those skilled in the art.

In addition, the sequence data may be stored and manipulated in a variety of data processor programs in a diversity of formats. For instance, the sequence data may be stored as text in a word processing file, such as Microsoft WORD or WORDPERFECT or as an ASCII file in a variety of database programs familiar to those of skill in the art, such as DB2, SYBASE, or ORACLE.

The computer readable media on which the sequence information is stored may be in a personal computer, a network, a server or other computer systems known to those skilled in the art. The computer or other system preferably includes the storage media described above, and a processor for accessing and manipulating the sequence data. Once the sequence data has been stored, it may be manipulated and searched to locate those stored sequences which contain a desired nucleic acid sequence or which encode a protein having a particular functional domain. For example, the stored sequence information may be compared to other

known sequences to identify homologies, motifs implicated in biological function, or structural motifs.

Programs which may be used to search or compare the stored sequences include the MacPattern (EMBL), BLAST, and BLAST2 program series (NCBI), basic local alignment search tool programs for nucleotide (BLASTN) and peptide (BLASTX) comparisons (Altschul *et al*, *J. Mol. Biol.* **215**: 403, 1990) and FASTA (Pearson and Lipman, *Proc. Natl. Acad. Sci. USA* **85**: 2444, 1988). The BLAST programs then extend the alignments on the basis of defined match and mismatch criteria.

Motifs which may be detected using the above programs and those described in Example 28 include sequences encoding leucine zippers, helix-turn-helix motifs, glycosylation sites, ubiquitination sites, alpha helices, and beta sheets, signal sequences encoding signal peptides which direct the secretion of the encoded proteins, sequences implicated in transcription regulation such as homeoboxes, acidic stretches, enzymatic active sites, substrate binding sites, and enzymatic cleavage sites.

Before searching the cDNAs in the NetGene™ database for sequence motifs of interest, cDNAs derived from mRNAs which were not of interest were identified and eliminated from further consideration as described in Example 18 below.

EXAMPLE 18

Elimination of Undesired Sequences from Further Consideration

5′ ESTs in the NetGene™ database which were derived from undesired sequences such as transfer RNAs, ribosomal RNAs, mitochondrial RNAs, prokaryotic RNAs, fungal RNAs, Alu sequences, L1 sequences, or repeat sequences were identified using the FASTA and BLASTN programs with the parameters listed in Table I.

To eliminate 5′ ESTs encoding tRNAs from further consideration, the 5′ EST sequences were compared to the sequences of 1190 known tRNAs obtained from EMBL release 38, of which 100 were human. The comparison was performed using FASTA on both strands of the 5′ ESTs. Sequences having more than 80% homology over more than 60 nucleotides were identified as tRNA. Of the 144,341 sequences screened, 26 were identified as tRNAs and eliminated from further consideration.

To eliminate 5' ESTs encoding rRNAs from further consideration, the 5' EST sequences were compared to the sequences of 2497 known rRNAs obtained from EMBL release 38, of which 73 were human. The comparison was performed using BLASTN on both strands of the 5' ESTs with the parameter S=108. Sequences having more than 80% homology over stretches longer than 40 nucleotides were identified as rRNAs. Of the 144,341 sequences screened, 3,312 were identified as rRNAs and eliminated from further consideration.

To eliminate 5' ESTs encoding mtRNAs from further consideration, the 5' EST sequences were compared to the sequences of the two known mitochondrial genomes for which the entire genomic sequences are available and all sequences transcribed from these mitochondrial genomes including tRNAs, rRNAs, and mRNAs for a total of 38 sequences. The comparison was performed using BLASTN on both strands of the 5' ESTs with the parameter S=108. Sequences having more than 80% homology over stretches longer than 40 nucleotides were identified as mtRNAs. Of the 144,341 sequences screened, 6,110 were identified as mtRNAs and eliminated from further consideration.

Sequences which might have resulted from exogenous contaminants were eliminated from further consideration by comparing the 5' EST sequences to release 46 of the EMBL bacterial and fungal divisions using BLASTN with the parameter S=144. All sequences having more than 90% homology over at least 40 nucleotides were identified as exogenous contaminants. Of the 42 cDNA libraries examined, the average percentages of prokaryotic and fungal sequences contained therein were 0.2% and 0.5% respectively. Among these sequences, only one could be identified as a sequence specific to fungi. The others were either fungal or prokaryotic sequences having homologies with vertebrate sequences or including repeat sequences which had not been masked during the electronic comparison.

In addition, the 5' ESTs were compared to 6093 Alu sequences and 1115 L1 sequences to mask 5' ESTs containing such repeat sequences. 5' ESTs including THE and MER repeats, SSTR sequences or satellite, micro-satellite, or telomeric repeats were also eliminated from further consideration. On average, 11.5% of the sequences in the libraries contained repeat sequences. Of this 11.5%, 7% contained Alu repeats, 3.3% contained L1 repeats and the remaining 1.2% were derived from the other screened types of repetitive sequences. These percentages are consistent with those found in cDNA libraries prepared by

other groups. For example, the cDNA libraries of Adams *et al.* contained between 0% and 7.4% Alu repeats depending on the source of the RNA which was used to prepare the cDNA library (Adams *et al.*, *Nature* 377:174, 1996).

The sequences of those 5′ ESTs remaining after the elimination of undesirable sequences were compared with the sequences of known human mRNAs to determine the accuracy of the sequencing procedures described above.

EXAMPLE 19

Measurement of Sequencing Accuracy by Comparison to Known Sequences

To further determine the accuracy of the sequencing procedure described above, the sequences of 5′ ESTs derived from known sequences were identified and compared to the original known sequences. First, a FASTA analysis with overhangs shorter than 5 bp on both ends was conducted on the 5′ ESTs to identify those matching an entry in the public human mRNA database. The 6655 5′ ESTs which matched a known human mRNA were then realigned with their cognate mRNA and dynamic programming was used to include substitutions, insertions, and deletions in the list of "errors" which would be recognized. Errors occurring in the last 10 bases of the 5′ EST sequences were ignored to avoid the inclusion of spurious cloning sites in the analysis of sequencing accuracy.

This analysis revealed that the sequences incorporated in the NetGene™ database had an accuracy of more than 99.5%.

To determine the efficiency with which the above selection procedures select cDNAs which include the 5′ ends of their corresponding mRNAs, the following analysis was performed.

EXAMPLE 20

Determination of Efficiency of 5′ EST Selection

To determine the efficiency at which the above selection procedures isolated 5′ ESTs which included sequences close to the 5′ end of the mRNAs from which they derived, the sequences of the ends of the 5′ ESTs derived from the elongation factor 1 subunit α and

ferritin heavy chain genes were compared to the known cDNA sequences of these genes. Since the transcription start sites of both genes are well characterized, they may be used to determine the percentage of derived 5′ ESTs which included the authentic transcription start sites.

For both genes, more than 95% of the obtained 5' ESTs actually included sequences close to or upstream of the 5′ end of the corresponding mRNAs.

To extend the analysis of the reliability of the procedures for isolating 5′ ESTs from ESTs in the NetGene™ database, a similar analysis was conducted using a database composed of human mRNA sequences extracted from GenBank database release 97 for comparison. The 5' ends of more than 85% of 5′ ESTs derived from mRNAs included in the GeneBank database were located close to the 5′ ends of the known sequence. As some of the mRNA sequences available in the GenBank database are deduced from genomic sequences, a 5′ end matching with these sequences will be counted as an internal match. Thus, the method used here underestimates the yield of ESTs including the authentic 5′ ends of their corresponding mRNAs.

The EST libraries made above included multiple 5′ ESTs derived from the same mRNA. The sequences of such 5′ ESTs were compared to one another and the longest 5′ ESTs for each mRNA were identified. Overlapping cDNAs were assembled into continuous sequences (contigs). The resulting continuous sequences were then compared to public databases to gauge their similarity to known sequences, as described in Example 21 below.

EXAMPLE 21

Clustering of the 5′ ESTs and Calculation of Novelty Indices for cDNA Libraries

For each sequenced EST library, the sequences were clustered by the 5′ end. Each sequence in the library was compared to the others with BLASTN2 (direct strand, parameters S=107). ESTs with High Scoring Segment Pairs (HSPs) at least 25 bp long, having 95% identical bases and beginning closer than 10 bp from each EST 5′ end were grouped. The longest sequence found in the cluster was used as representative of the group. A global clustering between libraries was then performed leading to the definition of super-contigs.

To assess the yield of new sequences within the EST libraries, a novelty rate (NR) was defined as: NR= 100 X (Number of new unique sequences found in the library/Total number of sequences from the library). Typically, novelty rating ranged between 10% and 41% depending on the tissue from which the EST library was obtained. For most of the libraries, the random sequencing of 5′ EST libraries was pursued until the novelty rate reached 20%.

Following characterization as described above, the collection of 5′ ESTs in NetGene™ was screened to identify those 5′ ESTs bearing potential signal sequences as described in Example 22 below.

EXAMPLE 22

Identification of Potential Signal Sequences in 5′ ESTs

The 5′ ESTs in the NetGene™ database were screened to identify those having an uninterrupted open reading frame (ORF) longer than 45 nucleotides beginning with an ATG codon and extending to the end of the EST. Approximately half of the cDNA sequences in NetGene™ contained such an ORF. The ORFs of these 5′ ESTs were then searched to identify potential signal motifs using slight modifications of the procedures disclosed in Von Heijne, *Nucleic Acids Res.* 14:4683-4690, 1986, the disclosure of which is incorporated herein by reference. Those 5′ EST sequences encoding a stretch of at least 15 amino acid long with a score of at least 3.5 in the Von Heijne signal peptide identification matrix were considered to possess a signal sequence. Those 5′ ESTs which matched a known human mRNA or EST sequence and had a 5′ end more than 20 nucleotides downstream of the known 5′ end were excluded from further analysis. The remaining cDNAs having signal sequences therein were included in a database called SignalTag™.

To confirm the accuracy of the above method for identifying signal sequences, the analysis of Example 23 was performed.

EXAMPLE 23

Confirmation of Accuracy of Identification of Potential Signal Sequences in 5′ ESTs

The accuracy of the above procedure for identifying signal sequences encoding signal peptides was evaluated by applying the method to the 43 amino acids located at the N terminus of all human SwissProt proteins. The computed Von Heijne score for each protein was compared with the known characterization of the protein as being a secreted protein or a non-secreted protein. In this manner, the number of non-secreted proteins having a score higher than 3.5 (false positives) and the number of secreted proteins having a score lower than 3.5 (false negatives) could be calculated.

Using the results of the above analysis, the probability that a peptide encoded by the 5′ region of the mRNA is in fact a genuine signal peptide based on its Von Heijne's score was calculated based on either the assumption that 10% of human proteins are secreted or the assumption that 20% of human proteins are secreted. The results of this analysis are shown in Figure 2 and table IV.

Using the above method of identification of secretory proteins, 5′ ESTs of the following polypeptides known to be secreted were obtained: human glucagon, gamma interferon induced monokine precursor, secreted cyclophilin-like protein, human pleiotropin, and human biotinidase precursor. Thus, the above method successfully identified those 5′ ESTs which encode a signal peptide.

To confirm that the signal peptide encoded by the 5′ ESTs actually functions as a signal peptide, the signal sequences from the 5′ ESTs may be cloned into a vector designed for the identification of signal peptides. Such vectors are designed to confer the ability to grow in selective medium only to host cells containing a vector with an operably linked signal sequence. For example, to confirm that a 5′ EST encodes a genuine signal peptide, the signal sequence of the 5′ EST may be inserted upstream and in frame with a non-secreted form of the yeast invertase gene in signal peptide selection vectors such as those described in U.S. Patent No. 5,536,637, the disclosure of which is incorporated herein by reference. Growth of host cells containing signal sequence selection vectors with the correctly inserted 5' EST signal sequence confirms that the 5′ EST encodes a genuine signal peptide.

Alternatively, the presence of a signal peptide may be confirmed by cloning the extended cDNAs obtained using the ESTs into expression vectors such as pXT1 (as described below in example 30), or by constructing promoter-signal sequence-reporter gene vectors which encode fusion proteins between the signal peptide and an assayable reporter protein. After introduction of these vectors into a suitable host cell, such as COS cells or NIH 3T3 cells, the growth medium may be harvested and analyzed for the presence of the secreted protein. The medium from these cells is compared to the medium from control cells containing vectors lacking the signal sequence or extended cDNA insert to identify vectors which encode a functional signal peptide or an authentic secreted protein.

Those 5′ ESTs which encoded a signal peptide, as determined by the method of Example 22 above, were further grouped into four categories based on their homology to known sequences as described in Example 24 below.

EXAMPLE 24

Categorization of 5′ ESTs Encoding a Signal Peptide

Those 5′ ESTs having a sequence not matching any known vertebrate sequence nor any publicly available EST sequence were designated "new." Of the sequences in the SignalTag™ database, 947 of the 5′ ESTs having a Von Heijne's score of at least 3.5 fell into this category.

Those 5′ ESTs having a sequence not matching any vertebrate sequence but matching a publicly known EST were designated "EST-ext", provided that the known EST sequence was extended by at least 40 nucleotides in the 5′ direction. Of the sequences in the SignalTag™ database, 150 of the 5′ ESTs having a Von Heijne's score of at least 3.5 fell into this category.

Those ESTs not matching any vertebrate sequence but matching a publicly known EST without extending the known EST by at least 40 nucleotides in the 5′ direction were designated "EST." Of the sequences in the SignalTag™ database, 599 of the 5′ ESTs having a Von Heijne's score of at least 3.5 fell into this category.

Those 5′ ESTs matching a human mRNA sequence but extending the known sequence by at least 40 nucleotides in the 5′ direction were designated "VERT-ext." Of the sequences in the SignalTag™ database, 23 of the 5′ ESTs having a Von Heijne's score of at

least 3.5 fell into this category. Included in this category was a 5' EST which extended the known sequence of the human translocase mRNA by more than 200 bases in the 5' direction. A 5' EST which extended the sequence of a human tumor suppressor gene in the 5' direction was also identified.

Table V shows the distribution of 5' ESTs in each category and the number of 5' ESTs in each category having a given minimum von Heijne's score.

3. Evaluation of Spatial and Temporal Expression of mRNAs Corresponding to the 5'ESTs or Extended cDNAs

Each of the 5' ESTs was also categorized based on the tissue from which its corresponding mRNA was obtained, as described below in Example 25.

EXAMPLE 25

Categorization of Expression Patterns

Table VI shows the distribution of 5' ESTs in each of the above defined category with respect to the tissue from which the 5'ESTs of the corresponding mRNA were obtained.

Table II provides the sequence identification numbers of 5' EST sequences derived from testis and other tisssues, the categories in which these sequences fall, and the von Heijne's score of the signal peptides which they encode. The 5' EST sequences and the amino acid sequences they encode are provided in the appended sequence listings. Table III provides the sequence ID numbers of the 5' ESTs and the sequences of the signal peptides which they encode. The sequences of the 5' ESTs and the polypeptides they encode are provided in the sequence listing appended hereto.

The sequences of DNA SEQ ID NOs: 38-270 can readily be screened for any errors therein and any sequence ambiguities can be resolved by resequencing a fragment containing such errors or amibiguities on both strands. Such fragments may be obtained from the plasmids stored in the inventors' laboratory or can be isolated using the techniques described herein. Resolution of any such ambiguities or errors may be facilitated by using primers which hybridize to sequences located close to the ambiguous or erroneous sequences. For example, the primers may hybridize to sequences within 50-75 bases of the amibiguity or

error. Upon resolution of an error or ambiguity, the corresponding corrections can be made in the protein sequences encoded by the DNA containing the error or amibiguity.

In addition to categorizing the 5′ ESTs with respect to their tissue of origin, the spatial and temporal expression patterns of the mRNAs corresponding to the 5′ ESTs, as well as their expression levels, may be determined as described in Example 26 below. Characterization of the spatial and temporal expression patterns and expression levels of these mRNAs is useful for constructing expression vectors capable of producing a desired level of gene product in a desired spatial or temporal manner, as will be discussed in more detail below.

Furthermore, 5′ ESTs whose corresponding mRNAs are associated with disease states may also be identified. For example, a particular disease may result from the lack of expression, over expression, or under expression of an mRNA corresponding to a 5′ EST. By comparing mRNA expression patterns and quantities in samples taken from healthy individuals with those from individuals suffering from a particular disease, 5′ ESTs responsible for the disease may be identified.

It will be appreciated that the results of the above characterization procedures for 5′ ESTs also apply to extended cDNAs (obtainable as described below) which contain sequences adjacent to the 5′ ESTs. It will also be appreciated that if desired, characterization may be delayed until extended cDNAs have been obtained rather than characterizing the ESTs themselves.

EXAMPLE 26

Evaluation of Expression Levels and Patterns of mRNAs Corresponding to 5′ ESTs or Extended cDNAs

Expression levels and patterns of mRNAs corresponding to 5′ ESTs or extended cDNAs (obtainable as described below in example 27) may be analyzed by solution hybridization with long probes as described in International Patent Application No. WO 97/05277, the entire contents of which are hereby incorporated by reference. Briefly, a 5′ EST, extended cDNA, or fragment thereof corresponding to the gene encoding the mRNA to be characterized is inserted at a cloning site immediately downstream of a bacteriophage (T3,

T7 or SP6) RNA polymerase promoter to produce antisense RNA. Preferably, the 5′ EST or extended cDNA has 100 or more nucleotides. The plasmid is linearized and transcribed in the presence of ribonucleotides comprising modified ribonucleotides (*i.e.* biotin-UTP and DIG-UTP). An excess of this doubly labeled RNA is hybridized in solution with mRNA isolated from cells or tissues of interest. The hybridizations are performed under standard stringent conditions (40-50°C for 16 hours in an 80% formamide, 0.4 M NaCl buffer, pH 7-8). The unhybridized probe is removed by digestion with ribonucleases specific for single-stranded RNA (*i.e.* RNases CL3, T1, Phy M, U2 or A). The presence of the biotin-UTP modification enables capture of the hybrid on a microtitration plate coated with streptavidin. The presence of the DIG modification enables the hybrid to be detected and quantified by ELISA using an anti-DIG antibody coupled to alkaline phosphatase.

The 5′ ESTs, extended cDNAs, or fragments thereof may also be tagged with nucleotide sequences for the serial analysis of gene expression (SAGE) as disclosed in UK Patent Application No. 2 305 241 A, the entire contents of which are incorporated by reference. In this method, cDNAs are prepared from a cell, tissue, organism or other source of nucleic acid for which gene expression patterns must be determined. The resulting cDNAs are separated into two pools. The cDNAs in each pool are cleaved with a first restriction endonuclease, called an anchoring enzyme, having a recognition site which is likely to be present at least once in most cDNAs. The fragments which contain the 5′ or 3′ most region of the cleaved cDNA are isolated by binding to a capture medium such as streptavidin coated beads. A first oligonucleotide linker having a first sequence for hybridization of an amplification primer and an internal restriction site for a so-called tagging endonuclease is ligated to the digested cDNAs in the first pool. Digestion with the second endonuclease produces short tag fragments from the cDNAs.

A second oligonucleotide having a second sequence for hybridization of an amplification primer and an internal restriction site is ligated to the digested cDNAs in the second pool. The cDNA fragments in the second pool are also digested with the tagging endonuclease to generate short tag fragments derived from the cDNAs in the second pool. The tags resulting from digestion of the first and second pools with the anchoring enzyme and the tagging endonuclease are ligated to one another to produce so-called ditags. In some embodiments, the ditags are concatamerized to produce ligation products containing from 2

to 200 ditags. The tag sequences are then determined and compared to the sequences of the 5′ ESTs or extended cDNAs to determine which 5′ ESTs or extended cDNAs are expressed in the cell, tissue, organism, or other source of nucleic acids from which the tags were derived. In this way, the expression pattern of the 5′ ESTs or extended cDNAs in the cell, tissue, organism, or other source of nucleic acids is obtained.

Quantitative analysis of gene expression may also be performed using arrays. As used herein, the term array means a one dimensional, two dimensional, or multidimensional arrangement of full length cDNAs (*i.e.* extended cDNAs which include the coding sequence for the signal peptide, the coding sequence for the mature protein, and a stop codon), extended cDNAs, 5′ ESTs or fragments thereof of sufficient length to permit specific detection of gene expression. Preferably, the fragments are at least 15 nucleotides in length. More preferably, the fragments are at least 100 nucleotide long. More preferably, the fragments are more than 100 nucleotides in length. In some embodiments, the fragments may be more than 500 nucleotide long.

For example, quantitative analysis of gene expression may be performed with full length cDNAs as defined below, extended cDNAs, 5′ ESTs, or fragments thereof in a complementary DNA microarray as described by Schena *et al.* (*Science* 270:467-470, 1995; *Proc. Natl. Acad. Sci. U.S.A.* 93:10614-10619, 1996). Full length cDNAs, extended cDNAs, 5′ ESTs or fragments thereof are amplified by PCR and arrayed from 96-well microtiter plates onto silylated microscope slides using high-speed robotics. Printed arrays are incubated in a humid chamber to allow rehydration of the array elements and rinsed, once in 0.2% SDS for 1 min, twice in water for 1 min and once for 5 min in sodium borohydride solution. The arrays are submerged in water for 2 min at 95°C, transferred into 0.2% SDS for 1 min, rinsed twice with water, air dried and stored in the dark at 25°C.

Cell or tissue mRNA is isolated or commercially obtained and probes are prepared by a single round of reverse transcription. Probes are hybridized to 1 cm^2 microarrays under a 14 x 14 mm glass coverslip for 6-12 hours at 60°C. Arrays are washed for 5 min at 25°C in low stringency wash buffer (1 x SSC/0.2% SDS), then for 10 min at room temperature in high stringency wash buffer (0.1 x SSC/0.2% SDS). Arrays are scanned in 0.1 x SSC using a fluorescence laser scanning device fitted with a custom filter set. Accurate differential

expression measurements are obtained by taking the average of the ratios of two independent hybridizations.

Quantitative analysis of the expression of genes may also be performed with full length cDNAs, extended cDNAs, 5′ ESTs, or fragments thereof in complementary DNA arrays as described by Pietu *et al.*. (*Genome Research* 6:492-503, 1996). The full length cDNAs, extended cDNAs, 5′ ESTs or fragments thereof are PCR amplified and spotted on membranes. Then, mRNAs originating from various tissues or cells are labeled with radioactive nucleotides. After hybridization and washing in controlled conditions, the hybridized mRNAs are detected by phospho-imaging or autoradiography. Duplicate experiments are performed and a quantitative analysis of differentially expressed mRNAs is then performed.

Alternatively, expression analysis of the 5′ ESTs or extended cDNAs can be done through high density nucleotide arrays as described by Lockhart *et al.* (*Nature Biotechnology* 14: 1675-1680, 1996) and Sosnowsky *et al.* (*Proc. Natl. Acad. Sci.* 94:1119-1123, 1997). Oligonucleotides of 15-50 nucleotides corresponding to sequences of the 5′ ESTs or extended cDNAs are synthesized directly on the chip (Lockhart *et al.*, *supra*) or synthesized and then addressed to the chip (Sosnowsky *et al.*, *supra*). Preferably, the oligonucleotides are about 20 nucleotides in length.

cDNA probes labeled with an appropriate compound, such as biotin, digoxigenin or fluorescent dye, are synthesized from the appropriate mRNA population and then randomly fragmented to an average size of 50 to 100 nucleotides. The said probes are then hybridized to the chip. After washing as described in Lockhart *et al*, *supra* and application of different electric fields (Sonowsky et *al*, *supra.*), the dyes or labeling compounds are detected and quantified. Duplicate hybridizations are performed. Comparative analysis of the intensity of the signal originating from cDNA probes on the same target oligonucleotide in different cDNA samples indicates a differential expression of the mRNA corresponding to the 5′ EST or extended cDNA from which the oligonucleotide sequence has been designed.

III. Use of 5′ ESTs to Clone Extended cDNAs and to Clone the Corresponding Genomic DNAs

Once 5′ ESTs which include the 5′ end of the corresponding mRNAs have been selected using the procedures described above, they can be utilized to isolate extended cDNAs which contain sequences adjacent to the 5′ ESTs. The extended cDNAs may include the entire coding sequence of the protein encoded by the corresponding mRNA, including the authentic translation start site, the signal sequence, and the sequence encoding the mature protein remaining after cleavage of the signal peptide. Such extended cDNAs are referred to herein as "full length cDNAs." Alternatively, the extended cDNAs may include only the sequence encoding the mature protein remaining after cleavage of the signal peptide, or only the sequence encoding the signal peptide.

Example 27 below describes a general method for obtaining extended cDNAs using 5' ESTs. Example 28 below provides experimental results, using the method explained in example 27, describing several extended cDNAs including the entire coding sequence and authentic 5′ end of the corresponding mRNA for several secreted proteins.

The methods of Examples 27, 28, and 29 can also be used to obtain extended cDNAs which encode less than the entire coding sequence of the secreted proteins encoded by the genes corresponding to the 5′ ESTs. In some embodiments, the extended cDNAs isolated using these methods encode at least 10 amino acids of one of the proteins encoded by the sequences of SEQ ID NOs: 38-270. In further embodiments, the extended cDNAs encode at least 20 amino acids of the proteins encoded by the sequences of SEQ ID NOs: 38-270. In further embodiments, the extended cDNAs encode at least 30 amino amino acids of the sequences of SEQ ID NOs: 38-270. In a preferred embodiment, the extended cDNAs encode a full length protein sequence, which includes the protein coding sequences of SEQ ID NOs: 38-270.

EXAMPLE 27

General Method for Using 5′ ESTs to Clone and Sequence cDNAs which Include the Entire Coding Region and the Authentic 5′ End of the Corresponding mRNA

The following general method has been used to quickly and efficiently isolate extended cDNAs having the authentic 5′ ends of their corresponding mRNAs as well as

the full protein coding sequence and including sequence adjacent to the sequences of the 5′ ESTs used to obtain them. This method may be applied to obtain extended cDNAs for any 5′ EST in the NetGene™ database, including those 5′ ESTs encoding polypeptides belonging to secreted proteins. The method is summarized in figure 3.

1. Obtention of Extended cDNAs

a) First strand synthesis

The method takes advantage of the known 5′ sequence of the mRNA. A reverse transcription reaction is conducted on purified mRNA with a poly 14dT primer containing a 49 nucleotide sequence at its 5′ end allowing the addition of a known sequence at the end of the cDNA which corresponds to the 3′ end of the mRNA. For example, the primer may have the following sequence: 5′-ATC GTT GAG ACT CGT ACC AGC AGA GTC ACG AGA GAG ACT ACA CGG TAC TGG TTT TTT TTT TTT TTVN -3′ (SEQ ID NO:14). Those skilled in the art will appreciate that other sequences may also be added to the poly dT sequence and used to prime the first strand synthesis. Using this primer and a reverse transcriptase such as the Superscript II (Gibco BRL) or Rnase H Minus M-MLV (Promega) enzyme, a reverse transcript anchored at the 3′ polyA site of the RNAs is generated.

After removal of the mRNA hybridized to the first cDNA strand by alkaline hydrolysis, the products of the alkaline hydrolysis and the residual poly dT primer are eliminated with an exclusion column such as an AcA34 (Biosepra) matrix as explained in Example 11.

b) Second strand synthesis

A pair of nested primers on each end is designed based on the known 5′ sequence from the 5′ EST and the known 3′ end added by the poly dT primer used in the first strand synthesis. Softwares used to design primers are either based on GC content and melting temperatures of oligonucleotides, such as OSP (Illier and Green, *PCR Meth. Appl.* 1:124-128, 1991), or based on the octamer frequency disparity method (Griffais *et al.*, *Nucleic Acids Res.* 19: 3887-3891, 1991) such as PC-Rare (http://bioinformatics.weizmann.ac.il/software/PC-Rare/doc/manuel.html).

Preferably, the nested primers at the 5′ end are separated from one another by four to nine bases. The 5′ primer sequences may be selected to have melting temperatures and specificities suitable for use in PCR.

Preferably, the nested primers at the 3′ end are separated from one another by four to nine bases. For example, the nested 3′ primers may have the following sequences: (5′- CCA GCA GAG TCA CGA GAG AGA CTA CAC GG -3′(SEQ ID NO:15), and 5′- CAC GAG AGA GAC TAC ACG GTA CTG G -3′ (SEQ ID NO:16). These primers were selected because they have melting temperatures and specificities compatible with their use in PCR. However, those skilled in the art will appreciate that other sequences may also be used as primers.

The first PCR run of 25 cycles is performed using the Advantage Tth Polymerase Mix (Clontech) and the outer primer from each of the nested pairs. A second 20 cycle PCR using the same enzyme and the inner primer from each of the nested pairs is then performed on 1/2500 of the first PCR product. Thereafter, the primers and nucleotides are removed.

2. Sequencing of Full Length Extended cDNAs or Fragments Thereof

Due to the lack of position constraints on the design of 5' nested primers compatible for PCR use using the OSP software, amplicons of two types are obtained. Preferably, the second 5' primer is located upstream of the translation initiation codon thus yielding a nested PCR product containing the whole coding sequence. Such a full length extended cDNA undergoes a direct cloning procedure as described in section a. However, in some cases, the second 5' primer is located downstream of the translation initiation codon, thereby yielding a PCR product containing only part of the ORF. Such incomplete PCR products are submitted to a modified procedure described in section b.

a) Nested PCR products containing complete ORFs

When the resulting nested PCR product contains the complete coding sequence, as predicted from the 5'EST sequence, it is cloned in an appropriate vector such as pED6dpc2, as described in section 3.

b) Nested PCR products containing incomplete ORFs

When the amplicon does not contain the complete coding sequence, intermediate steps are necessary to obtain both the complete coding sequence and a PCR product containing the full coding sequence. The complete coding sequence can be assembled from several partial sequences determined directly from different PCR products as described in the following section.

Once the full coding sequence has been completely determined, new primers compatible for PCR use are designed to obtain amplicons containing the whole coding region. However, in such cases, 3' primers compatible for PCR use are located inside the 3' UTR of the corresponding mRNA, thus yielding amplicons which lack part of this region, *i.e.* the polyA tract and sometimes the polyadenylation signal, as illustrated in figure 3. Such full length extended cDNAs are then cloned into an appropriate vector as described in section 3.

c) Sequencing extended cDNAs

Sequencing of extended cDNAs is performed using a Die Terminator approach with the AmpliTaq DNA polymerase FS kit available from Perkin Elmer.

In order to sequence PCR fragments, primer walking is performed using software such as OSP to choose primers and automated computer software such as ASMG (Sutton *et al., Genome Science Technol.* 1: 9-19, 1995) to construct contigs of walking sequences including the initial 5' tag using minimum overlaps of 32 nucleotides. Preferably, primer walking is performed until the sequences of full length cDNAs are obtained.

Completion of the sequencing of a given extended cDNA fragment is assessed as follows. Since sequences located after a polyA tract are difficult to determine precisely in the case of uncloned products, sequencing and primer walking processes for PCR products are interrupted when a polyA tract is identified in extended cDNAs obtained as described in case b. The sequence length is compared to the size of the nested PCR product obtained as described above. Due to the limited accuracy of the determination of the PCR product size by gel electrophoresis, a sequence is considered complete if the size of the obtained sequence is at least 70 % the size of the first nested PCR product. If the length of the sequence determined from the computer analysis is not at least 70% of the length of the nested PCR product, these PCR products are cloned and the sequence of the insertion is determined.

When Northern blot data are available, the size of the mRNA detected for a given PCR product is used to finally assess that the sequence is complete. Sequences which do not fulfill the above criteria are discarded and will undergo a new isolation procedure.

Sequence data of all extended cDNAs are then transferred to a proprietary database, where quality controls and validation steps are carried out as described in example 15.

3. Cloning of Full Length Extended cDNAs

The PCR product containing the full coding sequence is then cloned in an appropriate vector. For example, the extended cDNAs can be cloned into the expression vector pED6dpc2 (DiscoverEase, Genetics Institute, Cambridge, MA) as follows. pED6dpc2 vector DNA is prepared with blunt ends by performing an EcoRI digestion followed by a fill in reaction. The blunt ended vector is dephosphorylated. After removal of PCR primers and ethanol precipitation, the PCR product containing the full coding sequence or the extended cDNA obtained as described above is phosphorylated with a kinase subsequently removed by phenol-Sevag extraction and precipitation. The double stranded extended cDNA is then ligated to the vector and the resulting expression plasmid introduced into appropriate host cells.

Since the PCR products obtained as described above are blunt ended molecules that can be cloned in either direction, the orientation of several clones for each PCR product is determined. Then, 4 to 10 clones are ordered in microtiter plates and subjected to a PCR reaction using a first primer located in the vector close to the cloning site and a second primer located in the portion of the extended cDNA corresponding to the 3′ end of the mRNA. This second primer may be the antisense primer used in anchored PCR in the case of direct cloning (case a) or the antisense primer located inside the 3'UTR in the case of indirect cloning (case b). Clones in which the start codon of the extended cDNA is operably linked to the promoter in the vector so as to permit expression of the protein encoded by the extended cDNA are conserved and sequenced. In addition to the ends of cDNA inserts, approximately 50 bp of vector DNA on each side of the cDNA insert are also sequenced.

The cloned PCR products are then entirely sequenced according to the aforementioned procedure. In this case, contigation of long fragments is then performed

on walking sequences that have already contigated for uncloned PCR products during primer walking. Sequencing of cloned amplicons is complete when the resulting contigs include the whole coding region as well as overlapping sequences with vector DNA on both ends.

4. Computer analysis of Full Length Extended cDNA

Sequences of all full length extended cDNAs are then submitted to further analysis as described below. Before searching the extended full length cDNAs for sequences of interest, extended cDNAs which are not of interest (vector RNAs, transfer RNAs, ribosomal RNAs, mitochondrial RNAs, prokaryotic RNAs and fungal RNAs) are discarded using methods essentially similar to those described for 5'ESTs in Example 18.

a) Identification of structural features

Structural features, e.g. polyA tail and polyadenylation signal, of the sequences of full length extended cDNAs are subsequently determined as follows.

A polyA tail is defined as a homopolymeric stretch of at least 11 A with at most one alternative base within it. The polyA tail search is restricted to the last 100 nt of the sequence and limited to stretches of 11 consecutive A's because sequencing reactions are often not readable after such a polyA stretch. Stretches having more than 90% homology over 8 nucleotides are identified as polyA tails using BLAST2N.

To search for a polyadenylation signal, the polyA tail is clipped from the full-length sequence. The 50 bp preceding the polyA tail are first searched for the canonic polyadenylation AAUAAA signal and, if the canonic signal is not detected, for the alternative AUUAAA signal (Sheets *et al., Nuc. Acids Res.* **18**: 5799-5805, 1990). If neither of these consensus polyadenylation signals is found, the canonic motif is searched again allowing one mismatch to account for possible sequencing errors. More than 85 % of identified polyadenylation signals of either type actually ends 10 to 30 bp from the polyA tail. Alternative AUUAAA signals represents approximately 15 % of the total number of identified polyadenylation signals.

b) Identification of functional features

Functional features, e.g. ORFs and signal sequences, of the sequences of full length extended cDNAs were subsequently determined as follows.

The 3 upper strand frames of extended cDNAs are searched for ORFs defined as the maximum length fragments beginning with a translation intiation codon and ending with a stop codon. ORFs encoding at least 20 amino acids are preferred.

Each found ORF is then scanned for the presence of a signal peptide in the first 50 amino-acids or, where appropriate, within shorter regions down to 20 amino acids or less in the ORF, using the matrix method of von Heijne (*Nuc. Acids Res.* **14**: 4683-4690, 1986), the disclosure of which is incorporated herein by reference as described in Example 22.

c) Homology to either nucleotidic or proteic sequences

Categorization of full-length sequences may be achieved using procedures essentially similar to those described for 5'ESTs in Example 24.

Extended cDNAs prepared as described above may be subsequently engineered to obtain nucleic acids which include desired portions of the extended cDNA using conventional techniques such as subcloning, PCR, or *in vitro* oligonucleotide synthesis. For example, nucleic acids which include only the full coding sequences (*i.e.* the sequences encoding the signal peptide and the mature protein remaining after the signal peptide is cleaved off) may be obtained using techniques known to those skilled in the art. Alternatively, conventional techniques may be applied to obtain nucleic acids which contain only the coding sequences for the mature protein remaining after the signal peptide is cleaved off or nucleic acids which contain only the coding sequences for the signal peptides.

Similarly, nucleic acids containing any other desired portion of the coding sequences for the secreted protein may be obtained. For example, the nucleic acid may contain at least 10 consecutive bases of an extended cDNA such as one of the extended cDNAs described below. In another embodiment, the nucleic acid may contain at least 15 consecutive bases of an extended cDNA such as one of the extended cDNAs described below. Alternatively, the nucleic acid may contain at least 20 consecutive bases of an extended cDNA such as one of the extended cDNAs described below. In another embodiment, the nucleic acid may contain at least 25 consecutive bases of an extended cDNA such as one of the extended cDNAs described below. In yet another embodiment, the nucleic acid may contain at least 40

consecutive bases of an extended cDNA such as one of the extended cDNAs described below.

Once an extended cDNA has been obtained, it can be sequenced to determine the amino acid sequence it encodes. Once the encoded amino acid sequence has been determined, one can create and identify any of the many conceivable cDNAs that will encode that protein by simply using the degeneracy of the genetic code. For example, allelic variants or other homologous nucleic acids can be identified as described below. Alternatively, nucleic acids encoding the desired amino acid sequence can be synthesized *in vitro*.

In a preferred embodiment, the coding sequence may be selected using the known codon or codon pair preferences for the host organism in which the cDNA is to be expressed.

The extended cDNAs derived from the 5' ESTS of the present invention were obtained as described in Example 28 below.

EXAMPLE 28

Characterization of cloned extended cDNAs obtained using 5' ESTs

The procedure described in Example 27 above was used to obtain the extended cDNAs derived from the 5' ESTs of the present invention in a variety of tissues. The following list provides a few examples of thus obtained extended cDNAs.

Using this approach, the full length cDNA of SEQ ID NO:17 (internal identification number 48-19-3-G1-FL1) was obtained. This cDNA falls into the "EST-ext" category described above and encodes the signal peptide MKKVLLLITAILAVAVG (SEQ ID NO: 18) having a von Heijne score of 8.2.

The full length cDNA of SEQ ID NO:19 (internal identification number 58-34-2-E7-FL2) was also obtained using this procedure. This cDNA falls into the "EST-ext" category described above and encodes the signal peptide MWWFQQGLSFLPSALVIWTSA (SEQ ID NO:20) having a von Heijne score of 5.5.

Another full length cDNA obtained using the procedure described above has the sequence of SEQ ID NO:21 (internal identification number 51-27-1-E8-FL1). This cDNA, falls into the "EST-ext" category described above and encodes the signal peptide MVLTTLPSANSANSPVNMPTTGPNSLSYASSALSPCLT (SEQ ID NO:22) having a von Heijne score of 5.9.

The above procedure was also used to obtain a full length cDNA having the sequence of SEQ ID NO:23 (internal identification number 76-4-1-G5-FL1). This cDNA falls into the "EST-ext" category described above and encodes the signal peptide ILSTVTALTFAXA (SEQ ID NO:24) having a von Heijne score of 5.5.

The full length cDNA of SEQ ID NO:25 (internal identification number 51-3-3-B10-FL3) was also obtained using this procedure. This cDNA falls into the "new" category described above and encodes a signal peptide LVLTLCTLPLAVA (SEQ ID NO:26) having a von Heijne score of 10.1.

The full length cDNA of SEQ ID NO:27 (internal identification number 58-35-2-F10-FL2) was also obtained using this procedure. This cDNA falls into the "new" category described above and encodes a signal peptide LWLLFFLVTAIHA (SEQ ID NO:28) having a von Heijne score of 10.7.

Bacterial clones containing plasmids containing the full length cDNAs described above are presently stored in the inventor's laboratories under the internal identification numbers provided above. The inserts may be recovered from the stored materials by growing an aliquot of the appropriate bacterial clone in the appropriate medium. The plasmid DNA can then be isolated using plasmid isolation procedures familiar to those skilled in the art such as alkaline lysis minipreps or large scale alkaline lysis plasmid isolation procedures. If desired the plasmid DNA may be further enriched by centrifugation on a cesium chloride gradient, size exclusion chromatography, or anion exchange chromatography. The plasmid DNA obtained using these procedures may then be manipulated using standard cloning techniques familiar to those skilled in the art. Alternatively, a PCR can be done with primers designed at both ends of the cDNA insertion. The PCR product which corresponds to the cDNA can then be manipulated using standard cloning techniques familiar to those skilled in the art.

The polypeptides encoded by the extended cDNAs may be screened for the presence of known structural or functional motifs or for the presence of signatures, small amino acid sequences which are well conserved amongst the members of a protein family. The conserved regions have been used to derive consensus patterns or matrices included in the PROSITE data bank, in particular in the file prosite.dat (Release 13.0 of November 1995, located at http://expasy.hcuge.ch/sprot/prosite.html. Prosite_convert and prosite_scan

programs (http://ulrec3.unil.ch/ftpserveur/prosite_scan) may be used to find signatures on the extended cDNAs.

For each pattern obtained with the prosite_convert program from the prosite.dat file, the accuracy of the detection on a new protein sequence may be assessed by evaluating the frequency of irrelevant hits on the population of human secreted proteins included in the data bank SWISSPROT. The ratio between the number of hits on shuffled proteins (with a window size of 20 amino acids) and the number of hits on native (unshuffled) proteins may be used as an index. Every pattern for which the ratio is greater than 20% (one hit on shuffled proteins for 5 hits on native proteins) may be skipped during the search with prosite_scan. The program used to shuffle protein sequences (db_shuffled) and the program used to determine the statistics for each pattern in the protein data banks (prosite_statistics) are available on the ftp site http://ulrec3.unil.ch/ftpserveur/prosite_scan.

In addition to PCR based methods for obtaining extended cDNAs, traditional hybridization based methods may also be employed. These methods may also be used to obtain the genomic DNAs which encode the mRNAs from which the 5′ ESTs were derived, mRNAs corresponding to the extended cDNAs, or nucleic acids which are homologous to extended cDNAs or 5′ ESTs. Example 29 below provides examples of such methods.

EXAMPLE 29

Methods for Obtaining cDNAs which include the Entire Coding Region and the Authentic 5'End of the Corresponding mRNA

A full length cDNA library can be made using the strategies described in Examples 13, 14, 15, and 16 above by replacing the random nonamer used in Example 14 with an oligo-dT primer. For instance, the oligonucleotide of SEQ ID NO:14 may be used.

Alternatively, a cDNA library or genomic DNA library may be obtained from a commercial source or made using techniques familiar to those skilled in the art. Such cDNA or genomic DNA librairies may be used to isolate extended cDNAs obtained from 5′ EST or nucleic acids homologous to extended cDNAs or 5′ EST as follows. The cDNA library or genomic DNA library is hybridized to a detectable probe comprising at least 10 consecutive

nucleotides from the 5′ EST or extended cDNA using conventional techniques. Preferably, the probe comprises at least 12, 15, or 17 consecutive nucleotides from the 5′ EST or extended cDNA. More preferably, the probe comprises at least 20 to 30 consecutive nucleotides from the 5′ EST or extended cDNA. In some embodiments, the probe comprises more than 30 nucleotides from the 5′ EST or extended cDNA.

Techniques for identifying cDNA clones in a cDNA library which hybridize to a given probe sequence are disclosed in Sambrook *et al., Molecular Cloning: A Laboratory Manual 2d Ed.*, Cold Spring Harbor Laboratory Press, 1989, the disclosure of which is incorporated herein by reference. The same techniques may be used to isolate genomic DNAs.

Briefly, cDNA or genomic DNA clones which hybridize to the detectable probe are identified and isolated for further manipulation as follows. A probe comprising at least 10 consecutive nucleotides from the 5′ EST or extended cDNA is labeled with a detectable label such as a radioisotope or a fluorescent molecule. Preferably, the probe comprises at least 12, 15, or 17 consecutive nucleotides from the 5′ EST or extended cDNA. More preferably, the probe comprises 20 to 30 consecutive nucleotides from the 5′ EST or extended cDNA. In some embodiments, the probe comprises more than 30 nucleotides from the 5′ EST or extended cDNA.

Techniques for labeling the probe are well known and include phosphorylation with polynucleotide kinase, nick translation, *in vitro* transcription, and non radioactive techniques. The cDNAs or genomic DNAs in the library are transferred to a nitrocellulose or nylon filter and denatured. After blocking of non specific sites, the filter is incubated with the labeled probe for an amount of time sufficient to allow binding of the probe to cDNAs or genomic DNAs containing a sequence capable of hybridizing thereto.

By varying the stringency of the hybridization conditions used to identify extended cDNAs or genomic DNAs which hybridize to the detectable probe, extended cDNAS having different levels of homology to the probe can be identified and isolated as described below.

1. Identification of Extended cDNA or Genomic cDNA Sequences Having a High Degree of Homology to the Labeled Probe

To identify extended cDNAs or genomic DNAs having a high degree of homology to the probe sequence, the melting temperature of the probe may be calculated using the following formulas:

For probes between 14 and 70 nucleotides in length the melting temperature (Tm) is calculated using the formula: Tm=81.5+16.6(log [Na+])+0.41(fraction G+C)-(600/N) where N is the length of the probe.

If the hybridization is carried out in a solution containing formamide, the melting temperature may be calculated using the equation Tm=81.5+16.6(log [Na+])+0.41(fraction G+C)-(0.63% formamide)-(600/N) where N is the length of the probe.

Prehybridization may be carried out in 6X SSC, 5X Denhardt's reagent, 0.5% SDS, 100 µg denatured fragmented salmon sperm DNA or 6X SSC, 5X Denhardt's reagent, 0.5% SDS, 100 µg denatured fragmented salmon sperm DNA, 50% formamide. The formulas for SSC and Denhardt's solutions are listed in Sambrook *et al.*, *supra.*

Hybridization is conducted by adding the detectable probe to the prehybridization solutions listed above. Where the probe comprises double stranded DNA, it is denatured before addition to the hybridization solution. The filter is contacted with the hybridization solution for a sufficient period of time to allow the probe to hybridize to extended cDNAs or genomic DNAs containing sequences complementary thereto or homologous thereto. For probes over 200 nucleotides in length, the hybridization may be carried out at 15-25°C below the Tm. For shorter probes, such as oligonucleotide probes, the hybridization may be conducted at 15-25°C below the Tm. Preferably, for hybridizations in 6X SSC, the hybridization is conducted at approximately 68°C. Preferably, for hybridizations in 50% formamide containing solutions, the hybridization is conducted at approximately 42°C.

All of the foregoing hybridizations would be considered to be under "stringent" conditions.

Following hybridization, the filter is washed in 2X SSC, 0.1% SDS at room temperature for 15 minutes. The filter is then washed with 0.1X SSC, 0.5% SDS at room temperature for 30 minutes to 1 hour. Thereafter, the solution is washed at the hybridization

temperature in 0.1X SSC, 0.5% SDS. A final wash is conducted in 0.1X SSC at room temperature.

Extended cDNAs, nucleic acids homologous to extended cDNAs or 5′ ESTs, or genomic DNAs which have hybridized to the probe are identified by autoradiography or other conventional techniques.

2. Obtention of Extended cDNA or Genomic cDNA Sequences Having Lower Degrees of Homology to the Labeled Probe

The above procedure may be modified to identify extended cDNAs, nucleic acids homologous to extended cDNAs, or genomic DNAs having decreasing levels of homology to the probe sequence. For example, to obtain extended cDNAs, nucleic acids homologous to extended cDNAs, or genomic DNAs of decreasing homology to the detectable probe, less stringent conditions may be used. For example, the hybridization temperature may be decreased in increments of 5°C from 68°C to 42°C in a hybridization buffer having a sodium concentration of approximately 1M. Following hybridization, the filter may be washed with 2X SSC, 0.5% SDS at the temperature of hybridization. These conditions are considered to be "moderate" conditions above 50°C and "low" conditions below 50°C.

Alternatively, the hybridization may be carried out in buffers, such as 6X SSC, containing formamide at a temperature of 42°C. In this case, the concentration of formamide in the hybridization buffer may be reduced in 5% increments from 50% to 0% to identify clones having decreasing levels of homology to the probe. Following hybridization, the filter may be washed with 6X SSC, 0.5% SDS at 50°C. These conditions are considered to be "moderate" conditions above 25% formamide and "low" conditions below 25% formamide.

Extended cDNAs, nucleic acids homologous to extended cDNAs, or genomic DNAs which have hybridized to the probe are identified by autoradiography.

3. Determination of the Degree of Homology Between the Obtained Extended cDNAs and the Labeled Probe

If it is desired to obtain nucleic acids homologous to extended cDNAs, such as allelic variants thereof or nucleic acids encoding proteins related to the proteins encoded by the extended cDNAs, the level of homology between the hybridized nucleic acid and the

extended cDNA or 5' EST used as the probe may be further determined using BLAST2N; parameters may be adapted depending on the sequence length and degree of homology studied. To determine the level of homology between the hybridized nucleic acid and the extended cDNA or 5'EST from which the probe was derived, the nucleotide sequences of the hybridized nucleic acid and the extended cDNA or 5'EST from which the probe was derived are compared. For example, using the above methods, nucleic acids having at least 95% nucleic acid homology to the extended cDNA or 5'EST from which the probe was derived may be obtained and identified. Similarly, by using progressively less stringent hybridization conditions one can obtain and identify nucleic acids having at least 90%, at least 85%, at least 80% or at least 75% homology to the extended cDNA or 5'EST from which the probe was derived.

To determine whether a clone encodes a protein having a given amount of homology to the protein encoded by the extended cDNA or 5' EST, the amino acid sequence encoded by the extended cDNA or 5' EST is compared to the amino acid sequence encoded by the hybridizing nucleic acid. Homology is determined to exist when an amino acid sequence in the extended cDNA or 5' EST is closely related to an amino acid sequence in the hybridizing nucleic acid. A sequence is closely related when it is identical to that of the extended cDNA or 5' EST or when it contains one or more amino acid substitutions therein in which amino acids having similar characteristics have been substituted for one another. Using the above methods and algorithms such as FASTA with parameters depending on the sequence length and degree of homology studied, one can obtain nucleic acids encoding proteins having at least 95%, at least 90%, at least 85%, at least 80% or at least 75% homology to the proteins encoded by the extended cDNA or 5'EST from which the probe was derived.

In addition to the above described methods, other protocols are available to obtain extended cDNAs using 5' ESTs as outlined in the following paragraphs.

Extended cDNAs may be prepared by obtaining mRNA from the tissue, cell, or organism of interest using mRNA preparation procedures utilizing polyA selection procedures or other techniques known to those skilled in the art. A first primer capable of hybridizing to the polyA tail of the mRNA is hybridized to the mRNA and a reverse transcription reaction is performed to generate a first cDNA strand.

The first cDNA strand is hybridized to a second primer containing at least 10 consecutive nucleotides of the sequences of SEQ ID NOs 38-270. Preferably, the primer comprises at least 12, 15, or 17 consecutive nucleotides from the sequences of SEQ ID NOs 38-270. More preferably, the primer comprises 20 to 30 consecutive nucleotides from the sequences of SEQ ID NOs 38-270. In some embodiments, the primer comprises more than 30 nucleotides from the sequences of SEQ ID NOs 38-270. If it is desired to obtain extended cDNAs containing the full protein coding sequence, including the authentic translation initiation site, the second primer used contains sequences located upstream of the translation initiation site. The second primer is extended to generate a second cDNA strand complementary to the first cDNA strand. Alternatively, RT-PCR may be performed as described above using primers from both ends of the cDNA to be obtained.

Extended cDNAs containing 5' fragments of the mRNA may be prepared by hybridizing an mRNA comprising the sequence of the 5'EST for which an extended cDNA is desired with a primer comprising at least 10 consecutive nucleotides of the sequences complementary to the 5'EST and reverse transcribing the hybridized primer to make a first cDNA strand from the mRNAs. Preferably, the primer comprises at least 12, 15, or 17 consecutive nucleotides from the 5'EST. More preferably, the primer comprises 20 to 30 consecutive nucleotides from the 5'EST.

Thereafter, a second cDNA strand complementary to the first cDNA strand is synthesized. The second cDNA strand may be made by hybridizing a primer complementary to sequences in the first cDNA strand to the first cDNA strand and extending the primer to generate the second cDNA strand.

The double stranded extended cDNAs made using the methods described above are isolated and cloned. The extended cDNAs may be cloned into vectors such as plasmids or viral vectors capable of replicating in an appropriate host cell. For example, the host cell may be a bacterial, mammalian, avian, or insect cell.

Techniques for isolating mRNA, reverse transcribing a primer hybridized to mRNA to generate a first cDNA strand, extending a primer to make a second cDNA strand complementary to the first cDNA strand, isolating the double stranded cDNA and cloning the double stranded cDNA are well known to those skilled in the art and are described *in Current Protocols in Molecular Biology*, John Wiley and Sons, Inc. 1997 and Sambrook *et al.*,

Molecular Cloning: A Laboratory Manual, Second Edition, Cold Spring Harbor Laboratory Press, 1989, the entire disclosures of which are incorporated herein by reference.

Alternatively, procedures such as the one described in Example 29 may be used for obtaining full length cDNAs or extended cDNAs. In this approach, full length or extended cDNAs are prepared from mRNA and cloned into double stranded phagemids as follows. The cDNA library in the double stranded phagemids is then rendered single stranded by treatment with an endonuclease, such as the Gene II product of the phage F1, and an exonuclease (Chang *et al.*, *Gene* 127:95-8, 1993). A biotinylated oligonucleotide comprising the sequence of a 5′ EST, or a fragment containing at least 10 nucleotides thereof, is hybridized to the single stranded phagemids. Preferably, the fragment comprises at least 12, 15, or 17 consecutive nucleotides from the 5′ EST. More preferably, the fragment comprises 20-30 consecutive nucleotides from the 5′ EST. In some procedures, the fragment may comprise more than 30 consecutive nucleotides from the 5′ EST.

Hybrids between the biotinylated oligonucleotide and phagemids having inserts containing the 5′ EST sequence are isolated by incubating the hybrids with streptavidin coated paramagnetic beads and retrieving the beads with a magnet (Fry *et al.*, *Biotechniques*, 13: 124-131, 1992). Thereafter, the resulting phagemids containing the 5′ EST sequence are released from the beads and converted into double stranded DNA using a primer specific for the 5′ EST sequence. Alternatively, protocoles such as the Gene Trapper kit (Gibco BRL) may be used. The resulting double stranded DNA is transformed into bacteria. Extended cDNAs containing the 5′ EST sequence are identified by colony PCR or colony hybridization.

Using any of the above described methods in section III, a plurality of extended cDNAs containing full length protein coding sequences or sequences encoding only the mature protein remaining after the signal peptide is cleaved off may be provided as cDNA libraries for subsequent evaluation of the encoded proteins or use in diagnostic assays as described below.

IV. Expression of Proteins Encoded by Extended cDNAs Isolated Using 5′ ESTs

Extended cDNAs containing the full protein coding sequences of their corresponding mRNAs or portions thereof, such as cDNAs encoding the mature protein, may be used to

express the encoded secreted proteins or portions thereof as described in Example 30 below. If desired, the extended cDNAs may contain the sequences encoding the signal peptide to facilitate secretion of the expressed protein. It will be appreciated that a plurality of extended cDNAs containing the full protein coding sequences or portions thereof may be simultaneously cloned into expression vectors to create an expression library for analysis of the encoded proteins as described below.

EXAMPLE 30

Expression of the Proteins Encoded by the Genes Corresponding to 5'ESTS or Portions Thereof

To express the proteins encoded by the genes corresponding to 5' ESTs (or portions thereof), full length cDNAs containing the entire protein coding region or extended cDNAs containing sequences adjacent to the 5' ESTs (or portions thereof) are obtained as described in Examples 27-29 and cloned into a suitable expression vector. If desired, the nucleic acids may contain the sequences encoding the signal peptide to facilitate secretion of the expressed protein. The nucleic acids inserted into the expression vectors may also contain sequences upstream of the sequences encoding the signal peptide, such as sequences which regulate expression levels or sequences which confer tissue specific expression.

The nucleic acid encoding the protein or polypeptide to be expressed is operably linked to a promoter in an expression vector using conventional cloning technology. The expression vector may be any of the mammalian, yeast, insect or bacterial expression systems known in the art. Commercially available vectors and expression systems are available from a variety of suppliers including Genetics Institute (Cambridge, MA), Stratagene (La Jolla, California), Promega (Madison, Wisconsin), and Invitrogen (San Diego, California). If desired, to enhance expression and facilitate proper protein folding, the codon context and codon pairing of the sequence may be optimized for the particular expression organism in which the expression vector is introduced, as explained by Hatfield, *et al.*, U.S. Patent No. 5,082,767, incorporated herein by this reference.

The cDNA cloned into the expression vector may encode the entire protein (*i.e.* the signal peptide and the mature protein), the mature protein (*i.e.* the protein created by cleaving the signal peptide off), only the signal peptide or any other portion thereof.

The following is provided as one exemplary method to express the proteins encoded by the extended cDNAs corresponding to the 5′ ESTs or the nucleic acids described above. First, the methionine initiation codon for the gene and the polyA signal of the gene are identified. If the nucleic acid encoding the polypeptide to be expressed lacks a methionine to serve as the initiation site, an initiating methionine can be introduced next to the first codon of the nucleic acid using conventional techniques. Similarly, if the extended cDNA lacks a polyA signal, this sequence can be added to the construct by, for example, splicing out the polyA signal from pSG5 (Stratagene) using BglII and SalI restriction endonuclease enzymes and incorporating it into the mammalian expression vector pXT1 (Stratagene). pXT1 contains the LTRs and a portion of the *gag* gene from Moloney Murine Leukemia Virus. The position of the LTRs in the construct allow efficient stable transfection. The vector includes the Herpes Simplex thymidine kinase promoter and the selectable neomycin gene. The extended cDNA or portion thereof encoding the polypeptide to be expressed is obtained by PCR from the bacterial vector using oligonucleotide primers complementary to the extended cDNA or portion thereof and containing restriction endonuclease sequences for Pst I incorporated into the 5′primer and BglII at the 5′ end of the corresponding cDNA 3′ primer, taking care to ensure that the extended cDNA is positioned with the poly A signal. The purified fragment obtained from the resulting PCR reaction is digested with PstI, blunt ended with an exonuclease, digested with Bgl II, purified and ligated to pXT1 containing a poly A signal and prepared for this ligation (blunt/BglII).

The ligated product is transfected into mouse NIH 3T3 cells using Lipofectin (Life Technologies, Inc., Grand Island, New York) under conditions outlined in the product specification. Positive transfectants are selected after growing the transfected cells in 600 μg/ml G418 (Sigma, St. Louis, Missouri). Preferably the expressed protein is released into the culture medium, thereby facilitating purification.

Alternatively, the extended cDNAs may be cloned into pED6dpc2 as described above. The resulting pED6dpc2 constructs may be transfected into a suitable host cell, such as COS 1 cells. Methotrexate resistant cells are selected and expanded. Preferably, the protein expressed from the extended cDNA is released into the culture medium thereby facilitating purification.

Proteins in the culture medium are separated by gel electrophoresis. If desired, the proteins may be ammonium sulfate precipitated or separated based on size or charge prior to electrophoresis.

As a control, the expression vector lacking a cDNA insert is introduced into host cells or organisms and the proteins in the medium are harvested. The secreted proteins present in the medium are detected using techniques familiar to those skilled in the art such as Coomassie blue or silver staining or using antibodies against the protein encoded by the extended cDNA

Antibodies capable of specifically recognizing the protein of interest may be generated using synthetic 15-mer peptides having a sequence encoded by the appropriate 5′ EST, extended cDNA, or portion thereof. The synthetic peptides are injected into mice to generate antibody to the polypeptide encoded by the 5′ EST, extended cDNA, or portion thereof.

Secreted proteins from the host cells or organisms containing an expression vector which contains the extended cDNA derived from a 5′ EST or a portion thereof are compared to those from the control cells or organism. The presence of a band in the medium from the cells containing the expression vector which is absent in the medium from the control cells indicates that the extended cDNA encodes a secreted protein. Generally, the band corresponding to the protein encoded by the extended cDNA will have a mobility near that expected based on the number of amino acids in the open reading frame of the extended cDNA. However, the band may have a mobility different than that expected as a result of modifications such as glycosylation, ubiquitination, or enzymatic cleavage.

Alternatively, if the protein expressed from the above expression vectors does not contain sequences directing its secretion, the proteins expressed from host cells containing an expression vector with an insert encoding a secreted protein or portion thereof can be compared to the proteins expressed in control host cells containing the expression vector without an insert. The presence of a band in samples from cells containing the expression vector with an insert which is absent in samples from cells containing the expression vector without an insert indicates that the desired protein or portion thereof is being expressed. Generally, the band will have the mobility expected for the secreted protein or portion thereof. However, the band may have a mobility different than that expected as a result of modifications such as glycosylation, ubiquitination, or enzymatic cleavage.

The protein encoded by the extended cDNA may be purified using standard immunochromatography techniques. In such procedures, a solution containing the secreted protein, such as the culture medium or a cell extract, is applied to a column having antibodies against the secreted protein attached to the chromatography matrix. The secreted protein is allowed to bind the immunochromatography column. Thereafter, the column is washed to remove non-specifically bound proteins. The specifically bound secreted protein is then released from the column and recovered using standard techniques.

If antibody production is not possible, the extended cDNA sequence or portion thereof may be incorporated into expression vectors designed for use in purification schemes employing chimeric polypeptides. In such strategies, the coding sequence of the extended cDNA or portion thereof is inserted in frame with the gene encoding the other half of the chimera. The other half of the chimera may be β-globin or a nickel binding polypeptide. A chromatography matrix having antibody to β-globin or nickel attached thereto is then used to purify the chimeric protein. Protease cleavage sites may be engineered between the β-globin gene or the nickel binding polypeptide and the extended cDNA or portion thereof. Thus, the two polypeptides of the chimera may be separated from one another by protease digestion.

One useful expression vector for generating β-globin chimerics is pSG5 (Stratagene), which encodes rabbit β-globin. Intron II of the rabbit β-globin gene facilitates splicing of the expressed transcript, and the polyadenylation signal incorporated into the construct increases the level of expression. These techniques as described are well known to those skilled in the art of molecular biology. Standard methods are published in methods texts such as Davis *et al.*., (*Basic Methods in Molecular Biology*, Davis, Dibner, and Battey, ed., Elsevier Press, NY, 1986) and many of the methods are available from Stratagene, Life Technologies, Inc., or Promega. Polypeptide may additionally be produced from the construct using *in vitro* translation systems such as the *In vitro* Express™ Translation Kit (Stratagene).

Following expression and purification of the secreted proteins encoded by the 5′ ESTs, extended cDNAs, or fragments thereof, the purified proteins may be tested for the ability to bind to the surface of various cell types as described in Example 31 below. It will be appreciated that a plurality of proteins expressed from these cDNAs may be included in a

panel of proteins to be simultaneously evaluated for the activities specifically described below, as well as other biological roles for which assays for determining activity are available.

EXAMPLE 31

Analysis of Secreted Proteins to Determine Whether they Bind to the Cell Surface

The proteins encoded by the 5' ESTs, extended cDNAs, or fragments thereof are cloned into expression vectors such as those described in Example 30. The proteins are purified by size, charge, immunochromatography or other techniques familiar to those skilled in the art. Following purification, the proteins are labeled using techniques known to those skilled in the art. The labeled proteins are incubated with cells or cell lines derived from a variety of organs or tissues to allow the proteins to bind to any receptor present on the cell surface. Following the incubation, the cells are washed to remove non-specifically bound protein. The labeled proteins are detected by autoradiography. Alternatively, unlabeled proteins may be incubated with the cells and detected with antibodies having a detectable label, such as a fluorescent molecule, attached thereto.

Specificity of cell surface binding may be analyzed by conducting a competition analysis in which various amounts of unlabeled protein are incubated along with the labeled protein. The amount of labeled protein bound to the cell surface decreases as the amount of competitive unlabeled protein increases. As a control, various amounts of an unlabeled protein unrelated to the labeled protein is included in some binding reactions. The amount of labeled protein bound to the cell surface does not decrease in binding reactions containing increasing amounts of unrelated unlabeled protein, indicating that the protein encoded by the cDNA binds specifically to the cell surface.

As discussed above, secreted proteins have been shown to have a number of important physiological effects and, consequently, represent a valuable therapeutic resource. The secreted proteins encoded by the extended cDNAs or portions thereof made according to Examples 27-29 may be evaluated to determine their physiological activities as described below.

EXAMPLE 32

Assaying the Proteins Expressed from Extended cDNAs or Portions Thereof for Cytokine, Cell Proliferation or Cell Differentiation Activity

As discussed above, secreted proteins may act as cytokines or may affect cellular proliferation or differentiation. Many protein factors discovered to date, including all known cytokines, have exhibited activity in one or more factor dependent cell proliferation assays, and hence the assays serve as a convenient confirmation of cytokine activity. The activity of a protein encoded by the extended cDNAs is evidenced by any one of a number of routine factor dependent cell proliferation assays for cell lines including, without limitation, 32D, DA2, DA1G, T10, B9, B9/11, BaF3, MC9/G, M^+ (preB M^+), 2E8, RB5, DA1, 123, T1165, HT2, CTLL2, TF-1, Mo7c and CMK. The proteins encoded by the above extended cDNAs or portions thereof may be evaluated for their ability to regulate T cell or thymocyte proliferation in assays such as those described above or in the following references, which are incorporated herein by reference: *Current Protocols in Immunology*, Ed. by Coligan *et al.*, Greene Publishing Associates and Wiley-Interscience; Takai *et al. J. Immunol.* **137**:3494-3500, 1986., Bertagnolli *et al.*, J. *Immunol.* **145**:1706-1712, 1990., Bertagnolli *et al.*, *Cell. Immunol.* **133**:327-341, 1991; Bertagnolli, *et al., J. Immunol.* **149**:3778-3783, 1992; Bowman *et al., J. Immunol.* **152**:1756-1761, 1994.

In addition, numerous assays for cytokine production and/or the proliferation of spleen cells, lymph node cells and thymocytes are known. These include the techniques disclosed in *Current Protocols in Immunology, supra* **1**:3.12.1-3.12.14; and Schreiber In *Current Protocols in Immunology, supra* **1** : 6.8.1-6.8.8.

The proteins encoded by the cDNAs may also be assayed for the ability to regulate the proliferation and differentiation of hematopoietic or lymphopoietic cells. Many assays for such activity are familiar to those skilled in the art, including the assays in the following references, which are incorporated herein by reference: Bottomly *et al.*, In *Current Protocols in Immunology., supra.* **1** : 6.3.1-6.3.12,; deVries *et al., J. Exp. Med.* **173**:1205-1211, 1991; Moreau *et al.*, *Nature* **36**:690-692, 1988; Greenberger *et al.*, *Proc. Natl. Acad. Sci. U.S.A.* **80**:2931-2938, 1983; Nordan, R., In *Current Protocols in Immunology., supra.* 1 : 6.6.1-6.6.5; Smith et al., *Proc. Natl. Acad. Sci. U.S.A.* **83**:1857-1861, 1986; Bennett *et al.*, in

Current Protocols in Immunology supra **1** : 6.15.1; Ciarletta *et al.*, In *Current Protocols in Immunology. supra* **1** : 6.13.1.

The proteins encoded by the cDNAs may also be assayed for their ability to regulate T-cell responses to antigens. Many assays for such activity are familiar to those skilled in the art, including the assays described in the following references, which are incorporated herein by reference: Chapter 3 (*In Vitro* Assays for Mouse Lymphocyte Function), Chapter 6 (Cytokines and Their Cellular Receptors) and Chapter 7, (Immunologic Studies in Humans) in *Current Protocols in Immunology supra*; Weinberger *et al.*, *Proc. Natl. Acad. Sci. USA* 77:6091-6095, 1980; Weinberger *et al.*, *Eur. J. Immun.* **11**:405-411, 1981; Takai *et al.*, *J. Immunol.* 137:3494-3500, 1986; Takai *et al.*, *J. Immunol.* **140**:508-512, 1988.

Those proteins which exhibit cytokine, cell proliferation, or cell differentiation activity may then be formulated as pharmaceuticals and used to treat clinical conditions in which induction of cell proliferation or differentiation is beneficial. Alternatively, as described in more detail below, genes encoding these proteins or nucleic acids regulating the expression of these proteins may be introduced into appropriate host cells to increase or decrease the expression of the proteins as desired.

EXAMPLE 33

Assaying the Proteins Expressed from Extended cDNAs or Portions Thereof for Activity as Immune System Regulators

The proteins encoded by the cDNAs may also be evaluated for their effects as immune regulators. For example, the proteins may be evaluated for their activity to influence thymocyte or splenocyte cytotoxicity. Numerous assays for such activity are familiar to those skilled in the art including the assays described in the following references, which are incorporated herein by reference: Chapter 3 (*In Vitro* Assays for Mouse Lymphocyte Function 3.1-3.19) and Chapter 7 (Immunologic studies in Humans) in *Current Protocols in Immunology* , Coligan *et al.*, Eds, Greene Publishing Associates and Wiley-Interscience; Herrmann *et al.*, *Proc. Natl. Acad. Sci. USA* **78**:2488-2492, 1981; Herrmann *et al.*, *J. Immunol.* **128**:1968-1974, 1982; Handa *et al.*, *J. Immunol.* **135**:1564-1572, 1985; Takai *et al.*, *J. Immunol.* **137**:3494-3500, 1986; Takai *et al.*, *J. Immunol.* **140**:508-512, 1988;

Bowman *et al.*, *J. Virology* **61**:1992-1998; Bertagnolli *et al.*, *Cell. Immunol.* **133**:327-341, 1991; Brown *et al.*, *J. Immunol.* **153**:3079-3092, 1994.

The proteins encoded by the cDNAs may also be evaluated for their effects on T-cell dependent immunoglobulin responses and isotype switching. Numerous assays for such activity are familiar to those skilled in the art, including the assays disclosed in the following references, which are incorporated herein by reference: Maliszewski, *J. Immunol.* **144**:3028-3033, 1990; Mond *et al.* in *Current Protocols in Immunology*, **1** : 3.8.1-3.8.16, *supra*.

The proteins encoded by the cDNAs may also be evaluated for their effect on immune effector cells, including their effect on Th1 cells and cytotoxic lymphocytes. Numerous assays for such activity are familiar to those skilled in the art, including the assays disclosed in the following references, which are incorporated herein by reference: Chapter 3 (*In Vitro* Assays for Mouse Lymphocyte Function 3.1-3.19) and Chapter 7 (Immunologic Studies in Humans) in *Current Protocols in Immunology, supra*; Takai *et al.*, *J. Immunol.* **137**:3494-3500, 1986; Takai *et al.*, *J. Immunol.* **140**:508-512, 1988; Bertagnolli *et al.*, *J. Immunol.* **149**:3778-3783, 1992.

The proteins encoded by the cDNAs may also be evaluated for their effect on dendritic cell mediated activation of naive T-cells. Numerous assays for such activity are familiar to those skilled in the art, including the assays disclosed in the following references, which are incorporated herein by reference: Guery *et al.*, *J. Immunol.* **134**:536-544, 1995; Inaba *et al.*, *J. Exp. Med.* **173**:549-559, 1991; Macatonia *et al.*, *J. Immunol.* **154**:5071-5079, 1995; Porgador *et al.J. Exp. Med* **182**:255-260, 1995; Nair *et al.*, *J. Virol.* **67**:4062-4069, 1993; Huang *et al.*, *Science* **264**:961-965, 1994; Macatonia *et al.J. Exp. Med* **169**:1255-1264, 1989; Bhardwaj *et al.*, *Journal of Clinical Investigation* **94**:797-807, 1994; and Inaba *et al.*, *J. Exp. Med* **172**:631-640, 1990.

The proteins encoded by the cDNAs may also be evaluated for their influence on the lifetime of lymphocytes. Numerous assays for such activity are familiar to those skilled in the art, including the assays disclosed in the following references, which are incorporated herein by reference: Darzynkiewicz *et al.*, *Cytometry* **13**:795-808, 1992; Gorczyca *et al.*, *Leukemia* 7:659-670, 1993; Gorczyca *et al.*, *Cancer Res.* **53**:1945-1951, 1993; Itoh *et al.*, *Cell* **66**:233-243, 1991; Zacharchuk, *J. Immunol.* **145**:4037-4045, 1990; Zamai *et al.*, *Cytometry* **14**:891-897, 1993; Gorczyca *et al.*, *Int. J. Oncol.* **1**:639-648, 1992.

The proteins encoded by the cDNAs may also be evaluated for their influence on early steps of T-cell commitment and development. Numerous assays for such activity are familiar to those skilled in the art, including without limitation the assays disclosed in the following references, which are incorporated herein by references: Antica *et al.*, *Blood* **84**:111-117, 1994; Fine *et al.*, *Cell. Immunol.* 155:111-122, 1994; Galy *et al.*, *Blood* 85:2770-2778, 1995; Toki *et al.*, *Proc. Nat. Acad Sci. USA* **88**:7548-7551, 1991.

Those proteins which exhibit activity as immune system regulators activity may then be formulated as pharmaceuticals and used to treat clinical conditions in which regulation of immune activity is beneficial. For example, the protein may be useful in the treatment of various immune deficiencies and disorders (including severe combined immunodeficiency), e.g., in regulating (up or down) growth and proliferation of T and/or B lymphocytes, as well as effecting the cytolytic activity of NK cells and other cell populations. These immune deficiencies may be genetic or be caused by viral (e.g., HIV) as well as bacterial or fungal infections, or may result from autoimmune disorders. More specifically, infectious diseases caused by viral, bacterial, fungal or other infection may be treatable using a protein encoded by extended cDNAs derived from the 5' ESTs of the present invention, including infections by HIV, hepatitis viruses, herpesviruses, mycobacteria, Leishmania spp., plamodium and various fungal infections such as candidiasis. Of course, in this regard, a protein encoded by extended cDNAs derived from the 5' ESTs of the present invention may also be useful where a boost to the immune system generally may be desirable, *i.e.*, in the treatment of cancer.

Alternatively, proteins encoded by extended cDNAs derived from the 5' ESTs of the present invention may be used in treatment of autoimmune disorders including, for example, connective tissue disease, multiple sclerosis, systemic lupus erythematosus, rheumatoid arthritis, autoimmune pulmonary inflammation, Guillain-Barre syndrome, autoimmune thyroiditis, insulin dependent diabetes mellitis, myasthenia gravis, graft-versus-host disease and autoimmune inflammatory eye disease. Such a protein encoded by extended cDNAs derived from the 5' ESTs of the present invention may also to be useful in the treatment of allergic reactions and conditions, such as asthma (particularly allergic asthma) or other respiratory problems. Other conditions, in which immune suppression is desired (including, for example, organ transplantation), may also be treatable using a protein encoded by extended cDNAs derived from the 5' ESTs of the present invention.

Using the proteins of the invention it may also be possible to regulate immune responses either up or down.

Down regulation may involve inhibiting or blocking an immune response already in progress or may involve preventing the induction of an immune response. The functions of activated T-cells may be inhibited by suppressing T cell responses or by inducing specific tolerance in T cells, or both. Immunosuppression of T cell responses is generally an active non-antigen-specific process which requires continuous exposure of the T cells to the suppressive agent. Tolerance, which involves inducing non-responsiveness or anergy in T cells, is distinguishable from immunosuppression in that it is generally antigen-specific and persists after the end of exposure to the tolerizing agent. Operationally, tolerance can be demonstrated by the lack of a T cell response upon reexposure to specific antigen in the absence of the tolerizing agent.

Down regulating or preventing one or more antigen functions (including without limitation B lymphocyte antigen functions, such as, for example, B7 costimulation), e.g., preventing high level lymphokine synthesis by activated T cells, will be useful in situations of tissue, skin and organ transplantation and in graft-versus-host disease (GVHD). For example, blockage of T cell function should result in reduced tissue destruction in tissue transplantation. Typically, in tissue transplants, rejection of the transplant is initiated through its recognition as foreign by T cells, followed by an immune reaction that destroys the transplant. The administration of a molecule which inhibits or blocks interaction of a B7 lymphocyte antigen with its natural ligand(s) on immune cells (such as a soluble, monomeric form of a peptide having B7-2 activity alone or in conjunction with a monomeric form of a peptide having an activity of another B lymphocyte antigen (e.g., B7-1, B7-3) or blocking antibody), prior to transplantation, can lead to the binding of the molecule to the natural ligand(s) on the immune cells without transmitting the corresponding costimulatory signal. Blocking B lymphocyte antigen function in this matter prevents cytokine synthesis by immune cells, such as T cells, and thus acts as an immunosuppressant. Moreover, the lack of costimulation may also be sufficient to anergize the T cells, thereby inducing tolerance in a subject. Induction of long-term tolerance by B lymphocyte antigen-blocking reagents may avoid the necessity of repeated administration of these blocking reagents. To achieve

sufficient immunosuppression or tolerance in a subject, it may also be necessary to block the function of a combination of B lymphocyte antigens.

The efficacy of particular blocking reagents in preventing organ transplant rejection or GVHD can be assessed using animal models that are predictive of efficacy in humans. Examples of appropriate systems which can be used include allogeneic cardiac grafts in rats and xenogeneic pancreatic islet cell grafts in mice, both of which have been used to examine the immunosuppressive effects of CTLA4Ig fusion proteins *in vivo* as described in Lenschow *et al.*, *Science* 257:789-792, 1992 and Turka *et al.*, *Proc. Natl. Acad. Sci USA*, 89:11102-11105, 1992. In addition, murine models of GVHD (see Paul ed., *Fundamental Immunology*, Raven Press, New York, 1989, pp. 846-847) can be used to determine the effect of blocking B lymphocyte antigen function *in vivo* on the development of that disease.

Blocking antigen function may also be therapeutically useful for treating autoimmune diseases. Many autoimmune disorders are the result of inappropriate activation of T cells that are reactive against self tissue and which promote the production of cytokines and autoantibodies involved in the pathology of the diseases. Preventing the activation of autoreactive T cells may reduce or eliminate disease symptoms. Administration of reagents which block costimulation of T cells by disrupting receptor/ligand interactions of B lymphocyte antigens can be used to inhibit T cell activation and prevent production of autoantibodies or T cell-derived cytokines which potentially involved in the disease process. Additionally, blocking reagents may induce antigen-specific tolerance of autoreactive T cells which could lead to long-term relief from the disease. The efficacy of blocking reagents in preventing or alleviating autoimmune disorders can be determined using a number of well-characterized animal models of human autoimmune diseases. Examples include murine experimental autoimmune encephalitis, systemic lupus erythmatosis in MRL/pr/pr mice or NZB hybrid mice, murine autoimmuno collagen arthritis, diabetes mellitus in OD mice and BB rats, and murine experimental myasthenia gravis (see Paul ed., *supra*, pp. 840-856).

Upregulation of an antigen function (preferably a B lymphocyte antigen function), as a means of up regulating immune responses, may also be useful in therapy. Upregulation of immune responses may involve either enhancing an existing immune response or eliciting an initial immune response as shown by the following examples. For instance, enhancing an immune response through stimulating B lymphocyte antigen function may be useful in cases

of viral infection. In addition, systemic viral diseases such as influenza, the common cold, and encephalitis might be alleviated by the administration of stimulatory form of B lymphocyte antigens systemically.

Alternatively, antiviral immune responses may be enhanced in an infected patient by removing T cells from the patient, costimulating the T cells *in vitro* with viral antigen-pulsed APCs either expressing a peptide encoded by extended cDNAs derived from the 5' ESTs of the present invention or together with a stimulatory form of a soluble peptide encoded by extended cDNAs derived from the 5' ESTs of the present invention and reintroducing the *in vitro* primed T cells into the patient. The infected cells would now be capable of delivering a costimulatory signal to T cells *in vivo*, thereby activating the T cells.

In another application, upregulation or enhancement of antigen function (preferably B lymphocyte antigen function) may be useful in the induction of tumor immunity. Tumor cells (e.g., sarcoma, melanoma, lymphoma, leukemia, neuroblastoma, carcinoma) transfected with a nucleic acid encoding at least one peptide encoded by extended cDNAs derived from the 5' ESTs of the present invention can be administered to a subject to overcome tumor-specific tolerance in the subject. If desired, the tumor cell can be transfected to express a combination of peptides. For example, tumor cells obtained from a patient can be transfected *ex vivo* with an expression vector directing the expression of a peptide having B7-2-like activity alone, or in conjunction with a peptide having B7-1-like activity and/or B7-3-like activity. The transfected tumor cells are returned to the patient to result in expression of the peptides on the surface of the transfected cell. Alternatively, gene therapy techniques can be used to target a tumor cell for transfection *in vivo*.

The presence of the peptide encoded by extended cDNAs derived from the 5' ESTs of the present invention having the activity of a B lymphocyte antigen(s) on the surface of the tumor cell provides the necessary costimulation signal to T cells to induce a T cell mediated immune response against the transfected tumor cells. In addition, tumor cells which lack or which fail to reexpress sufficient amounts of MHC class I or MHC class II molecules can be transfected with nucleic acids encoding all or a portion of (e.g., a cytoplasmic-domain truncated portion) of an MHC class I α chain and β_2 microglobulin or an MHC class II α chain and an MHC class II β chain to thereby express MHC class I or MHC class II proteins on the cell surface, respectively. Expression of the appropriate MHC class I or class II

molecules in conjunction with a peptide having the activity of a B lymphocyte antigen (e.g., B7-1, B7-2, B7-3) induces a T cell mediated immune response against the transfected tumor cell. Optionally, a gene encoding an antisense construct which blocks expression of an MHC class II associated protein, such as the invariant chain, can also be cotransfected with a DNA encoding a peptide having the activity of a B lymphocyte antigen to promote presentation of tumor associated antigens and induce tumor specific immunity. Thus, the induction of a T cell mediated immune response in a human subject may be sufficient to overcome tumor-specific tolerance in the subject. Alternatively, as described in more detail below, genes encoding these immune system regulator proteins or nucleic acids regulating the expression of such proteins may be introduced into appropriate host cells to increase or decrease the expression of the proteins as desired.

EXAMPLE 34

Assaying the Proteins Expressed from Extended cDNAs or Portions Thereof for Hematopoiesis Regulating Activity

The proteins encoded by the extended cDNAs or portions thereof may also be evaluated for their hematopoiesis regulating activity. For example, the effect of the proteins on embryonic stem cell differentiation may be evaluated. Numerous assays for such activity are familiar to those skilled in the art, including the assays disclosed in the following references, which are incorporated herein by reference: Johansson *et al. Cell. Biol.* **15**:141-151, 1995; Keller *et al., Mol. Cell. Biol.* **13**:473-486, 1993; McClanahan *et al., Blood* **81**:2903-2915, 1993.

The proteins encoded by the extended cDNAs or portions thereof may also be evaluated for their influence on the lifetime of stem cells and stem cell differentiation. Numerous assays for such activity are familiar to those skilled in the art, including the assays disclosed in the following references, which are incorporated herein by reference: Freshney, Methylcellulose Colony Forming Assays, in *Culture of Hematopoietic Cells.*, Freshney, *et al.*. Eds. pp. 265-268, Wiley-Liss, Inc., New York, NY. 1994; Hirayama *et al., Proc. Natl. Acad. Sci. USA* **89**:5907-5911, 1992; McNiece and Briddell, in *Culture of Hematopoietic Cells, supra*; Neben *et al., Exp. Hematol.* **22**:353-359, 1994; Ploemacher and Cobblestone In

*Culture of Hematopoietic Cells, supra*1-21, Spooncer *et al*, in *Culture of Hematopoietic Cells, supra*163-179 and Sutherland in *Culture of Hematopoietic Cells, supra*. 139-162.

Those proteins which exhibit hematopoiesis regulatory activity may then be formulated as pharmaceuticals and used to treat clinical conditions in which regulation of hematopoeisis is beneficial, such as in the treatment of myeloid or lymphoid cell deficiencies. Involvement in regulating hematopoiesis is indicated even by marginal biological activity in support of colony forming cells or of factor-dependent cell lines. For example, proteins supporting the growth and proliferation of erythroid progenitor cells alone or in combination with other cytokines, indicates utility, for example, in treating various anemias or for use in conjunction with irradiation/chemotherapy to stimulate the production of erythroid precursors and/or erythroid cells. Proteins supporting the growth and proliferation of myeloid cells such as granulocytes and monocytes/macrophages (*i.e.*, traditional CSF activity) may be useful, for example, in conjunction with chemotherapy to prevent or treat consequent myelo-suppression. Proteins supporting the growth and proliferation of megakaryocytes and consequently of platelets allows prevention or treatment of various platelet disorders such as thrombocytopenia, and generally may be used in place of or complementary to platelet transfusions. Proteins supporting the growth and proliferation of hematopoietic stem cells which are capable of maturing to any and all of the above-mentioned hematopoietic cells may therefore find therapeutic utility in various stem cell disorders (such as those usually treated with transplantion, including, without limitation, aplastic anemia and paroxysmal nocturnal hemoglobinuria), as well as in repopulating the stem cell compartment post irradiation/chemotherapy, either *in vivo* or *ex vivo* (*i.e.*, in conjunction with bone marrow transplantation or with peripheral progenitor cell transplantation (homologous or heterologous)) as normal cells or genetically manipulated for gene therapy. Alternatively, as described in more detail below, genes encoding hematopoiesis regulating activity proteins or nucleic acids regulating the expression of such proteins may be introduced into appropriate host cells to increase or decrease the expression of the proteins as desired.

EXAMPLE 35

Assaying the Proteins Expressed from Extended cDNAs or Portions Thereof for Regulation of Tissue Growth

The proteins encoded by the extended cDNAs or portions thereof may also be evaluated for their effect on tissue growth. Numerous assays for such activity are familiar to those skilled in the art, including the assays disclosed in International Patent Publication No. WO95/16035, International Patent Publication No. WO95/05846 and International Patent Publication No. WO91/07491, which are incorporated herein by reference.

Assays for wound healing activity include, without limitation, those described in: Winter, *Epidermal Wound Healing*, pps. 71-112, Maibach and Rovee, eds., Year Book Medical Publishers, Inc., Chicago, as modified by Eaglstein and Mertz, *J. Invest. Dermatol.* 71:382-84, 1978, which are incorporated herein by reference.

Those proteins which are involved in the regulation of tissue growth may then be formulated as pharmaceuticals and used to treat clinical conditions in which regulation of tissue growth is beneficial. For example, a protein encoded by extended cDNAs derived from the 5' ESTs of the present invention also may have utility in compositions used for bone, cartilage, tendon, ligament and/or nerve tissue growth or regeneration, as well as for wound healing and tissue repair and replacement, and in the treatment of burns, incisions and ulcers.

A protein encoded by extended cDNAs derived from the 5' ESTs of the present invention, which induces cartilage and/or bone growth in circumstances where bone is not normally formed, has application in the healing of bone fractures and cartilage damage or defects in humans and other animals. Such a preparation employing a protein of the invention may have prophylactic use in closed as well as open fracture reduction and also in the improved fixation of artificial joints. *De novo* bone synthesis induced by an osteogenic agent contributes to the repair of congenital, trauma induced, or oncologic resection induced craniofacial defects, and also is useful in cosmetic plastic surgery.

A protein of this invention may also be used in the treatment of periodontal disease, and in other tooth repair processes. Such agents may provide an environment to attract bone-forming cells, stimulate growth of bone-forming cells or induce differentiation of bone-forming cell progenitors. A protein of the invention may also be useful in the treatment of osteoporosis or osteoarthritis, such as through stimulation of bone and/or cartilage repair or by blocking inflammation or processes of tissue destruction (collagenase activity, osteoclast activity, etc.) mediated by inflammatory processes.

Another category of tissue regeneration activity that may be attributable to the protein encoded by extended cDNAs derived from the 5' ESTs of the present invention is tendon/ligament formation. A protein encoded by extended cDNAs derived from the 5' ESTs of the present invention, which induces tendon/ligament-like tissue or other tissue formation in circumstances where such tissue is not normally formed, has application in the healing of tendon or ligament tears, deformities and other tendon or ligament defects in humans and other animals. Such a preparation employing a tendon/ligament-like tissue inducing protein may have prophylactic use in preventing damage to tendon or ligament tissue, as well as use in the improved fixation of tendon or ligament to bone or other tissues, and in repairing defects to tendon or ligament tissue. *De novo* tendon/ligament-like tissue formation induced by a composition encoded by extended cDNAs derived from the 5' ESTs of the present invention contributes to the repair of tendon or ligaments defects of congenital, traumatic or other origin and is also useful in cosmetic plastic surgery for attachment or repair of tendons or ligaments. The compositions encoded by extended cDNAs derived from the 5' ESTs of the present invention may provide an environment to attract tendon- or ligament-forming cells, stimulate growth of tendon- or ligament-forming cells, induce differentiation of progenitors of tendon- or ligament-forming cells, or induce growth of tendon/ligament cells or progenitors *ex vivo* for return *in vivo* to effect tissue repair. The compositions of the invention may also be useful in the treatment of tendinitis, carpal tunnel syndrome and other tendon or ligament defects. The compositions may also include an appropriate matrix and/or sequestering agent as a carrier as is well known in the art.

The protein encoded by extended cDNAs derived from the 5' ESTs of the present invention may also be useful for proliferation of neural cells and for regeneration of nerve and brain tissue, *i.e.*, for the treatment of central and peripheral nervous system diseases and neuropathies, as well as mechanical and traumatic disorders, which involve degeneration, death or trauma to neural cells or nerve tissue. More specifically, a protein may be used in the treatment of diseases of the peripheral nervous system, such as peripheral nerve injuries, peripheral neuropathy and localized neuropathies, and central nervous system diseases, such as Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic lateral sclerosis, and Shy-Drager syndrome. Further conditions which may be treated in accordance with the present invention include mechanical and traumatic disorders, such as spinal cord disorders,

head trauma and cerebrovascular diseases such as stroke. Peripheral neuropathies resulting from chemotherapy or other medical therapies may also be treatable using a protein of the invention.

Proteins of the invention may also be useful to promote better or faster closure of non-healing wounds, including without limitation pressure ulcers, ulcers associated with vascular insufficiency, surgical and traumatic wounds, and the like.

It is expected that a protein encoded by extended cDNAs derived from the 5' ESTs of the present invention may also exhibit activity for generation or regeneration of other tissues, such as organs (including, for example, pancreas, liver, intestine, kidney, skin, endothelium) muscle (smooth, skeletal or cardiac) and vascular (including vascular endothelium) tissue, or for promoting the growth of cells comprising such tissues. Part of the desired effects may be by inhibition or modulation of fibrotic scarring to allow normal tissue to generate. A protein of the invention may also exhibit angiogenic activity.

A protein encoded by extended cDNAs derived from the 5' ESTs of the present invention may also be useful for gut protection or regeneration and treatment of lung or liver fibrosis, reperfusion injury in various tissues, and conditions resulting from systemic cytokinc damage.

A protein encoded by extended cDNAs derived from the 5' ESTs of the present invention may also be useful for promoting or inhibiting differentiation of tissues described above from precursor tissues or cells; or for inhibiting the growth of tissues described above.

Alternatively, as described in more detail below, genes encoding tissue growth regulating activity proteins or nucleic acids regulating the expression of such proteins may be introduced into appropriate host cells to increase or decrease the expression of the proteins as desired.

EXAMPLE 36

Assaying the Proteins Expressed from Extended cDNAs or Portions Thereof for Regulation of Reproductive Hormones

The proteins encoded by the extended cDNAs or portions thereof may also be evaluated for their ability to regulate reproductive hormones, such as follicle stimulating hormone. Numerous assays for such activity are familiar to those skilled in the art, including

the assays disclosed in the following references, which are incorporated herein by reference: Vale *et al.*, *Endocrinol.* **91**:562-572, 1972; Ling *et al.*, *Nature* **321**:779-782, 1986; Vale *et al.*, *Nature* **321**:776-779, 1986; Mason *et al..*, *Nature* **318**:659-663, 1985; Forage *et al.*, *Proc. Natl. Acad. Sci. USA* **83**:3091-3095, 1986, Chapter 6.12 in *Current Protocols in Immunology*, Coligan *et al.* Eds. Greene Publishing Associates and Wiley-Intersciece ; Taub *et al.*, *J. Clin. Invest.* **95**:1370-1376, 1995; Lind *et al.*, *APMIS* **103**:140-146, 1995; Muller *et al.*, *Eur. J. Immunol.* **25**:1744-1748; Gruber *et al.*, *J. Immunol.* **152**:5860-5867, 1994; Johnston *et al.*, *J Immunol.* **153**:1762-1768, 1994.

Those proteins which exhibit activity as reproductive hormones or regulators of cell movement may then be formulated as pharmaceuticals and used to treat clinical conditions in which regulation of reproductive hormones are beneficial. For example, a protein encoded by extended cDNAs derived from the 5' ESTs of the present invention may also exhibit activin- or inhibin-related activities. Inhibins are characterized by their ability to inhibit the release of follicle stimulating hormone (FSH), while activins are characterized by their ability to stimulate the release of FSH. Thus, a protein encoded by extended cDNAs derived from the 5' ESTs of the present invention, alone or in heterodimers with a member of the inhibin α family, may be useful as a contraceptive based on the ability of inhibins to decrease fertility in female mammals and decrease spermatogenesis in male mammals. Administration of sufficient amounts of other inhibins can induce infertility in these mammals. Alternatively, the protein of the invention, as a homodimer or as a heterodimer with other protein subunits of the inhibin-B group, may be useful as a fertility inducing therapeutic, based upon the ability of activin molecules in stimulating FSH release from cells of the anterior pituitary. See, for example, United States Patent 4,798,885, the disclosure of which is incorporated herein by reference. A protein of the invention may also be useful for advancement of the onset of fertility in sexually immature mammals, so as to increase the lifetime reproductive performance of domestic animals such as cows, sheep and pigs.

Alternatively, as described in more detail below, genes encoding reproductive hormone regulating activity proteins or nucleic acids regulating the expression of such proteins may be introduced into appropriate host cells to increase or decrease the expression of the proteins as desired.

EXAMPLE 37

Assaying the Proteins Expressed from Extended cDNAs or Portions Thereof for Chemotactic/Chemokinetic Activity

The proteins encoded by the extended cDNAs or portions thereof may also be evaluated for chemotactic/chemokinetic activity. For example, a protein encoded by extended cDNAs derived from the 5' ESTs of the present invention may have chemotactic or chemokinetic activity (e.g., act as a chemokine) for mammalian cells, including, for example, monocytes, fibroblasts, neutrophils, T-cells, mast cells, eosinophils, epithelial and/or endothelial cells. Chemotactic and chemokinetic proteins can be used to mobilize or attract a desired cell population to a desired site of action. Chemotactic or chemokinetic proteins provide particular advantages in treatment of wounds and other trauma to tissues, as well as in treatment of localized infections. For example, attraction of lymphocytes, monocytes or neutrophils to tumors or sites of infection may result in improved immune responses against the tumor or infecting agent.

A protein or peptide has chemotactic activity for a particular cell population if it can stimulate, directly or indirectly, the directed orientation or movement of such cell population. Preferably, the protein or peptide has the ability to directly stimulate directed movement of cells. Whether a particular protein has chemotactic activity for a population of cells can be readily determined by employing such protein or peptide in any known assay for cell chemotaxis.

The activity of a protein of the invention may, among other means, be measured by the following methods:

Assays for chemotactic activity (which will identify proteins that induce or prevent chemotaxis) consist of assays that measure the ability of a protein to induce the migration of cells across a membrane as well as the ability of a protein to induce the adhesion of one cell population to another cell population. Suitable assays for movement and adhesion include, without limitation, those described in: *Current Protocols in Immunology*, Ed by Coligan, Kruisbeek, Margulies, Shevach and Strober, Pub. Greene Publishing Associates and Wiley-Interscience, Chapter **6.12**: 6.12.1-6.12.28; Taub *et al., J. Clin. Invest.* **95**:1370-1376, 1995; Lind *et al., APMIS* **103**:140-146, 1995; Mueller *et al., Eur. J. Immunol.* 25:1744-1748;

Gruber *et al., J. Immunol.* 152:5860-5867, 1994; Johnston *et al. J. Immunol.*, 153:1762-1768, 1994.

EXAMPLE 38

Assaying the Proteins Expressed from Extended cDNAs or Portions Thereof for Regulation of Blood Clotting

The proteins encoded by the extended cDNAs or portions thereof may also be evaluated for their effects on blood clotting. Numerous assays for such activity are familiar to those skilled in the art, including the assays disclosed in the following references, which are incorporated herein by reference: Linet *et al., J. Clin. Pharmacol.* 26:131-140, 1986; Burdick *et al., Thrombosis Res.* 45:413-419, 1987; Humphrey *et al., Fibrinolysis* 5:71-79, 1991; Schaub, *Prostaglandins* 35:467-474, 1988.

Those proteins which are involved in the regulation of blood clotting may then be formulated as pharmaceuticals and used to treat clinical conditions in which regulation of blood clotting is beneficial. For example, a protein of the invention may also exhibit hemostatic or thrombolytic activity. As a result, such a protein is expected to be useful in treatment of various coagulations disorders (including hereditary disorders, such as hemophilias) or to enhance coagulation and other hemostatic events in treating wounds resulting from trauma, surgery or other causes. A protein of the invention may also be useful for dissolving or inhibiting formation of thromboses and for treatment and prevention of conditions resulting therefrom (such as infarction of cardiac and central nervous system vessels (e.g., stroke)). Alternatively, as described in more detail below, genes encoding blood clotting activity proteins or nucleic acids regulating the expression of such proteins may be introduced into appropriate host cells to increase or decrease the expression of the proteins as desired.

EXAMPLE 39

Assaying the Proteins Expressed from Extended cDNAs or Portions Thereof for Involvement in Receptor/Ligand Interactions

The proteins encoded by the extended cDNAs or a portion thereof may also be evaluated for their involvement in receptor/ligand interactions. Numerous assays for such

involvement are familiar to those skilled in the art, including the assays disclosed in the following references, which are incorporated herein by reference: Chapter 7. 7.28.1-7.28.22 in *Current Protocols in Immunology*, Coligan *et al.* Eds. Greene Publishing Associates and Wiley-Interscience; Takai *et al.*, *Proc. Natl. Acad. Sci. USA* **84**:6864-6868, 1987; Bierer *et al.*, *J. Exp. Med.* **168**:1145-1156, 1988; Rosenstein *et al.*, *J. Exp. Med.* **169**:149-160, 1989; Stoltenborg *et al.*, *J. Immunol. Methods* **175**:59-68, 1994; Stitt *et al.*, *Cell* **80**:661-670, 1995; Gyuris *et al.*, *Cell* **75**:791-803, 1993.

For example, the proteins encoded by extended cDNAs derived from the 5' ESTs of the present invention may also demonstrate activity as receptors, receptor ligands or inhibitors or agonists of receptor/ligand interactions. Examples of such receptors and ligands include, without limitation, cytokine receptors and their ligands, receptor kinases and their ligands, receptor phosphatases and their ligands, receptors involved in cell-cell interactions and their ligands (including without limitation, cellular adhesion molecules (such as selectins, integrins and their ligands) and receptor/ligand pairs involved in antigen presentation, antigen recognition and development of cellular and humoral immune responses). Receptors and ligands are also useful for screening of potential peptide or small molecule inhibitors of the relevant receptor/ligand interaction. A protein encoded by extended cDNAs derived from the 5' ESTs of the present invention (including, without limitation, fragments of receptors and ligands) may themselves be useful as inhibitors of receptor/ligand interactions. Alternatively, as described in more detail below, genes encoding proteins involved in receptor/ligand interactions or nucleic acids regulating the expression of such proteins may be introduced into appropriate host cells to increase or decrease the expression of the proteins as desired.

EXAMPLE 40

Assaying the Proteins Expressed from Extended cDNAs or Portions Thereof for Anti-Inflammatory Activity

The proteins encoded by the extended cDNAs or a portion thereof may also be evaluated for anti-inflammatory activity. The anti-inflammatory activity may be achieved by providing a stimulus to cells involved in the inflammatory response, by inhibiting or promoting cell-cell interactions (such as, for example, cell adhesion), by inhibiting or promoting chemotaxis of cells involved in the inflammatory process, inhibiting or promoting

cell extravasation, or by stimulating or suppressing production of other factors which more directly inhibit or promote an inflammatory response. Proteins exhibiting such activities can be used to treat inflammatory conditions including chronic or acute conditions, including without limitation inflammation associated with infection (such as septic shock, sepsis or systemic inflammatory response syndrome), ischemia-reperfusioninury, endotoxin lethality, arthritis, complement-mediated hyperacute rejection, nephritis, cytokine- or chemokine-induced lung injury, inflammatory bowel disease, Crohn's disease or resulting from over production of cytokines such as TNF or IL-1. Proteins of the invention may also be useful to treat anaphylaxis and hypersensitivity to an antigenic substance or material. Alternatively, as described in more detail below, genes encoding anti-inflammatory activity proteins or nucleic acids regulating the expression of such proteins may be introduced into appropriate host cells to increase or decrease the expression of the proteins as desired.

EXAMPLE 41

Assaying the Proteins Expressed from Extended cDNAs or Portions Thereof for Tumor Inhibition Activity

The proteins encoded by the extended cDNAs or a portion thereof may also be evaluated for tumor inhibition activity. In addition to the activities described above for immunological treatment or prevention of tumors, a protein of the invention may exhibit other anti-tumor activities. A protein may inhibit tumor growth directly or indirectly (such as, for example, via ADCC). A protein may exhibit its tumor inhibitory activity by acting on tumor tissue or tumor precursor tissue, by inhibiting formation of tissues necessary to support tumor growth (such as, for example, by inhibiting angiogenesis), by causing production of other factors, agents or cell types which inhibit tumor growth, or by suppressing, eliminating or inhibiting factors, agents or cell types which promote tumor growth. Alternatively, as described in more detail below, genes tumor inhibition activity proteins or nucleic acids regulating the expression of such proteins may be introduced into appropriate host cells to increase or decrease the expression of the proteins as desired.

A protein of the invention may also exhibit one or more of the following additional activities or effects: inhibiting the growth, infection or function of, or killing, infectious agents,

including, without limitation, bacteria, viruses, fungi and other parasites; effecting (suppressing or enhancing) bodily characteristics, including, without limitation, height, weight, hair color, eye color, skin, fat to lean ratio or other tissue pigmentation, or organ or body part size or shape (such as, for example, breast augmentation or diminution, change in bone form or shape); effecting biorhythms or circadian cycles or rhythms; effecting the fertility of male or female subjects; effecting the metabolism, catabolism, anabolism, processing, utilization, storage or elimination of dietary fat, lipid, protein, carbohydrate, vitamins, minerals, cofactors or other nutritional factors or component(s); effecting behavioral characteristics, including, without limitation, appetite, libido, stress, cognition (including cognitive disorders), depression (including depressive disorders) and violent behaviors; providing analgesic effects or other pain reducing effects; promoting differentiation and growth of embryonic stem cells in lineages other than hematopoietic lineages; hormonal or endocrine activity; in the case of enzymes, correcting deficiencies of the enzyme and treating deficiency-related diseases; treatment of hyperproliferative disorders (such as, for example, psoriasis); immunoglobulin-like activity (such as, for example, the ability to bind antigens or complement); and the ability to act as an antigen in a vaccine composition to raise an immune response against such protein or another material or entity which is cross-reactive with such protein. Alternatively, as described in more detail below, genes encoding proteins involved in any of the above mentioned activities or nucleic acids regulating the expression of such proteins may be introduced into appropriate host cells to increase or decrease the expression of the proteins as desired.

EXAMPLE 42

Identification of Proteins which Interact with
Polypeptides Encoded by Extended cDNAs

Proteins which interact with the polypeptides encoded by cDNAs derived from the 5′ ESTs or fragments thereof, such as receptor proteins, may be identified using two hybrid systems such as the Matchmaker Two Hybrid System 2 (Catalog No. K1604-1, Clontech). As described in the manual accompanying the kit which is incorporated herein by reference, the the cDNAs derived from 5′ ESTs, or fragments thereof, are inserted into an expression vector such that they are in frame with DNA encoding the DNA binding domain of the yeast

transcriptional activator GAL4. cDNAs in a cDNA library which encode proteins which might interact with the polypeptides encoded by the extended cDNAs or portions thereof are inserted into a second expression vector such that they are in frame with DNA encoding the activation domain of GAL4. The two expression plasmids are transformed into yeast and the yeast are plated on selection medium which selects for expression of selectable markers on each of the expression vectors as well as GAL4 dependent expression of the HIS3 gene. Transformants capable of growing on medium lacking histidine are screened for GAL4 dependent lacZ expression. Those cells which are positive in both the histidine selection and the lacZ assay contain plasmids encoding proteins which interact with the polypeptide encoded by the extended cDNAs or portions thereof.

Alternatively, the system described in Lustig *et al.*, *Methods in Enzymology* **283**: 83-99, 1997, and in U.S. Patent No. 5,654,150, the disclosure of which is incorporated herein by reference, may be used for identifying molecules which interact with the polypeptides encoded by extended cDNAs. In such systems, *in vitro* transcription reactions are performed on a pool of vectors containing extended cDNA inserts cloned downstream of a promoter which drives *in vitro* transcription. The resulting pools of mRNAs are introduced into *Xenopus laevis* oocytes. The oocytes are then assayed for a desired activity.

Alternatively, the pooled *in vitro* transcription products produced as described above may be translated *in vitro*. The pooled *in vitro* translation products can be assayed for a desired activity or for interaction with a known polypeptide.

Proteins or other molecules interacting with polypeptides encoded by extended cDNAs can be found by a variety of additional techniques. In one method, affinity columns containing the polypeptide encoded by the extended cDNA or a portion thereof can be constructed. In some versions, of this method the affinity column contains chimeric proteins in which the protein encoded by the extended cDNA or a portion thereof is fused to glutathione S-transferase. A mixture of cellular proteins or pool of expressed proteins as described above and is applied to the affinity column. Proteins interacting with the polypeptide attached to the column can then be isolated and analyzed on 2-D electrophoresis gel as described in Ramunsen *et al.*, *Electrophoresis* **18**:588-598, 1997, the disclosure of which is incorporated herein by reference. Alternatively, the proteins retained on the affinity column can be purified by electrophoresis based methods

and sequenced. The same method can be used to isolate antibodies, to screen phage display products, or to screen phage display human antibodies.

Proteins interacting with polypeptides encoded by extended cDNAs or portions thereof can also be screened by using an Optical Biosensor as described in Edwards and Leatherbarrow, *Analytical Biochemistry* **246**:1-6, 1997, the disclosure of which is incorporated herein by reference. The main advantage of the method is that it allows the determination of the association rate between the protein and other interacting molecules. Thus, it is possible to specifically select interacting molecules with a high or low association rate. Typically a target molecule is linked to the sensor surface (through a carboxymethl dextran matrix) and a sample of test molecules is placed in contact with the target molecules. The binding of a test molecule to the target molecule causes a change in the refractive index and/ or thickness. This change is detected by the Biosensor provided it occurs in the evanescent field (which extend a few hundred nanometers from the sensor surface). In these screening assays, the target molecule can be one of the polypeptides encoded by extended cDNAs or a portion thereof and the test sample can be a collection of proteins extracted from tissues or cells, a pool of expressed proteins, combinatorial peptide and/ or chemical libraries, or phage displayed peptides. The tissues or cells from which the test proteins are extracted can originate from any species.

In other methods, a target protein is immobilized and the test population is a collection of unique polypeptides encoded by the extended cDNAs or portions thereof.

To study the interaction of the proteins encoded by the extended cDNAs or portions thereof with drugs, the microdialysis coupled to HPLC method described by Wang *et al., Chromatographia* **44**:205-208, 1997 or the affinity capillary electrophoresis method described by Busch *et al., J. Chromatogr.* 777:311-328, 1997, the disclosures of which are incorporated herein by reference can be used.

It will be appreciated by those skilled in the art that the proteins expressed from the extended cDNAs or portions may be assayed for numerous activities in addition to those specifically enumerated above. For example, the expressed proteins may be evaluated for applications involving control and regulation of inflammation, tumor proliferation or

metastasis, infection, or other clinical conditions. In addition, the proteins expressed from the extended cDNAs or portions thereof may be useful as nutritional agents or cosmetic agents.

The proteins expressed from the cDNAs or portions thereof may be used to generate antibodies capable of specifically binding to the expressed protein or fragments thereof as described in Example 40 below. The antibodies may capable of binding a full length protein encoded by a cDNA derived from a 5′ EST, a mature protein (*i.e.* the protein generated by cleavage of the signal peptide) encoded by a cDNA derived from a 5′ EST, or a signal peptide encoded by a cDNA derived from a 5′ EST. Alternatively, the antibodies may be capable of binding fragments of at least 10 amino acids of the proteins encoded by the above cDNAs. In some embodiments, the antibodies may be capable of binding fragments of at least 15 amino acids of the proteins encoded by the above cDNAs. In other embodiments, the antibodies may be capable of binding fragments of at least 25 amino acids of the proteins expressed from the extended cDNAs which comprise at least 25 amino acids of the proteins encoded by the above cDNAs. In further embodiments, the antibodies may be capable of binding fragments of at least 40 amino acids of the proteins encoded by the above cDNAs.

EXAMPLE 43

Production of an Antibody to a Human Protein

Substantially pure protein or polypeptide is isolated from the transfected or transformed cells as described in Example 30. The concentration of protein in the final preparation is adjusted, for example, by concentration on an Amicon filter device, to the level of a few μg/ml. Monoclonal or polyclonal antibody to the protein can then be prepared as follows:

1. Monoclonal Antibody Production by Hybridoma Fusion

Monoclonal antibody to epitopes of any of the peptides identified and isolated as described can be prepared from murine hybridomas according to the classical method of Kohler, and Milstein, *Nature* **256**:495, 1975 or derivative methods thereof. Briefly, a mouse is repetitively inoculated with a few micrograms of the selected protein or peptides derived therefrom over a period of a few weeks. The mouse is then sacrificed, and the antibody producing cells of the spleen isolated. The spleen cells are fused by means of polyethylene glycol with mouse myeloma cells, and the excess unfused cells

destroyed by growth of the system on selective media comprising aminopterin (HAT media). The successfully fused cells are diluted and aliquots of the dilution placed in wells of a microtiter plate where growth of the culture is continued. Antibody-producing clones are identified by detection of antibody in the supernatant fluid of the wells by immunoassay procedures, such as ELISA, as originally described by Engvall, *Meth. Enzymol.* 70:419, 1980, the disclosure of which is incorporated herein by reference and derivative methods thereof. Selected positive clones can be expanded and their monoclonal antibody product harvested for use. Detailed procedures for monoclonal antibody production are described in Davis *et al.* in *Basic Methods in Molecular Biology* Elsevier, New York. Section 21-2, the disclosure of which is incorporated herein by reference.

2. Polyclonal Antibody Production by Immunization

Polyclonal antiserum containing antibodies to heterogenous epitopes of a single protein can be prepared by immunizing suitable animals with the expressed protein or peptides derived therefrom, which can be unmodified or modified to enhance immunogenicity. Effective polyclonal antibody production is affected by many factors related both to the antigen and the host species. For example, small molecules tend to be less immunogenic than others and may require the use of carriers and adjuvant. Also, host animals response vary depending on site of inoculations and doses, with both inadequate or excessive doses of antigen resulting in low titer antisera. Small doses (ng level) of antigen administered at multiple intradermal sites appears to be most reliable. An effective immunization protocol for rabbits can be found in Vaitukaitis. *et al, J. Clin. Endocrinol. Metab.* 33:988-991 (1971), the disclosure of which is incorporated herein by reference.

Booster injections can be given at regular intervals, and antiserum harvested when antibody titer thereof, as determined semi-quantitatively, for example, by double immunodiffusion in agar against known concentrations of the antigen, begins to fall. See, for example, Ouchterlony, *et al.*, Chap. 19 in: *Handbook of Experimental Immunology* D. Wier (ed) Blackwell (1973), the disclosure of which is incorporated herein by reference. Plateau concentration of antibody is usually in the range of 0.1 to 0.2 mg/ml of serum (about 12 μM). Affinity of the antisera for the antigen is determined by preparing competitive binding curves,

as described, for example, by Fisher, D., Chap. 42 in: *Manual of Clinical Immunology*, 2d Ed. (Rose and Friedman, Eds.) Amer. Soc. For Microbiol., Washington, D.C. (1980) , the disclosure of which is incorporated herein by reference..

Antibody preparations prepared according to either protocol are useful in quantitative immunoassays which determine concentrations of antigen-bearing substances in biological samples; they are also used semi-quantitatively or qualitatively to identify the presence of antigen in a biological sample. The antibodies may also be used in therapeutic compositions for killing cells expressing the protein or reducing the levels of the protein in the body.

V. Use of 5' ESTs or Sequences Obtainable Therefrom or Portions Thereof as Reagents

The 5' ESTs of the present invention (or cDNAs or genomic DNAs obtainable therefrom) may be used as reagents in isolation procedures, diagnostic assays, and forensic procedures. For example, sequences from the 5' ESTs (or cDNAs or genomic DNAs obtainable therefrom) may be detectably labeled and used as probes to isolate other sequences capable of hybridizing to them. In addition, sequences from 5' ESTs (or cDNAs or genomic DNAs obtainable therefrom) may be used to design PCR primers to be used in isolation, diagnostic, or forensic procedures.

1. Use of 5' ESTs or Sequences Obtainable Therefrom or Portions Thereof in Isolation, Diagnostic and Forensic Procedures

EXAMPLE 44

Preparation of PCR Primers and Amplification of DNA

The 5' EST sequences (or cDNAs or genomic DNAs obtainable therefrom) may be used to prepare PCR primers for a variety of applications, including isolation procedures for cloning nucleic acids capable of hybridizing to such sequences, diagnostic techniques and forensic techniques. The PCR primers are at least 10 bases, and preferably at least 12, 15, or 17 bases in length. More preferably, the PCR primers are at least 20-30 bases in length. In some embodiments, the PCR primers may be more than 30 bases in length. It is preferred

that the primer pairs have approximately the same G/C ratio, so that melting temperatures are approximately the same. A variety of PCR techniques are familiar to those skilled in the art. For a review of PCR technology, see Molecular Cloning to Genetic Engineering, White Ed. *in Methods in Molecular Biology* 67: Humana Press, Totowa 1997, the disclosure of which is incorporated herein by reference. In each of these PCR procedures, PCR primers on either side of the nucleic acid sequences to be amplified are added to a suitably prepared nucleic acid sample along with dNTPs and a thermostable polymerase such as Taq polymerase, Pfu polymerase, or Vent polymerase. The nucleic acid in the sample is denatured and the PCR primers are specifically hybridized to complementary nucleic acid sequences in the sample. The hybridized primers are extended. Thereafter, another cycle of denaturation, hybridization, and extension is initiated. The cycles are repeated multiple times to produce an amplified fragment containing the nucleic acid sequence between the primer sites.

EXAMPLE 45

Use of 5'ESTs as Probes

Probes derived from 5' ESTs (or cDNAs or genomic DNAs obtainable therefrom), including full length cDNAs or genomic sequences, may be labeled with detectable labels familiar to those skilled in the art, including radioisotopes and non-radioactive labels, to provide a detectable probe. The detectable probe may be single stranded or double stranded and may be made using techniques known in the art, including *in vitro* transcription, nick translation, or kinase reactions. A nucleic acid sample containing a sequence capable of hybridizing to the labeled probe is contacted with the labeled probe. If the nucleic acid in the sample is double stranded, it may be denatured prior to contacting the probe. In some applications, the nucleic acid sample may be immobilized on a surface such as a nitrocellulose or nylon membrane. The nucleic acid sample may comprise nucleic acids obtained from a variety of sources, including genomic DNA, cDNA libraries, RNA, or tissue samples.

Procedures used to detect the presence of nucleic acids capable of hybridizing to the detectable probe include well known techniques such as Southern blotting, Northern blotting, dot blotting, colony hybridization, and plaque hybridization. In some applications, the nucleic acid capable of hybridizing to the labeled probe may be cloned into vectors such as expression vectors, sequencing vectors, or *in vitro* transcription vectors to facilitate the characterization

and expression of the hybridizing nucleic acids in the sample. For example, such techniques may be used to isolate and clone sequences in a genomic library or cDNA library which are capable of hybridizing to the detectable probe as described in Example 30 above.

PCR primers made as described in Example 44 above may be used in forensic analyses, such as the DNA fingerprinting techniques described in Examples 46-50 below. Such analyses may utilize detectable probes or primers based on the sequences of the the 5′ ESTs or of cDNAs or genomic DNAs isolated using the 5′ ESTs.

EXAMPLE 46

Forensic Matching by DNA Sequencing

In one exemplary method, DNA samples are isolated from forensic specimens of, for example, hair, semen, blood or skin cells by conventional methods. A panel of PCR primers based on a number of the 5′ ESTs of Example 25, or cDNAs or genomic DNAs isolated therefrom as described above, is then utilized in accordance with Example 44 to amplify DNA of approximately 100-200 bases in length from the forensic specimen. Corresponding sequences are obtained from a test subject. Each of these identification DNAs is then sequenced using standard techniques, and a simple database comparison determines the differences, if any, between the sequences from the subject and those from the sample. Statistically significant differences between the suspect's DNA sequences and those from the sample conclusively prove a lack of identity. This lack of identity can be proven, for example, with only one sequence. Identity, on the other hand, should be demonstrated with a large number of sequences, all matching. Preferably, a minimum of 50 statistically identical sequences of 100 bases in length are used to prove identity between the suspect and the sample.

EXAMPLE 47

Positive Identification by DNA Sequencing

The technique outlined in the previous example may also be used on a larger scale to provide a unique fingerprint-type identification of any individual. In this technique, primers are prepared from a large number of 5’EST sequences from Example 25, or cDNA or genomic DNA sequences obtainable therefrom. Preferably, 20 to 50 different primers are

used. These primers are used to obtain a corresponding number of PCR-generated DNA segments from the individual in question in accordance with Example 44. Each of these DNA segments is sequenced, using the methods set forth in Example 46. The database of sequences generated through this procedure uniquely identifies the individual from whom the sequences were obtained. The same panel of primers may then be used at any later time to absolutely correlate tissue or other biological specimen with that individual.

EXAMPLE 48

Southern Blot Forensic Identification

The procedure of Example 47 is repeated to obtain a panel of at least 10 amplified sequences from an individual and a specimen. Preferably, the panel contains at least 50 amplified sequences. More preferably, the panel contains 100 amplified sequences. In some embodiments, the panel contains 200 amplified sequences. This PCR-generated DNA is then digested with one or a combination of, preferably, four base specific restriction enzymes. Such enzymes are commercially available and known to those of skill in the art. After digestion, the resultant gene fragments are size separated in multiple duplicate wells on an agarose gel and transferred to nitrocellulose using Southern blotting techniques well known to those with skill in the art. For a review of Southern blotting see Davis *et al.* (Basic Methods in Molecular Biology, 1986, Elsevier Press. pp 62-65) , the disclosure of which is incorporated herein by reference.

A panel of probes based on the sequences of 5′ ESTs (or cDNAs or genomic DNAs obtainable therefrom), or fragments thereof of at least 10 bases, are radioactively or colorimetrically labeled using methods known in the art, such as nick translation or end labeling, and hybridized to the Southern blot using techniques known in the art (Davis *et al.*, supra). Preferably, the probe comprises at least 12, 15, or 17 consecutive nucleotides from the 5′ EST (or cDNAs or genomic DNAs obtainable therefrom). More preferably, the probe comprises at least 20-30 consecutive nucleotides from the 5′ EST (or cDNAs or genomic DNAs obtainable therefrom). In some embodiments, the probe comprises more than 30 nucleotides from the 5′ EST (or cDNAs or genomic DNAs obtainable therefrom).

Preferably, at least 5 to 10 of these labeled probes are used, and more preferably at least about 20 or 30 are used to provide a unique pattern. The resultant bands appearing

from the hybridization of a large sample of 5' EST (or cDNAs or genomic DNAs obtainable therefrom) will be a unique identifier. Since the restriction enzyme cleavage will be different for every individual, the band pattern on the Southern blot will also be unique. Increasing the number of 5' EST (or cDNAs or genomic DNAs obtainable therefrom) probes will provide a statistically higher level of confidence in the identification since there will be an increased number of sets of bands used for identification.

EXAMPLE 49

Dot Blot Identification Procedure

Another technique for identifying individuals using the 5' EST sequences disclosed herein utilizes a dot blot hybridization technique.

Genomic DNA is isolated from nuclei of subject to be identified. Oligonucleotide probes of approximately 30 bp in length are synthesized that correspond to at least 10, preferably 50 sequences from the 5' ESTs or cDNAs or genomic DNAs obtainable therefrom. The probes are used to hybridize to the genomic DNA through conditions known to those in the art. The oligonucleotides are end labeled with P^{32} using polynucleotide kinase (Pharmacia). Dot Blots are created by spotting the genomic DNA onto nitrocellulose or the like using a vacuum dot blot manifold (BioRad, Richmond California). The nitrocellulose filter containing the genomic sequences is baked or UV linked to the filter, prehybridized and hybridized with labeled probe using techniques known in the art (Davis et *al., supra*). The ^{32}P labeled DNA fragments are sequentially hybridized with successively stringent conditions to detect minimal differences between the 30 bp sequence and the DNA. Tetramethylammonium chloride is useful for identifying clones containing small numbers of nucleotide mismatches (Wood *et al., Proc. Natl. Acad. Sci. USA* **82(6)**:1585-1588, 1985) which is hereby incorporated by reference. A unique pattern of dots distinguishes one individual from another individual.

5' EST sequences (or cDNAs or genomic DNAs obtainable therefrom) or oligonucleotides containing at least 10 consecutive bases from these sequences can be used as probes in the following alternative fingerprinting technique. Preferably, the probe comprises at least 12, 15, or 17 consecutive nucleotides from the 5' EST sequences (or cDNAs or genomic DNAs obtainable therefrom). More preferably, the probe comprises at least 20-30

consecutive nucleotides from the 5′ EST sequences (or cDNAs or genomic DNAs obtainable therefrom). In some embodiments, the probe comprises more than 30 nucleotides from the 5′ EST sequences (or cDNAs or genomic DNAs obtainable therefrom).

Preferably, a plurality of probes having sequences from different genes are used in the alternative fingerprinting technique. Example 50 below provides a representative alternative fingerprinting procedure in which the probes are derived from 5'EST.

EXAMPLE 50

Alternative "Fingerprint" Identification Technique

20-mer oligonucleotides are prepared from a large number, e.g. 50, 100, or 200, of 5'EST using commercially available oligonucleotide services such as Genset, Paris, France. Cell samples from the test subject are processed for DNA using techniques well known to those with skill in the art. The nucleic acid is digested with restriction enzymes such as EcoRI and XbaI. Following digestion, samples are applied to wells for electrophoresis. The procedure, as known in the art, may be modified to accommodate polyacrylamide electrophoresis, however in this example, samples containing 5 ug of DNA are loaded into wells and separated on 0.8% agarose gels. The gels are transferred onto nitrocellulose using standard Southern blotting techniques.

10 ng of each of the oligonucleotides are pooled and end-labeled with ^{32}P. The nitrocellulose is prehybridized with blocking solution and hybridized with the labeled probes. Following hybridization and washing, the nitrocellulose filter is exposed to X-Omat AR X-ray film. The resulting hybridization pattern will be unique for each individual.

It is additionally contemplated within this example that the number of probe sequences used can be varied for additional accuracy or clarity.

The proteins encoded by the extended cDNAs may also be used to generate antibodies as explained in Examples 30 and 43 in order to identify the tissue type or cell species from which a sample is derived as described in example 51.

EXAMPLE 51

Identification of Tissue Types or Cell Species by Means of Labeled Tissue Specific Antibodies

Identification of specific tissues is accomplished by the visualization of tissue specific antigens by means of antibody preparations according to Examples 30 and 43 which are conjugated, directly or indirectly to a detectable marker. Selected labeled antibody species bind to their specific antigen binding partner in tissue sections, cell suspensions, or in extracts of soluble proteins from a tissue sample to provide a pattern for qualitative or semi-qualitative interpretation.

Antisera for these procedures must have a potency exceeding that of the native preparation, and for that reason, antibodies are concentrated to a mg/ml level by isolation of the gamma globulin fraction, for example, by ion-exchange chromatography or by ammonium sulfate fractionation. Also, to provide the most specific antisera, unwanted antibodies, for example to common proteins, must be removed from the gamma globulin fraction, for example by means of insoluble immunoabsorbents, before the antibodies are labeled with the marker. Either monoclonal or heterologous antisera is suitable for either procedure.

A. Immunohistochemical techniques

Purified, high-titer antibodies, prepared as described above, are conjugated to a detectable marker, as described, for example, by Fudenberg, Chap. 26 in: *Basic and Clinical Immunology*, 3rd Ed. Lange, Los Altos, California, 1980, or Rose,. *et al.*, Chap. **12** in: *Methods in Immunodiagnosis*, 2d Ed. John Wiley and Sons, New York (1980), the disclosures of which are incorporated herein by reference.

A fluorescent marker, either fluorescein or rhodamine, is preferred, but antibodies can also be labeled with an enzyme that supports a color producing reaction with a substrate, such as horseradish peroxidase. Markers can be added to tissue-bound antibody in a second step, as described below. Alternatively, the specific antitissue antibodies can be labeled with ferritin or other electron dense particles, and localization of the ferritin coupled antigen-antibody complexes achieved by means of an electron microscope. In yet another approach, the antibodies are radiolabeled, with, for example ^{125}I, and detected by overlaying the antibody treated preparation with photographic emulsion.

Preparations to carry out the procedures can comprise monoclonal or polyclonal antibodies to a single protein or peptide identified as specific to a tissue type, for example, brain tissue, or antibody preparations to several antigenically distinct tissue specific antigens can be used in panels, independently or in mixtures, as required.

Tissue sections and cell suspensions are prepared for immunohistochemical examination according to common histological techniques. Multiple cryostat sections (about 4 μm, unfixed) of the unknown tissue and known control, are mounted and each slide covered with different dilutions of the antibody preparation. Sections of known and unknown tissues should also be treated with preparations to provide a positive control, a negative control, for example, pre-immune sera, and a control for non-specific staining, for example, buffer.

Treated sections are incubated in a humid chamber for 30 min at room temperature, rinsed, then washed in buffer for 30-45 min. Excess fluid is blotted away, and the marker developed.

If the tissue specific antibody was not labeled in the first incubation, it can be labeled at this time in a second antibody-antibody reaction, for example, by adding fluorescein- or enzyme-conjugated antibody against the immunoglobulin class of the antiserum-producing species, for example, fluorescein labeled antibody to mouse IgG. Such labeled sera are commercially available.

The antigen found in the tissues by the above procedure can be quantified by measuring the intensity of color or fluorescence on the tissue section, and calibrating that signal using appropriate standards.

B. Identification of tissue specific soluble proteins

The visualization of tissue specific proteins and identification of unknown tissues from that procedure is carried out using the labeled antibody reagents and detection strategy as described for immunohistochemistry; however the sample is prepared according to an electrophoretic technique to distribute the proteins extracted from the tissue in an orderly array on the basis of molecular weight for detection.

A tissue sample is homogenized using a Virtis apparatus; cell suspensions are disrupted by Dounce homogenization or osmotic lysis, using detergents in either case as required to disrupt cell membranes, as is the practice in the art. Insoluble cell components

such as nuclei, microsomes, and membrane fragments are removed by ultracentrifugation, and the soluble protein-containing fraction concentrated if necessary and reserved for analysis.

A sample of the soluble protein solution is resolved into individual protein species by conventional SDS polyacrylamide electrophoresis as described, for example, by Davis, *et al.*, Section **19-2** in: *Basic Methods in Molecular Biology*, Leder ed., Elsevier, New York, 1986, the disclosure of which is incorporated herein by reference, using a range of amounts of polyacrylamide in a set of gels to resolve the entire molecular weight range of proteins to be detected in the sample. A size marker is run in parallel for purposes of estimating molecular weights of the constituent proteins. Sample size for analysis is a convenient volume of from 5 to 55 µl, and containing from about 1 to 100 µg protein. An aliquot of each of the resolved proteins is transferred by blotting to a nitrocellulose filter paper, a process that maintains the pattern of resolution. Multiple copies are prepared. The procedure, known as Western Blot Analysis, is well described in Davis, L. *et al., supra* Section 19-3. One set of nitrocellulose blots is stained with Coomassie blue dye to visualize the entire set of proteins for comparison with the antibody bound proteins. The remaining nitrocellulose filters are then incubated with a solution of one or more specific antisera to tissue specific proteins prepared as described in Examples 30 and 43. In this procedure, as in procedure A above, appropriate positive and negative sample and reagent controls are run.

In either procedure A or B, a detectable label can be attached to the primary tissue antigen-primary antibody complex according to various strategies and permutations thereof. In a straightforward approach, the primary specific antibody can be labeled; alternatively, the unlabeled complex can be bound by a labeled secondary anti-IgG antibody. In other approaches, either the primary or secondary antibody is conjugated to a biotin molecule, which can, in a subsequent step, bind an avidin conjugated marker. According to yet another strategy, enzyme labeled or radioactive protein A, which has the property of binding to any IgG, is bound in a final step to either the primary or secondary antibody.

The visualization of tissue specific antigen binding at levels above those seen in control tissues to one or more tissue specific antibodies, prepared from the gene sequences identified from extended cDNA sequences, can identify tissues of unknown origin, for example, forensic samples, or differentiated tumor tissue that has metastasized to foreign bodily sites.

In addition to their applications in forensics and identification, 5′ ESTs (or cDNAs or genomic DNAs obtainable therefrom) may be mapped to their chromosomal locations. Example 52 below describes radiation hybrid (RH) mapping of human chromosomal regions using 5'ESTs. Example 53 below describes a representative procedure for mapping an 5′ EST to its location on a human chromosome. Example 54 below describes mapping of 5′ ESTs on metaphase chromosomes by Fluorescence In Situ Hybridization (FISH). Those skilled in the art will appreciate that the method of Examples 52-54 may also be used to map cDNAs or genomic DNAs obtainable from the 5′ ESTs to their chromosomal locations.

2. Use of 5' ESTs or Sequences Obtainable Therefrom or Portions Thereof in Chromosome Mapping

EXAMPLE 52

Radiation hybrid mapping of 5'ESTs to the human genome

Radiation hybrid (RH) mapping is a somatic cell genetic approach that can be used for high resolution mapping of the human genome. In this approach, cell lines containing one or more human chromosomes are lethally irradiated, breaking each chromosome into fragments whose size depends on the radiation dose. These fragments are rescued by fusion with cultured rodent cells, yielding subclones containing different portions of the human genome. This technique is described by Benham *et al.*, *Genomics* 4:509-517, 1989; and Cox *et al.*, *Science* 250:245-250, 1990, the entire contents of which are hereby incorporated by reference. The random and independent nature of the subclones permits efficient mapping of any human genome marker. Human DNA isolated from a panel of 80-100 cell lines provides a mapping reagent for ordering 5'EST. In this approach, the frequency of breakage between markers is used to measure distance, allowing construction of fine resolution maps as has been done using conventional ESTs (Schuler *et al.*, *Science* 274:540-546, 1996, hereby incorporated by reference).

RH mapping has been used to generate a high-resolution whole genome radiation hybrid map of human chromosome 17q22-q25.3 across the genes for growth hormone (GH) and thymidine kinase (TK) (Foster *et al.*, *Genomics* 33:185-192, 1996), the region surrounding the Gorlin syndrome gene (Obermayr *et al.*, *Eur. J. Hum. Genet.* 4:242-245,

1996), 60 loci covering the entire short arm of chromosome 12 (Raeymaekers *et al.*, *Genomics* 29:170-178, 1995), the region of human chromosome 22 containing the neurofibromatosis type 2 locus (Frazer *et al.*, *Genomics* 14:574-584, 1992) and 13 loci on the long arm of chromosome 5 (Warrington *et al.*, *Genomics* 11:701-708, 1991).

EXAMPLE 53

Mapping of 5'ESTs to HumanChromosomes using PCR techniques

5' ESTs (or cDNAs or genomic DNAs obtainable therefrom) may be assigned to human chromosomes using PCR based methodologies. In such approaches, oligonucleotide primer pairs are designed from the 5' ESTs (or cDNAs or genomic DNAs obtainable therefrom) to minimize the chance of amplifying through an intron. Preferably, the oligonucleotide primers are 18-23 bp in length and are designed for PCR amplification. The creation of PCR primers from known sequences is well known to those with skill in the art. For a review of PCR technology see Erlich in *PCR Technology; Principles and Applications for DNA Amplification*, Freeman and Co., New York, 1992, the disclosure of which is incorporated herein by reference.

The primers are used in polymerase chain reactions (PCR) to amplify templates from total human genomic DNA. PCR conditions are as follows: 60 ng of genomic DNA is used as a template for PCR with 80 ng of each oligonucleotide primer, 0.6 unit of Taq polymerase, and 1 μCu of a ^{32}P-labeled deoxycytidine triphosphate. The PCR is performed in a microplate thermocycler (Techne) under the following conditions: 30 cycles of 94°C, 1.4 min; 55°C, 2 min; and 72°C, 2 min; with a final extension at 72°C for 10 min. The amplified products are analyzed on a 6% polyacrylamide sequencing gel and visualized by autoradiography. If the length of the resulting PCR product is identical to the distance between the ends of the primer sequences in the extended cDNA from which the primers are derived, then the PCR reaction is repeated with DNA templates from two panels of human-rodent somatic cell hybrids, BIOS PCRable DNA (BIOS Corporation) and NIGMS Human-Rodent Somatic Cell Hybrid Mapping Panel Number 1 (NIGMS, Camden, NJ).

PCR is used to screen a series of somatic cell hybrid cell lines containing defined sets of human chromosomes for the presence of a given 5' EST (or cDNA or genomic DNA obtainable therefrom). DNA is isolated from the somatic hybrids and used as starting

templates for PCR reactions using the primer pairs from the 5′ EST (or cDNA or genomic DNA obtainable therefrom). Only those somatic cell hybrids with chromosomes containing the human gene corresponding to the 5′ EST (or cDNA or genomic DNA obtainable therefrom) will yield an amplified fragment. The 5′ EST (or cDNA or genomic DNA obtainable therefrom) are assigned to a chromosome by analysis of the segregation pattern of PCR products from the somatic hybrid DNA templates. The single human chromosome present in all cell hybrids that give rise to an amplified fragment is the chromosome containing that 5′EST (or cDNA or genomic DNA obtainable therefrom). For a review of techniques and analysis of results from somatic cell gene mapping experiments, see Ledbetter *et al.*, *Genomics* 6:475-481, 1990, the disclosure of which is incorporated herein by reference.

EXAMPLE 54

Mapping of Extended 5′ ESTs to Chromosomes Using Fluorescence *In Situ* Hybridization

Fluorescence in situ hybridization allows the 5'EST (or cDNA or genomic DNA obtainable therefrom) to be mapped to a particular location on a given chromosome. The chromosomes to be used for fluorescence in situ hybridization techniques may be obtained from a variety of sources including cell cultures, tissues, or whole blood.

In a preferred embodiment, chromosomal localization of an 5'EST (or cDNA or genomic DNA obtainable therefrom) is obtained by FISH as described by Cherif *et al.* (*Proc. Natl. Acad. Sci. U.S.A.*, 87:6639-6643, 1990) , the disclosure of which is incorporated herein by reference.. Metaphase chromosomes are prepared from phytohemagglutinin (PHA)-stimulated blood cell donors. PHA-stimulated lymphocytes from healthy males are cultured for 72 h in RPMI-1640 medium. For synchronization, methotrexate (10 μM) is added for 17 h, followed by addition of 5-bromodeoxyuridine (5-BrdU, 0.1 mM) for 6 h. Colcemid (1 μg/ml) is added for the last 15 min before harvesting the cells. Cells are collected, washed in RPMI, incubated with a hypotonic solution of KCl (75 mM) at 37°C for 15 min and fixed in three changes of methanol:acetic acid (3:1). The cell suspension is dropped onto a glass slide and air dried. The 5'EST (or cDNA or genomic DNA obtainable therefrom) is labeled with biotin-16 dUTP by nick translation according to the manufacturer's instructions (Bethesda Research Laboratories, Bethesda, MD), purified using a Sephadex G-50 column (Pharmacia,

Upsala, Sweden) and precipitated. Just prior to hybridization, the DNA pellet is dissolved in hybridization buffer (50% formamide, 2 X SSC, 10% dextran sulfate, 1 mg/ml sonicated salmon sperm DNA, pH 7) and the probe is denatured at 70°C for 5-10 min.

Slides kept at -20°C are treated for 1 h at 37°C with RNase A (100 μg/ml), rinsed three times in 2 X SSC and dehydrated in an ethanol series. Chromosome preparations are denatured in 70% formamide, 2 X SSC for 2 min at 70°C, then dehydrated at 4°C. The slides are treated with proteinase K (10 μg/100 ml in 20 mM Tris-HCl, 2 mM $CaCl_2$) at 37°C for 8 min and dehydrated. The hybridization mixture containing the probe is placed on the slide, covered with a coverslip, sealed with rubber cement and incubated overnight in a humid chamber at 37°C. After hybridization and post-hybridization washes, the biotinylated probe is detected by avidin-FITC and amplified with additional layers of biotinylated goat anti-avidin and avidin-FITC. For chromosomal localization, fluorescent R-bands are obtained as previously described (Cherif *et al.*, *supra*.). The slides are observed under a LEICA fluorescence microscope (DMRXA). Chromosomes are counterstained with propidium iodide and the fluorescent signal of the probe appears as two symmetrical yellow-green spots on both chromatids of the fluorescent R-band chromosome (red). Thus, a particular 5'EST (or cDNA or genomic DNA obtainable therefrom) may be localized to a particular cytogenetic R-band on a given chromosome.

Once the 5'EST (or cDNA or genomic DNA obtainable therefrom) have been assigned to particular chromosomes using the techniques described in Examples 52-54 above, they may be utilized to construct a high resolution map of the chromosomes on which they are located or to identify the chromosomes in a sample.

EXAMPLE 55

Use of 5'EST to Construct or Expand Chromosome Maps

Chromosome mapping involves assigning a given unique sequence to a particular chromosome as described above. Once the unique sequence has been mapped to a given chromosome, it is ordered relative to other unique sequences located on the same chromosome. One approach to chromosome mapping utilizes a series of yeast artificial chromosomes (YACs) bearing several thousand long inserts derived from the chromosomes

of the organism from which the extended cDNAs (or genomic DNAs obtainable therefrom) are obtained. This approach is described in Nagaraja *et al., Genome Research* 7:210-222, 1997, the disclosure of which is incorporated herein by reference. Briefly, in this approach each chromosome is broken into overlapping pieces which are inserted into the YAC vector. The YAC inserts are screened using PCR or other methods to determine whether they include the 5'EST (or cDNA or genomic DNA obtainable therefrom) whose position is to be determined. Once an insert has been found which includes the 5'EST (or cDNA or genomic DNA obtainable therefrom), the insert can be analyzed by PCR or other methods to determine whether the insert also contains other sequences known to be on the chromosome or in the region from which the 5'EST (or cDNA or genomic DNA obtainable therefrom) was derived. This process can be repeated for each insert in the YAC library to determine the location of each of the extended cDNAs (or genomic DNAs obtainable therefrom) relative to one another and to other known chromosomal markers. In this way, a high resolution map of the distribution of numerous unique markers along each of the organisms chromosomes may be obtained.

As described in Example 56 below extended cDNAs (or genomic DNAs obtainable therefrom) may also be used to identify genes associated with a particular phenotype, such as hereditary disease or drug response.

3. Use of 5'ESTs or Sequences Obtained Therefrom or Fragments Thereof in Gene Identification

EXAMPLE 56

Identification of genes associated with hereditary diseases or drug response

This example illustrates an approach useful for the association of 5'ESTs (or cDNA or genomic DNA obtainable therefrom) with particular phenotypic characteristics. In this example, a particular 5'EST (or cDNA or genomic DNA obtainable therefrom) is used as a test probe to associate that 5'EST (or cDNA or genomic DNA obtainable therefrom) with a particular phenotypic characteristic.

5'ESTs (or cDNA or genomic DNA obtainable therefrom) are mapped to a particular location on a human chromosome using techniques such as those described in Examples 52 and 53 or other techniques known in the art. A search of Mendelian Inheritance in Man (McKusick in *Mendelian Inheritance in Man* (available on line through Johns Hopkins University Welch Medical Library) reveals the region of the human chromosome which contains the 5'EST (or cDNA or genomic DNA obtainable therefrom) to be a very gene rich region containing several known genes and several diseases or phenotypes for which genes have not been identified. The gene corresponding to this 5'EST (or cDNA or genomic DNA obtainable therefrom) thus becomes an immediate candidate for each of these genetic diseases.

Cells from patients with these diseases or phenotypes are isolated and expanded in culture. PCR primers from the 5'EST (or cDNA or genomic DNA obtainable therefrom) are used to screen genomic DNA, mRNA or cDNA obtained from the patients. 5'ESTs (or cDNA or genomic DNA obtainable therefrom) that are not amplified in the patients can be positively associated with a particular disease by further analysis. Alternatively, the PCR analysis may yield fragments of different lengths when the samples are derived from an individual having the phenotype associated with the disease than when the sample is derived from a healthy individual, indicating that the gene containing the 5'EST may be responsible for the genetic disease.

VI. Use of 5'EST (or cDNA or Genomic DNA Obtainable Therefrom) to Construct Vectors

The present 5'ESTs (or cDNA or genomic DNA obtainable therefrom) may also be used to construct secretion vectors capable of directing the secretion of the proteins encoded by genes therein. Such secretion vectors may facilitate the purification or enrichment of the proteins encoded by genes inserted therein by reducing the number of background proteins from which the desired protein must be purified or enriched. Exemplary secretion vectors are described in Example 57 below.

1. Construction of Secretion Vectors

EXAMPLE 57

Construction of Secretion Vectors

The secretion vectors include a promoter capable of directing gene expression in the host cell, tissue, or organism of interest. Such promoters include the Rous Sarcoma Virus promoter, the SV40 promoter, the human cytomegalovirus promoter, and other promoters familiar to those skilled in the art.

A signal sequence from a 5′ EST (or cDNAs or genomic DNAs obtainable therefrom) is operably linked to the promoter such that the mRNA transcribed from the promoter will direct the translation of the signal peptide. The host cell, tissue, or organism may be any cell, tissue, or organism which recognizes the signal peptide encoded by the signal sequence in the 5' EST (or cDNA or genomic DNA obtainable therefrom). Suitable hosts include mammalian cells, tissues or organisms, avian cells, tissues, or organisms, insect cells, tissues or organisms, or yeast.

In addition, the secretion vector contains cloning sites for inserting genes encoding the proteins which are to be secreted. The cloning sites facilitate the cloning of the insert gene in frame with the signal sequence such that a fusion protein in which the signal peptide is fused to the protein encoded by the inserted gene is expressed from the mRNA transcribed from the promoter. The signal peptide directs the extracellular secretion of the fusion protein.

The secretion vector may be DNA or RNA and may integrate into the chromosome of the host, be stably maintained as an extrachromosomal replicon in the host, be an artificial chromosome, or be transiently present in the host. Many nucleic acid backbones suitable for use as secretion vectors are known to those skilled in the art, including retroviral vectors, SV40 vectors, Bovine Papilloma Virus vectors, yeast integrating plasmids, yeast episomal plasmids, yeast artificial chromosomes, human artificial chromosomes, P element vectors, baculovirus vectors, or bacterial plasmids capable of being transiently introduced into the host.

The secretion vector may also contain a polyA signal such that the polyA signal is located downstream of the gene inserted into the secretion vector.

After the gene encoding the protein for which secretion is desired is inserted into the secretion vector, the secretion vector is introduced into the host cell, tissue, or organism using

calcium phosphate precipitation, DEAE-Dextran, electroporation, liposome-mediated transfection, viral particles or as naked DNA. The protein encoded by the inserted gene is then purified or enriched from the supernatant using conventional techniques such as ammonium sulfate precipitation, immunoprecipitation, immunochromatography, size exclusion chromatography, ion exchange chromatography, and HPLC. Alternatively, the secreted protein may be in a sufficiently enriched or pure state in the supernatant or growth media of the host to permit it to be used for its intended purpose without further enrichment.

The signal sequences may also be inserted into vectors designed for gene therapy. In such vectors, the signal sequence is operably linked to a promoter such that mRNA transcribed from the promoter encodes the signal peptide. A cloning site is located downstream of the signal sequence such that a gene encoding a protein whose secretion is desired may readily be inserted into the vector and fused to the signal sequence. The vector is introduced into an appropriate host cell. The protein expressed from the promoter is secreted extracellularly, thereby producing a therapeutic effect.

The 5′ ESTs may also be used to clone sequences located upstream of the 5′ ESTs which are capable of regulating gene expression, including promoter sequences, enhancer sequences, and other upstream sequences which influence transcription or translation levels. Once identified and cloned, these upstream regulatory sequences may be used in expression vectors designed to direct the expression of an inserted gene in a desired spatial, temporal, developmental, or quantitative fashion. Example 58 describes a method for cloning sequences upstream of the extended cDNAs or 5′ ESTs.

2. Identification of Upstream Sequences With Promoting or Regulatory Activities

EXAMPLE 58

Use of Extended cDNAs or 5′ ESTs to Clone Upstream Sequences from Genomic DNA

Sequences derived from extended cDNAs or 5′ ESTs may be used to isolate the promoters of the corresponding genes using chromosome walking techniques. In one chromosome walking technique, which utilizes the GenomeWalker™ kit available from Clontech, five complete genomic DNA samples are each digested with a different restriction

enzyme which has a 6 base recognition site and leaves a blunt end. Following digestion, oligonucleotide adapters are ligated to each end of the resulting genomic DNA fragments.

For each of the five genomic DNA libraries, a first PCR reaction is performed according to the manufacturer's instructions (which are incorporated herein by reference) using an outer adaptor primer provided in the kit and an outer gene specific primer. The gene specific primer should be selected to be specific for the extended cDNA or 5′ EST of interest and should have a melting temperature, length, and location in the extended cDNA or 5'EST which is consistent with its use in PCR reactions. Each first PCR reaction contains 5 ng of genomic DNA, 5 µl of 10X Tth reaction buffer, 0.2 mM of each dNTP, 0.2 µM each of outer adaptor primer and outer gene specific primer, 1.1 mM of $Mg(OAc)_2$, and 1 µl of the Tth polymerase 50X mix in a total volume of 50 µl. The reaction cycle for the first PCR reaction is as follows: 1 min - 94°C / 2 sec - 94°C, 3 min - 72°C (7 cycles) / 2 sec - 94°C, 3 min - 67°C (32 cycles) / 5 min - 67°C.

The product of the first PCR reaction is diluted and used as a template for a second PCR reaction according to the manufacturer's instructions using a pair of nested primers which are located internally on the amplicon resulting from the first PCR reaction. For example, 5 µl of the reaction product of the first PCR reaction mixture may be diluted 180 times. Reactions are made in a 50 µl volume having a composition identical to that of the first PCR reaction except the nested primers are used. The first nested primer is specific for the adaptor, and is provided with the GenomeWalker™ kit. The second nested primer is specific for the particular extended cDNA or 5′ EST for which the promoter is to be cloned and should have a melting temperature, length, and location in the extended cDNA or 5′ EST which is consistent with its use in PCR reactions. The reaction parameters of the second PCR reaction are as follows: 1 min - 94°C / 2 sec - 94°C, 3 min - 72°C (6 cycles) / 2 sec - 94°C, 3 min - 67°C (25 cycles) / 5 min - 67°C. The product of the second PCR reaction is purified, cloned, and sequenced using standard techniques.

Alternatively, two or more human genomic DNA libraries can be constructed by using two or more restriction enzymes. The digested genomic DNA is cloned into vectors which can be converted into single stranded, circular, or linear DNA. A biotinylated oligonucleotide comprising at least 15 nucleotides from the extended cDNA or 5′ EST

sequence is hybridized to the single stranded DNA. Hybrids between the biotinylated oligonucleotide and the single stranded DNA containing the extended cDNA or EST sequence are isolated as described in Example 29 above. Thereafter, the single stranded DNA containing the extended cDNA or EST sequence is released from the beads and converted into double stranded DNA using a primer specific for the extended cDNA or 5′ EST sequence or a primer corresponding to a sequence included in the cloning vector. The resulting double stranded DNA is transformed into bacteria. DNAs containing the 5′ EST or extended cDNA sequences are identified by colony PCR or colony hybridization.

Once the upstream genomic sequences have been cloned and sequenced as described above, prospective promoters and transcription start sites within the upstream sequences may be identified by comparing the sequences upstream of the extended cDNAs or 5′ ESTs with databases containing known transcription start sites, transcription factor binding sites, or promoter sequences.

In addition, promoters in the upstream sequences may be identified using promoter reporter vectors as described in Example.

EXAMPLE 59

Identification of Promoters in Cloned Upstream Sequences

The genomic sequences upstream of the extended cDNAs or 5′ ESTs are cloned into a suitable promoter reporter vector, such as the pSEAP-Basic, pSEAP-Enhancer, pβgal-Basic, pβgal-Enhancer, or pEGFP-1 Promoter Reporter vectors available from Clontech. Briefly, each of these promoter reporter vectors include multiple cloning sites positioned upstream of a reporter gene encoding a readily assayable protein such as secreted alkaline phosphatase, β galactosidase, or green fluorescent protein. The sequences upstream of the extended cDNAs or 5′ ESTs are inserted into the cloning sites upstream of the reporter gene in both orientations and introduced into an appropriate host cell. The level of reporter protein is assayed and compared to the level obtained from a vector which lacks an insert in the cloning site. The presence of an elevated expression level in the vector containing the insert with respect to the control vector indicates the presence of a promoter in the insert. If necessary, the upstream sequences can be cloned into vectors which contain an enhancer for

augmenting transcription levels from weak promoter sequences. A significant level of expression above that observed with the vector lacking an insert indicates that a promoter sequence is present in the inserted upstream sequence.

Appropriate host cells for the promoter reporter vectors may be chosen based on the results of the above described determination of expression patterns of the extended cDNAs and ESTs. For example, if the expression pattern analysis indicates that the mRNA corresponding to a particular extended cDNA or 5′ EST is expressed in fibroblasts, the promoter reporter vector may be introduced into a human fibroblast cell line.

Promoter sequences within the upstream genomic DNA may be further defined by constructing nested deletions in the upstream DNA using conventional techniques such as Exonuclease III digestion. The resulting deletion fragments can be inserted into the promoter reporter vector to determine whether the deletion has reduced or obliterated promoter activity. In this way, the boundaries of the promoters may be defined. If desired, potential individual regulatory sites within the promoter may be identified using site directed mutagenesis or linker scanning to obliterate potential transcription factor binding sites within the promoter individually or in combination. The effects of these mutations on transcription levels may be determined by inserting the mutations into the cloning sites in the promoter reporter vectors.

EXAMPLE 60

Cloning and Identification of Promoters

Using the method described in Example 58 above with 5′ ESTs, sequences upstream of several genes were obtained. Using the primer pairs GGG AAG ATG GAG ATA GTA TTG CCT G (SEQ ID NO:29) and CTG CCA TGT ACA TGA TAG AGA GAT TC (SEQ ID NO:30), the promoter having the internal designation P13H2 (SEQ ID NO:31) was obtained.

Using the primer pairs GTA CCA GGGG ACT GTG ACC ATT GC (SEQ ID NO:32) and CTG TGA CCA TTG CTC CCA AGA GAG (SEQ ID NO:33), the promoter having the internal designation P15B4 (SEQ ID NO:34) was obtained.

Using the primer pairs CTG GGA TGG AAG GCA CGG TA (SEQ ID NO:35) and GAG ACC ACA CAG CTA GAC AA (SEQ ID NO:36), the promoter having the internal designation P29B6 (SEQ ID NO:37) was obtained.

Figure 4 provides a schematic description of the promoters isolated and the way they are assembled with the corresponding 5' tags. The upstream sequences were screened for the presence of motifs resembling transcription factor binding sites or known transcription start sites using the computer program MatInspector release 2.0, August 1996.

Table VII describes the transcription factor binding sites present in each of these promoters. The columns labeled matrice provides the name of the MatInspector matrix used. The column labeled position provides the 5' position of the promoter site. Numeration of the sequence starts from the transcription site as determined by matching the genomic sequence with the 5' EST sequence. The column labeled "orientation" indicates the DNA strand on which the site is found, with the + strand being the coding strand as determined by matching the genomic sequence with the sequence of the 5' EST. The column labeled "score" provides the MatInspector score found for this site. The column labeled "length" provides the length of the site in nucleotides. The column labeled "sequence" provides the sequence of the site found.

Bacterial clones containing plasmids containing the promoter sequences described above described above are presently stored in the inventor's laboratories under the internal identification numbers provided above. The inserts may be recovered from the deposited materials by growing an aliquot of the appropriate bacterial clone in the appropriate medium. The plasmid DNA can then be isolated using plasmid isolation procedures familiar to those skilled in the art such as alkaline lysis minipreps or large scale alkaline lysis plasmid isolation procedures. If desired the plasmid DNA may be further enriched by centrifugation on a cesium chloride gradient, size exclusion chromatography, or anion exchange chromatography. The plasmid DNA obtained using these procedures may then be manipulated using standard cloning techniques familiar to those skilled in the art. Alternatively, a PCR can be done with primers designed at both ends of the EST insertion. The PCR product which corresponds to the 5' EST can then be manipulated using standard cloning techniques familiar to those skilled in the art.

The promoters and other regulatory sequences located upstream of the extended cDNAs or 5′ ESTs may be used to design expression vectors capable of directing the expression of an inserted gene in a desired spatial, temporal, developmental, or quantitative manner. A promoter capable of directing the desired spatial, temporal, developmental, and quantitative patterns may be selected using the results of the expression analysis described in Example 26 above. For example, if a promoter which confers a high level of expression in muscle is desired, the promoter sequence upstream of an extended cDNA or 5′ EST derived from an mRNA which is expressed at a high level in muscle, as determined by the method of Example 26, may be used in the expression vector.

Preferably, the desired promoter is placed near multiple restriction sites to facilitate the cloning of the desired insert downstream of the promoter, such that the promoter is able to drive expression of the inserted gene. The promoter may be inserted in conventional nucleic acid backbones designed for extrachromosomal replication, integration into the host chromosomes or transient expression. Suitable backbones for the present expression vectors include retroviral backbones, backbones from eukaryotic episomes such as SV40 or Bovine Papilloma Virus, backbones from bacterial episomes, or artificial chromosomes.

Preferably, the expression vectors also include a polyA signal downstream of the multiple restriction sites for directing the polyadenylation of mRNA transcribed from the gene inserted into the expression vector.

Following the identification of promoter sequences using the procedures of Examples 58-60, proteins which interact with the promoter may be identified as described in Example 61 below.

EXAMPLE 61

Identification of Proteins Which Interact with Promoter Sequences, Upstream Regulatory Sequences, or mRNA

Sequences within the promoter region which are likely to bind transcription factors may be identified by homology to known transcription factor binding sites or through conventional mutagenesis or deletion analyses of reporter plasmids containing the promoter sequence. For example, deletions may be made in a reporter plasmid containing the promoter sequence of interest operably linked to an assayable reporter gene. The reporter plasmids

carrying various deletions within the promoter region are transfected into an appropriate host cell and the effects of the deletions on expression levels is assessed. Transcription factor binding sites within the regions in which deletions reduce expression levels may be further localized using site directed mutagenesis, linker scanning analysis, or other techniques familiar to those skilled in the art.

Nucleic acids encoding proteins which interact with sequences in the promoter may be identified using one-hybrid systems such as those described in the manual accompanying the Matchmaker One-Hybrid System kit available from Clontech (Catalog No. K1603-1), the disclosure of which is incorporated herein by reference. Briefly, the Matchmaker One-hybrid system is used as follows. The target sequence for which it is desired to identify binding proteins is cloned upstream of a selectable reporter gene and integrated into the yeast genome. Preferably, multiple copies of the target sequences are inserted into the reporter plasmid in tandem. A library comprised of fusions between cDNAs to be evaluated for the ability to bind to the promoter and the activation domain of a yeast transcription factor, such as GAL4, is transformed into the yeast strain containing the integrated reporter sequence. The yeast are plated on selective media to select cells expressing the selectable marker linked to the promoter sequence. The colonies which grow on the selective media contain genes encoding proteins which bind the target sequence. The inserts in the genes encoding the fusion proteins are further characterized by sequencing. In addition, the inserts may be inserted into expression vectors or *in vitro* transcription vectors. Binding of the polypeptides encoded by the inserts to the promoter DNA may be confirmed by techniques familiar to those skilled in the art, such as gel shift analysis or DNAse protection analysis.

VII. Use of 5′ ESTs (or cDNAs or Genomic DNAs Obtainable Therefrom) in Gene Therapy

The present invention also comprises the use of 5'ESTs (or cDNA or genomic DNA obtainable therefrom) in gene therapy strategies, including antisense and triple helix strategies as described in Examples 62 and 63 below. In antisense approaches, nucleic acid sequences complementary to an mRNA are hybridized to the mRNA intracellularly, thereby blocking the expression of the protein encoded by the mRNA. The antisense sequences may prevent gene

expression through a variety of mechanisms. For example, the antisense sequences may inhibit the ability of ribosomes to translate the mRNA. Alternatively, the antisense sequences may block transport of the mRNA from the nucleus to the cytoplasm, thereby limiting the amount of mRNA available for translation. Another mechanism through which antisense sequences may inhibit gene expression is by interfering with mRNA splicing. In yet another strategy, the antisense nucleic acid may be incorporated in a ribozyme capable of specifically cleaving the target mRNA.

EXAMPLE 62

Preparation and Use of Antisense Oligonucleotides

The antisense nucleic acid molecules to be used in gene therapy may be either DNA or RNA sequences. They may comprise a sequence complementary to the sequence of the 5'EST (or cDNA or genomic DNA obtainable therefrom). The antisense nucleic acids should have a length and melting temperature sufficient to permit formation of an intracellular duplex with sufficient stability to inhibit the expression of the mRNA in the duplex. Strategies for designing antisense nucleic acids suitable for use in gene therapy are disclosed in Green *et al.*, *Ann. Rev. Biochem.* 55:569-597, 1986; and Izant and Weintraub, *Cell* **36**:1007-1015, 1984, which are hereby incorporated by reference.

In some strategies, antisense molecules are obtained from a nucleotide sequence encoding a protein by reversing the orientation of the coding region with respect to a promoter so as to transcribe the opposite strand from that which is normally transcribed in the cell. The antisense molecules may be transcribed using *in vitro* transcription systems such as those which employ T7 or SP6 polymerase to generate the transcript. Another approach involves transcription of the antisense nucleic acids *in vivo* by operably linking DNA containing the antisense sequence to a promoter in an expression vector.

Alternatively, oligonucleotides which are complementary to the strand normally transcribed in the cell may be synthesized *in vitro*. Thus, the antisense nucleic acids are complementary to the corresponding mRNA and are capable of hybridizing to the mRNA to create a duplex. In some embodiments, the antisense sequences may contain modified sugar phosphate backbones to increase stability and make them less sensitive to RNase activity.

Examples of modifications suitable for use in antisense strategies are described by Rossi *et al.*, *Pharmacol. Ther.* 50(2):245-254, 1991, which is hereby incorporated by reference.

Various types of antisense oligonucleotides complementary to the sequence of the 5'EST (or cDNA or genomic DNA obtainable therefrom) may be used. In one preferred embodiment, stable and semi-stable antisense oligonucleotides described in International Application No. PCT WO94/23026, hereby incorporated by reference, are used. In these molecules, the 3′ end or both the 3′ and 5′ ends are engaged in intramolecular hydrogen bonding between complementary base pairs. These molecules are better able to withstand exonuclease attacks and exhibit increased stability compared to conventional antisense oligonucleotides.

In another preferred embodiment, the antisense oligodeoxynucleotides against herpes simplex virus types 1 and 2 described in International Application No. WO 95/04141, hereby incorporated by reference, are used.

In yet another preferred embodiment, the covalently cross-linked antisense oligonucleotides described in International Application No. WO 96/31523, hereby incorporated by reference, are used. These double- or single-stranded oligonucleotides comprise one or more, respectively, inter- or intra-oligonucleotide covalent cross-linkages, wherein the linkage consists of an amide bond between a primary amine group of one strand and a carboxyl group of the other strand or of the same strand, respectively, the primary amine group being directly substituted in the 2' position of the strand nucleotide monosaccharide ring, and the carboxyl group being carried by an aliphatic spacer group substituted on a nucleotide or nucleotide analog of the other strand or the same strand, respectively.

The antisense oligodeoxynucleotides and oligonucleotides disclosed in International Application No. WO 92/18522, incorporated by reference, may also be used. These molecules are stable to degradation and contain at least one transcription control recognition sequence which binds to control proteins and are effective as decoys therefore. These molecules may contain "hairpin" structures, "dumbbell" structures, "modified dumbbell" structures, "cross-linked" decoy structures and "loop" structures.

In another preferred embodiment, the cyclic double-stranded oligonucleotides described in European Patent Application No. 0 572 287 A2, hereby incorporated by

reference are used. These ligated oligonucleotide "dumbbells" contain the binding site for a transcription factor and inhibit expression of the gene under control of the transcription factor by sequestering the factor.

Use of the closed antisense oligonucleotides disclosed in International Application No. WO 92/19732, hereby incorporated by reference, is also contemplated. Because these molecules have no free ends, they are more resistant to degradation by exonucleases than are conventional oligonucleotides. These oligonucleotides may be multifunctional, interacting with several regions which are not adjacent to the target mRNA.

The appropriate level of antisense nucleic acids required to inhibit gene expression may be determined using *in vitro* expression analysis. The antisense molecule may be introduced into the cells by diffusion, injection, infection, transfection or h-region-mediated import using procedures known in the art. For example, the antisense nucleic acids can be introduced into the body as a bare or naked oligonucleotide, oligonucleotide encapsulated in lipid, oligonucleotide sequence encapsidated by viral protein, or as an oligonucleotide operably linked to a promoter contained in an expression vector. The expression vector may be any of a variety of expression vectors known in the art, including retroviral or viral vectors, vectors capable of extrachromosomal replication, or integrating vectors. The vectors may be DNA or RNA.

The antisense molecules are introduced onto cell samples at a number of different concentrations preferably between 1×10^{-10}M to 1×10^{-4}M. Once the minimum concentration that can adequately control gene expression is identified, the optimized dose is translated into a dosage suitable for use *in vivo*. For example, an inhibiting concentration in culture of 1×10^{-7} translates into a dose of approximately 0.6 mg/kg bodyweight. Levels of oligonucleotide approaching 100 mg/kg bodyweight or higher may be possible after testing the toxicity of the oligonucleotide in laboratory animals. It is additionally contemplated that cells from the vertebrate are removed, treated with the antisense oligonucleotide, and reintroduced into the vertebrate.

It is further contemplated that the antisense oligonucleotide sequence is incorporated into a ribozyme sequence to enable the antisense to specifically bind and cleave its target mRNA. For technical applications of ribozyme and antisense oligonucleotides see Rossi *et al.*, *supra*.

In a preferred application of this invention, the polypeptide encoded by the gene is first identified, so that the effectiveness of antisense inhibition on translation can be monitored using techniques that include but are not limited to antibody-mediated tests such as RIAs and ELISA, functional assays, or radiolabeling.

The 5′ ESTs of the present invention (or cDNAs or genomic DNAs obtainable therefrom) may also be used in gene therapy approaches based on intracellular triple helix formation. Triple helix oligonucleotides are used to inhibit transcription from a genome. They are particularly useful for studying alterations in cell activity as it is associated with a particular gene. The 5′ EST sequences (or cDNAs or genomic DNAs obtainable therefrom) of the present invention or, more preferably, a portion of those sequences, can be used to inhibit gene expression in individuals having diseases associated with expression of a particular gene. Similarly, a portion of 5′ EST sequences (or cDNAs or genomic DNAs obtainable therefrom) can be used to study the effect of inhibiting transcription of a particular gene within a cell. Traditionally, homopurine sequences were considered the most useful for triple helix strategies. However, homopyrimidine sequences can also inhibit gene expression. Such homopyrimidine oligonucleotides bind to the major groove at homopurine:homopyrimidine sequences. Thus, both types of sequences from the 5'EST or from the gene corresponding to the 5'EST are contemplated within the scope of this invention.

EXAMPLE 63

Preparation and Use of Triple Helix Probes

The sequences of the 5′ ESTs (or cDNAs or genomic DNAs obtainable therefrom) are scanned to identify 10-mer to 20-mer homopyrimidine or homopurine stretches which could be used in triple-helix based strategies for inhibiting gene expression. Following identification of candidate homopyrimidine or homopurine stretches, their efficiency in inhibiting gene expression is assessed by introducing varying amounts of oligonucleotides containing the candidate sequences into tissue culture cells which normally express the target gene. The oligonucleotides may be prepared on an oligonucleotide synthesizer or they may be purchased commercially from a company specializing in custom oligonucleotide synthesis, such as GENSET, Paris, France.

The oligonucleotides may be introduced into the cells using a variety of methods known to those skilled in the art, including but not limited to calcium phosphate precipitation, DEAE-Dextran, electroporation, liposome-mediated transfection or native uptake.

Treated cells are monitored for altered cell function or reduced gene expression using techniques such as Northern blotting, RNase protection assays, or PCR based strategies to monitor the transcription levels of the target gene in cells which have been treated with the oligonucleotide. The cell functions to be monitored are predicted based upon the homologies of the target gene corresponding to the extended cDNA from which the oligonucleotide was derived with known gene sequences that have been associated with a particular function. The cell functions can also be predicted based on the presence of abnormal physiologies within cells derived from individuals with a particular inherited disease, particularly when the extended cDNA is associated with the disease using techniques described in Example 56.

The oligonucleotides which are effective in inhibiting gene expression in tissue culture cells may then be introduced *in vivo* using the techniques described above and in Example 62 at a dosage calculated based on the *in vitro* results, as described in Example 62.

In some embodiments, the natural (beta) anomers of the oligonucleotide units can be replaced with alpha anomers to render the oligonucleotide more resistant to nucleases. Further, an intercalating agent such as ethidium bromide, or the like, can be attached to the 3′ end of the alpha oligonucleotide to stabilize the triple helix. For information on the generation of oligonucleotides suitable for triple helix formation see Griffin *et al.*, *Science* 245:967-971, 1989, which is hereby incorporated by this reference.

EXAMPLE 64

Use of cDNAs Obtained Using the 5′ ESTs to Express an Encoded Protein in a Host Organism

The cDNAs obtained as described above using the 5′ ESTs of the present invention may also be used to express an encoded protein in a host organism to produce a beneficial effect. In such procedures, the encoded protein may be transiently expressed in the host organism or stably expressed in the host organism. The encoded protein may have any of the activities described above. The encoded protein may be a protein which the host organism

lacks or, alternatively, the encoded protein may augment the existing levels of the protein in the host organism.

A full length extended cDNA encoding the signal peptide and the mature protein, or an extended cDNA encoding only the mature protein is introduced into the host organism. The extended cDNA may be introduced into the host organism using a variety of techniques known to those of skill in the art. For example, the extended cDNA may be injected into the host organism as naked DNA such that the encoded protein is expressed in the host organism, thereby producing a beneficial effect.

Alternatively, the extended cDNA may be cloned into an expression vector downstream of a promoter which is active in the host organism. The expression vector may be any of the expression vectors designed for use in gene therapy, including viral or retroviral vectors. The expression vector may be directly introduced into the host organism such that the encoded protein is expressed in the host organism to produce a beneficial effect. In another approach, the expression vector may be introduced into cells *in vitro*. Cells containing the expression vector are thereafter selected and introduced into the host organism, where they express the encoded protein to produce a beneficial effect.

EXAMPLE 65

Use of Signal Peptides Encoded by 5' ESTs or Sequences obtained Therefrom to Import Proteins Into Cells

The short core hydrophobic region (h) of signal peptides encoded by the 5'ESTS or extended cDNAs derived from SEQ ID NOs: 38-270 may also be used as a carrier to import a peptide or a protein of interest, so-called cargo, into tissue culture cells (Lin *et al.*, *J. Biol. Chem.*, **270**: 14225-14258, 1995; Du *et al.*, *J. Peptide Res.*, **51**: 235-243, 1998; Rojas *et al.*, *Nature Biotech.*, **16**: 370-375, 1998).

When cell permeable peptides of limited size (approximately up to 25 amino acids) are to be translocated across cell membrane, chemical synthesis may be used in order to add the h region to either the C-terminus or the N-terminus to the cargo peptide of interest. Alternatively, when longer peptides or proteins are to be imported into cells, nucleic acids can be genetically engineered, using techniques familiar to those skilled in the art, in order to link the extended cDNA sequence encoding the h region to the 5' or the 3' end of a DNA

sequence-coding for a cargo polypeptide. Such genetically engineered nucleic acids are then translated either *in vitro* or *in vivo* after transfection into appropriate cells, using conventional techniques to produce the resulting cell permeable polypeptide. Suitable hosts cells are then simply incubated with the cell permeable polypeptide which is then translocated across the membrane.

This method may be applied to study diverse intracellular functions and cellular processes. For instance, it has been used to probe functionally relevant domains of intracellular proteins and to examine protein-protein interactions involved in signal transduction pathways (Lin *et al., supra*; Lin *et al., J. Biol. Chem.*, 271: 5305-5308, 1996; Rojas *et al., J. Biol. Chem.*, 271: 27456-27461, 1996; Liu *et al., Proc. Natl. Acad. Sci. USA*, 93: 11819-11824, 1996; Rojas *et al., Bioch. Biophys. Res. Commun.*, 234: 675-680, 1997).

Such techniques may be used in cellular therapy to import proteins producing therapeutic effects. For instance, cells isolated from a patient may be treated with imported therapeutic proteins and then re-introduced into the host organism.

Alternatively, the h region of signal peptides of the present invention could be used in combination with a nuclear localization signal to deliver nucleic acids into cell nucleus. Such oligonucleotides may be antisense oligonucleotides or oligonucleotides designed to form triple helixes, as described in examples 62 and 63 respectively, in order to inhibit processing and/or maturation of a target cellular RNA.

As discussed above, the cDNAs or portions thereof obtained using the 5′ ESTs of the present invention can be used for various purposes. The polynucleotides can be used to express recombinant protein for analysis, characterization or therapeutic use; as markers for tissues in which the corresponding protein is preferentially expressed (either constitutively or at a particular stage of tissue differentiation or development or in disease states); as molecular weight markers on Southern gels; as chromosome markers or tags (when labeled) to identify chromosomes or to map related gene positions; to compare with endogenous DNA sequences in patients to identify potential genetic disorders; as probes to hybridize and thus discover novel, related DNA sequences; as a source of information to derive PCR primers for genetic fingerprinting; for selecting and making oligomers for attachment to a "gene chip" or other support, including for examination for expression patterns; to raise anti-protein

antibodies using DNA immunization techniques; and as an antigen to raise anti-DNA antibodies or elicit another immune response. Where the polynucleotide encodes a protein which binds or potentially binds to another protein (such as, for example, in a receptor-ligand interaction), the polynucleotide can also be used in interaction trap assays (such as, for example, that described in Gyuris *et al.*, *Cell* 75:791-803, 1993, the disclosure of which is hereby incorporated by reference) to identify polynucleotides encoding the other protein with which binding occurs or to identify inhibitors of the binding interaction.

The proteins or polypeptides provided by the present invention can similarly be used in assays to determine biological activity, including in a panel of multiple proteins for high-throughput screening; to raise antibodies or to elicit another immune response; as a reagent (including the labeled reagent) in assays designed to quantitatively determine levels of the protein (or its receptor) in biological fluids; as markers for tissues in which the corresponding protein is preferentially expressed (either constitutively or at a particular stage of tissue differentiation or development or in a disease state); and, of course, to isolate correlative receptors or ligands. Where the protein binds or potentially binds to another protein (such as, for example, in a receptor-ligand interaction), the protein can be used to identify the other protein with which binding occurs or to identify inhibitors of the binding interaction. Proteins involved in these binding interactions can also be used to screen for peptide or small molecule inhibitors or agonists of the binding interaction.

Any or all of these research utilities are capable of being developed into reagent grade or kit format for commercialization as research products.

Methods for performing the uses listed above are well known to those skilled in the art. References disclosing such methods include without limitation *Molecular Cloning; A Laboratory Manual*, 2d ed., Cold Spring Harbor Laboratory Press, Sambrook,. Fritsch and Maniatis eds., 1989, and *Methods in Enzymology; Guide to Molecular Cloning Techniques*, Academic Press, Berger and Kimmel eds., 1987.

Polynucleotides and proteins of the present invention can also be used as nutritional sources or supplements. Such uses include without limitation use as a protein or amino acid supplement, use as a carbon source, use as a nitrogen source and use as a source of carbohydrate. In such cases the protein or polynucleotide of the invention can be added to the feed of a particular organism or can be administered as a separate solid or liquid

preparation, such as in the form of powder, pills, solutions, suspensions or capsules. In the case of microorganisms, the protein or polynucleotide of the invention can be added to the medium in or on which the microorganism is cultured.

Although this invention has been described in terms of certain preferred embodiments, other embodiments which will be apparent to those of ordinary skill in the art in view of the disclosure herein are also within the scope of this invention. Accordingly, the scope of the invention is intended to be defined only by reference to the appended claims. All documents cited herein are incorporated herein by reference in their entirety.

	Search characteristic		Selection Characteristics		
Step	Program	Strand	Parameters	Identity (%)	Length (bp)
miscellanaeous	blastn	both	S=61 X=16	90	17
tRNA	fasta	both	-	80	60
rRNA	blastn	both	S=108	80	40
mtRNA	blastn	both	S=108	80	40
Procaryotic	blastn	both	S=144	90	40
Fungal	blastn	both	S=144	90	40
Alu	fasta*	both	-	70	40
L1	blastn	both	S=72	70	40
Repeats	blastn	both	S=72	70	40
Promoters	blastn	top	S=54 X=16	90	15†
Vertebrate	fasta*	both	S=108	90	30
ESTs	blastn	both	S=108 X=16	90	30
Proteins	blastx¤	top	E = 0.001	-	-

Table 1: Parameters used for each step of EST analysis

* use "Quick Fast" Database scanner
† alignement further constrained to begin closer than 10bp to EST\5' end
¤ using BLOSUM62 substitution matrix

TABLE II

SEQ. ID NO.	CATEGORY	VON HEIJNE SCORE	TISSUE SOURCE	INTERNAL DESIGNATION
ID38	new	13.2	Testis	51-39-3-H2-PU
ID39	new	12	Testis	51-34-3-F8-PU
ID40	new	11	Testis	51-43-1-C5-PU
ID41	new	10.6	Testis	51-2-4-C4-PU
ID42	new	10.4	Ovary	26-49-1-A5-PU
ID43	new	10.1	Testis	51-3-3-B10-PU
ID44	new	9.8	Testis	51-15-4-A12-PU
ID45	new	9.8	Testis	51-14-1-G6-PU
ID46	new	9.5	Spleen	53-1-4-A1-PU
ID47	new	9.4	Ovary	26-40-1-A11-PU
ID48	new	9.4	Testis	51-19-4-A10-PU
ID49	new	9.2	Ovary	26-25-2-D2-PU
ID50	new	9.2	Testis	51-17-2-C6-PU
ID51	new	9.2	Ovary	26-40-3-A6-PU
ID52	new	9.1	Ovary	26-49-1-A9-PU
ID53	new	9.1	Spleen	20-7-2-D6-PU
ID54	new	9.1	Testis	51-2-1-A11-PU
ID55	new	9	Testis	51-43-3-G3-PU
ID56	new	8.9	Ovary	26-47-2-B1-PU
ID57	new	8.8	Ovary	26-11-1-G8-PU
ID58	new	8.8	Testis	51-37-4-E11-PU
ID59	new	8.7	Ovary	26-25-2-G1-PU
ID60	new	8.5	Testis	51-13-1-F7-PU
ID61	new	8.4	Spleen	20-2-1-D7-PU
ID62	new	8.1	Ovary	26-12-2-B5-PU
ID63	new	8	Testis	51-1-1-G12-PU
ID64	new	7.6	Spleen	20-8-2-F3-PU
ID65	new	7.5	Spleen	20-10-3-D4-PU
ID66	new	7.5	Spleen	20-3-3-G4-PU
ID67	new	7.5	Testis	51-10-3-B6-PU
ID68	new	7.5	Ovary	26-27-3-E8-PU
ID69	new	7.4	Testis	51-44-4-A6-PU
ID70	new	7.3	Testis	51-7-2-A6-PU
ID71	new	7.3	Ovary	26-31-1-D11-PU
ID72	new	7.1	Testis	51-28-2-G1-PU
ID73	new	6.9	Spleen	20-10-1-B12-PU
ID74	new	6.9	Testis	51-39-1-A5-PU
ID75	new	6.9	Ovary	26-23-2-A11-PU
ID76	new	6.9	Testis	51-1-4-C5-PU
ID77	new	6.8	Spleen	53-2-4-D8-PU
ID78	new	6.8	Spleen	20-3-2-C11-PU
ID79	new	6.8	Testis	51-29-4-B4-PU
ID80	new	6.8	Ovary	26-27-3-E11-PU
ID81	new	6.6	Ovary	26-10-1-H8-PU
ID82	new	6.5	Testis	51-18-2-G10-PU
ID83	new	6.5	Spleen	20-2-1-H12-PU
ID84	new	6.4	Testis	51-10-3-G3-PU
ID85	new	6.4	Uterus	74-9-4-H2-PU
ID86	new	6.4	Ovary	26-23-3-G2-PU
ID87	new	6.4	Testis	51-2-4-F5-PU
ID88	new	6.4	Uterus	74-4-3-C4-PU

SEQ. ID NO.	CATEGORY	VON HEIJNE SCORE	TISSUE SOURCE	INTERNAL DESIGNATION
ID89	new	6.3	Testis	51-31-3-D1-PU
ID90	new	6.3	Spleen	20-5-1-H1-PU
ID91	new	6.2	Ovary	26-41-1-G3-PU
ID92	new	6.2	Uterus	74-11-4-G3-PU
ID93	new	6.1	Ovary	26-4-4-E9-PU
ID94	new	6.1	Spleen	20-2-3-C2-PU
ID95	new	6.1	Ovary	26-48-1-A9-PU
ID96	new	6	Spleen	20-1-2-C7-PU
ID97	new	6	Ovary	26-28-4-H1-PU
ID98	new	6	Uterus	74-8-4-C11-PU
ID99	new	6	Ovary	26-6-3-B9-PU
ID100	new	5.9	Testis	51-16-4-B10-PU
ID101	new	5.9	Testis	51-47-3-F9-PU
ID102	new	5.9	Testis	51-4-2-D10-PU
ID103	new	5.9	Ovary	26-10-4-D9-PU
ID104	new	5.8	Testis	51-18-1-C3-PU
ID105	new	5.8	Ovary	26-45-2-C4-PU
ID106	new	5.7	Ovary	26-26-3-D7-PU
ID107	new	5.7	Ovary	26-5-3-A8-PU
ID108	new	5.7	Ovary	26-47-1-C6-PU
ID109	new	5.6	Testis	51-19-1-F10-PU
ID110	new	5.6	Testis	51-11-4-G10-PU
ID111	new	5.5	Testis	51-39-3-F7-PU
ID112	new	5.5	Testis	51-2-1-E10-PU
ID113	new	5.4	Testis	51-26-2-F5-PU
ID114	new	5.4	Ovary	26-2-2-G10-PU
ID115	new	5.4	Testis	51-35-4-G9-PU
ID116	new	5.4	Ovary	26-39-1-A6-PU
ID117	new	5.3	Ovary	26-47-1-E2-PU
ID118	new	5.3	Testis	51-26-2-C7-PU
ID119	new	5.2	Uterus	74-11-3-F8-PU
ID120	new	5.2	Spleen	53-3-1-E2-PU
ID121	new	5.2	Testis	51-31-3-G12-PU
ID122	new	5.1	Spleen	20-6-4-G5-PU
ID123	new	5.1	Uterus	74-6-3-F1-PU
ID124	new	5.1	Uterus	74-11-1-F8-PU
ID125	new	5.1	Ovary	26-7-4-B3-PU
ID126	new	5	Ovary	26-5-3-F10-PU
ID127	new	5	Ovary	26-49-3-C2-PU
ID128	new	5	Testis	51-29-3-E1-PU
ID129	new	5	Ovary	26-26-3-D2-PU
ID130	new	5	Uterus	74-9-4-B4-PU
ID131	new	5	Testis	51-1-3-E9-PU
ID132	new	4.9	Ovary	26-5-1-C6-PU
ID133	new	4.9	Ovary	26-3-1-H5-PU
ID134	new	4.9	Ovary	26-51-4-D9-PU
ID135	new	4.9	Ovary	26-27-3-D7-PU
ID136	new	4.8	Uterus	74-3-4-D8-PU
ID137	new	4.8	Ovary	26-29-1-E1-PU
ID138	new	4.8	Spleen	20-3-1-H3-PU
ID139	new	4.8	Testis	51-3-3-D8-PU
ID140	new	4.8	Spleen	20-5-3-D9-PU
ID141	new	4.7	Testis	51-44-4-H4-PU

SEQ. ID NO.	CATEGORY	VON HEIJNE SCORE	TISSUE SOURCE	INTERNAL DESIGNATION
ID142	new	4.7	Testis	51-5-4-G12-PU
ID143	new	4.7	Spleen	20-9-2-F7-PU
ID144	new	4.7	Spleen	53-3-2-A10-PU
ID145	new	4.6	Ovary	26-30-4-C1-PU
ID146	new	4.6	Testis	51-29-3-H6-PU
ID147	new	4.6	Testis	51-5-3-G2-PU
ID148	new	4.6	Testis	51-11-3-D5-PU
ID149	new	4.6	Testis	51-7-1-E7-PU
ID150	new	4.6	Testis	51-27-1-G12-PU
ID151	new	4.6	Uterus	74-4-1-F5-PU
ID152	new	4.5	Ovary	26-24-1-F8-PU
ID153	new	4.5	Spleen	20-7-3-F6-PU
ID154	new	4.5	Ovary	26-1-2-A8-PU
ID155	new	4.4	Testis	51-1-3-H9-PU
ID156	new	4.4	Testis	51-27-1-E8-PU
ID157	new	4.3	Testis	51-44-4-B2-PU
ID158	new	4.3	Ovary	26-44-1-C3-PU
ID159	new	4.3	Spleen	20-4-2-E2-PU
ID160	new	4.3	Testis	51-19-4-F5-PU
ID161	new	4.3	Spleen	20-8-4-D7-PU
ID162	new	4.3	Testis	51-24-1-B11-PU
ID163	new	4.3	Spleen	20-6-2-G10-PU
ID164	new	4.2	Testis	51-6-4-F8-PU
ID165	new	4.2	Testis	51-36-2-A9-PU
ID166	new	4.2	Ovary	26-7-3-H10-PU
ID167	new	4.2	Testis	51-1-3-D9-PU
ID168	new	4.2	Spleen	20-2-1-B11-PU
ID169	new	4.2	Uterus	74-6-4-A5-PU
ID170	new	4.2	Testis	51-14-3-F3-PU
ID171	new	4.1	Ovary	26-33-3-E2-PU
ID172	new	4	Testis	51-26-4-C7-PU
ID173	new	4	Testis	51-25-3-F3-PU
ID174	new	4	Ovary	26-8-3-D5-PU
ID175	new	4	Testis	51-42-3-F9-PU
ID176	new	4	Ovary	26-27-1-C5-PU
ID177	new	4	Ovary	26-1-1-G2-PU
ID178	new	3.9	Ovary	26-8-3-H3-PU
ID179	new	3.9	Ovary	26-40-2-A9-PU
ID180	new	3.9	Ovary	26-24-4-A5-PU
ID181	new	3.9	Uterus	74-5-3-B12-PU
ID182	new	3.8	Testis	51-37-2-G12-PU
ID183	new	3.8	Spleen	20-8-2-E7-PU
ID184	new	3.8	Testis	51-2-1-H9-PU
ID185	new	3.8	Ovary	26-46-4-D12-PU
ID186	new	3.8	Ovary	26-40-1-A12-PU
ID187	new	3.7	Testis	51-3-4-E2-PU
ID188	new	3.7	Ovary	26-47-3-G12-PU
ID189	new	3.7	Ovary	26-2-4-E12-PU
ID190	new	3.7	Uterus	74-4-4-D6-PU
ID191	new	3.7	Testis	51-36-4-A3-PU
ID192	new	3.7	Uterus	74-11-1-B8-PU
ID193	new	3.7	Spleen	20-10-2-G2-PU
ID194	new	3.7	Testis	51-37-4-D6-PU

SEQ. ID NO.	CATEGORY	VON HEIJNE SCORE	TISSUE SOURCE	INTERNAL DESIGNATION
ID195	new	3.6	Ovary	26-27-4-G9-PU
ID196	new	3.6	Testis	51-2-3-A6-PU
ID197	new	3.6	Ovary	26-24-2-A3-PU
ID198	new	3.6	Uterus	74-3-3-F6-PU
ID199	new	3.5	Spleen	20-10-2-B2-PU
ID200	new	3.5	Testis	51-13-2-G2-PU
ID201	new	3.5	Testis	51-17-4-A4-PU
ID202	new	3.5	Spleen	20-10-3-E5-PU
ID203	new	3.5	Testis	51-30-1-B6-PU
ID204	new	3.5	Ovary	26-40-2-G12-PU
ID205	new	3.5	Ovary	26-9-3-G4-PU
ID206	ext-est-not-vrt	12.7	Testis	51-18-4-A4-PU
ID207	ext-est-not-vrt	7.4	Ovary	26-44-1-B5-PU
ID208	ext-est-not-vrt	7.3	Testis	51-20-1-A2-PU
ID209	ext-est-not-vrt	7.1	Ovary	26-2-1-A12-PU
ID210	ext-est-not-vrt	6.7	Testis	51-2-1-A7-PU
ID211	ext-est-not-vrt	5.6	Spleen	53-1-1-C10-PU
ID212	ext-est-not-vrt	5.6	Uterus	74-10-1-B10-PU
ID213	ext-est-not-vrt	5.3	Testis	51-31-4-A1-PU
ID214	ext-est-not-vrt	4.4	Testis	51-25-1-A2-PU
ID215	ext-est-not-vrt	4.1	Testis	51-35-2-F8-PU
ID216	ext-est-not-vrt	3.9	Testis	51-8-3-E7-PU
ID217	ext-est-not-vrt	3.9	Testis	51-34-2-H6-PU
ID218	ext-est-not-vrt	3.5	Uterus	74-7-2-F11-PU
ID219	est-not-ext	10.5	Testis	51-18-1-G7-PU
ID220	est-not-ext	9.5	Testis	51-23-1-G1-PU
ID221	est-not-ext	8.3	Ovary	26-8-1-B12-PU
ID222	est-not-ext	8.3	Testis	51-41-1-F10-PU
ID223	est-not-ext	8.2	Ovary	26-12-1-A2-PU
ID224	est-not-ext	8.1	Spleen	53-3-3-B8-PU
ID225	est-not-ext	8	Testis	51-4-4-A12-PU
ID226	est-not-ext	7.8	Testis	51-18-1-H7-PU
ID227	est-not-ext	7.6	Spleen	20-6-4-G3-PU
ID228	est-not-ext	7.5	Testis	51-2-3-F10-PU
ID229	est-not-ext	7.1	Testis	51-7-2-C2-PU
ID230	est-not-ext	7.1	Testis	51-6-4-F9-PU
ID231	est-not-ext	6.5	Spleen	20-6-1-D11-PU
ID232	est-not-ext	6.4	Ovary	26-26-1-A11-PU
ID233	est-not-ext	6.4	Testis	51-9-3-A12-PU
ID234	est-not-ext	6.2	Ovary	26-8-3-F5-PU
ID235	est-not-ext	6.1	Ovary	26-27-2-A12-PU
ID236	est-not-ext	6	Uterus	74-11-3-H4-PU
ID237	est-not-ext	5.8	Ovary	26-51-2-G10-PU
ID238	est-not-ext	5.8	Testis	51-23-1-G2-PU
ID239	est-not-ext	5.7	Uterus	74-1-2-H1-PU
ID240	est-not-ext	5.7	Testis	51-9-1-E7-PU
ID241	est-not-ext	5.3	Testis	51-1-4-E9-PU
ID242	est-not-ext	4.8	Testis	51-6-4-G2-PU
ID243	est-not-ext	4.8	Spleen	20-2-1-C5-PU
ID244	est-not-ext	4.7	Testis	51-23-1-H2-PU
ID245	est-not-ext	4.6	Testis	51-19-3-H6-PU
ID246	est-not-ext	4.6	Testis	51-10-3-D11-PU
ID247	est-not-ext	4.6	Testis	51-20-2-G7-PU

SEQ. ID NO.	CATEGORY	VON HEIJNE SCORE	TISSUE SOURCE	INTERNAL DESIGNATION
ID248	est-not-ext	4.6	Ovary	26-38-4-C2-PU
ID249	est-not-ext	4.5	Ovary	26-44-3-C5-PU
ID250	est-not-ext	4.4	Ovary	26-47-4-H1-PU
ID251	est-not-ext	4.4	Spleen	20-5-2-C3-PU
ID252	est-not-ext	4.3	Testis	51-21-3-B10-PU
ID253	est-not-ext	4.3	Spleen	20-4-4-B3-PU
ID254	est-not-ext	4.2	Ovary	26-5-1-F8-PU
ID255	est-not-ext	4.1	Testis	51-22-3-B10-PU
ID256	est-not-ext	4.1	Testis	51-18-1-G1-PU
ID257	est-not-ext	4.1	Testis	51-12-2-H4-PU
ID258	est-not-ext	3.9	Testis	51-25-1-A12-PU
ID259	est-not-ext	3.8	Spleen	20-2-1-B4-PU
ID260	est-not-ext	3.8	Spleen	20-7-2-A6-PU
ID261	est-not-ext	3.8	Ovary	26-27-4-D3-PU
ID262	est-not-ext	3.8	Ovary	26-5-4-F9-PU
ID263	est-not-ext	3.8	Uterus	74-3-1-B9-PU
ID264	est-not-ext	3.7	Spleen	20-8-4-A11-PU
ID265	est-not-ext	3.6	Testis	51-15-4-G10-PU
ID266	est-not-ext	3.6	Testis	51-2-1-A10-PU
ID267	est-not-ext	3.5	Spleen	53-1-1-A10-PU
ID268	est-not-ext	3.5	Testis	51-15-4-H10-PU
ID269	ext-vrt-not-genomic	8.1	Ovary	26-36-1-D11-PU
ID270	ext-vrt-not-genomic	4	Testis	51-39-2-D9-PU

TABLE III

SEQ. ID NO.	SIGNAL PEPTIDE
ID38	MGEASPPAPARRHLLVLLLLLSTLVIPSAA
ID39	MAPQTLLPVLVLCVLLLQAQG
ID40	MWTLKSSLVLLLCLTCSYA
ID41	MLPLLLLPLLWGGSLQ
ID42	METGALRRPQLLPLLLLLCGPSQDQC
ID43	MERLVLTLCTLPLAVA
ID44	MMLPQWLLLLFLLFFFLFLLTRG
ID45	MKPVLPLQXLVVFCLALQLVPG
ID46	MFRQRQETAQRSTQSCRCPRDGLFFSLFSAPLASA
ID47	MGSSACEIAVGTKRLLLALPLALVLG
ID48	MSNQRLPLIFSLLFICFFGESFC
ID49	MLWFLSFLLALLSLNC
ID50	MLXISLEIXSFICCVIVLISLSWT
ID51	MVFRNCILFILTFFSHTFC
ID52	MLAACPLSPGCQS
ID53	MAWSPLFLTLITHCTVSWA
ID54	MLKSVLVSLCSWSPPLTS
ID55	MTSKXILVSFILAALSLSTTFS
ID56	MKSLSLXLAVXLGLATAVSA
ID57	MWAMESGHLLWALLFMQSLWP
ID58	MAQTWAXLLVMGSLPSASWS
ID59	MKCGFLAYLLITLLYVWPVINA
ID60	MRKPAAGFLPSLLKVLLLPLAPAAA
ID61	MRQSLLFLTSVVPFVLA
ID62	MELSQMSELMGLSVLLGLLALMATA
ID63	MQDAPLSCLSPTKWSSVSSADSTEKSASAAGTRNLPFQFCLRQALRMKAAGILTLIGCLV TGVES
ID64	MALAFCLCMAEAILLFSPEHSLFFFCSRKARIRLHWAGQTLAILCAALGLGFIISSRTRS ELPHLVSWHSWVGALTLLATAVQALCGLCLLCPRAA
ID65	MLRFPTCFPSXRVXGXKQLPQEIIXLVWSPXRDXIXLANTAGEVLLHRLASFHRVWS
ID66	MFMVLEVVVSRVTSSLAMLSDSFHMLSDVLALVVALVAERFA
ID67	MENQLWHNTVRCCNQYQESPHDAEDILLLLLGLIVLVNI
ID68	MLSXKITLLTLSPNSVCC
ID69	MEGPRGWLVLCVLAISLA
ID70	MKSLLFTLAVFMLLAQLVSG
ID71	MLKLILLFSLLISIVC
ID72	MTPWCLACLGRRPLASLQWSLTLAWC
ID73	MTMRHNWTPDLSPLWVLLLCAHVVTL
ID74	MTGNNRDLFCATLSCMPATS
ID75	MTMRHNWTPDLSPLWVLLLCAHVVTL
ID76	MKPLLETLYLLGMLVPGGLG
ID77	MNQADPRLRAVCLWTLTSAAMSRGDNCTDLLALGIPSITQAWGLWVLLGAVTLLFLISLA AHLSQ
ID78	MHRQISFLLLRKPRKNWFCQNHVNLRKRYLLSILSSLTMVIC
ID79	MKQWLCWVLRLEGRQGLGVGEPRGLRLCLGALSAXTFVSFLHA
ID80	MRLGLCFWVPHRGEMSFSSHYSRGTWYQWDLSLLMLTLISWFRWCLPAVSTVELLFFLFP ILFIRS
ID81	MDFWEEYRRGDVPFSWCPIRSYLMSVCPVTGKVNLNHLVKVASARFLHQVTIFPFLYSVK ANYCFLNFDVPQYAWEIHSFAAPSILIVIIIVITITSACSA
ID82	MSTSSSSSWDNLLESLSLSTVWNWIQA
ID83	MVFATIGFSLKSGLALGSAGLLWCLA

SEQ. ID NO.	SIGNAL PEPTIDE
ID84	MVLLLSGSVSVGVC
ID85	MCSQKRAVSNQGLMDLGLCXLCXVXNVFA
ID86	MLIVLTLHSPSCDT
ID87	MTRLCLPRPEAREDPIPVPPRGLGAGEGSGSPVRPPVSTWGPSWAQLLDSVLWLGALGLTIQ
ID88	MVLTCLFLSLISTYP
ID89	MLIPVFSFSLQLLSSSST
ID90	MAAAXLSGPSAGSAAGVPGGTGGLSAVSSGPRLRLLLLESVSGLLQP
ID91	MHNWLFLFVFTFCNC
ID92	MHVECFYFLSTALGSQA
ID93	MSPGSALALLWSLPASDLG
ID94	MALALGSIPSSIA
ID95	MLAFLFCTLFSLVVHP
ID96	MAQMPLTGSYQDLEYFLECMFLHLLYTLQTISSLSG
ID97	MALLMGLWVRTVLQG
ID98	MINHLYLAILIXSLKLTIG
ID99	MGRQGTLEIEGILCVITWLEANLGKQKDENHYYKKLSLLYLCSFPLPGTS
ID100	MELTNKQTGTDRHEQVLRRVKQDKRISAWWCVLLEWSQG
ID101	MAKRQNPTSVLGLLFSISDTWA
ID102	MNVLPFSYYYILFCLSLQIFRVSLA
ID103	MKCLKVNPFLFLVFNFFSYISXFLSPVCG
ID104	MSWTVPVVRASQRVSSVGANXLCLGMALCPRQA
ID105	MGFLXLMTLTTHVHS
ID106	MLFRVLLLAQLFLGSG
ID107	MRVPEDLASKILLPGCAPGSLPLSTSAPPLRG
ID108	MFPHXETQVKCFWQGLRRSDLCLCQCILARA
ID109	MKSLLFTLAVFMXLAQLVSG
ID110	MHLYSCSCMRLLNVACCIPFSSS
ID111	MRAPLVLSPLSYQCSS
ID112	MQVPHLRVWTQVXDTFIGYRNLGFTSMCILFHCLLS
ID113	MQKLMAVPMITRAQGGDTCTRQILWLMHQSFQKSNS
ID114	MCXAGFXDHPRAARHARTSRHPLPWVCVSQXPAHRSLCLWPACLC
ID115	MTSKFILVSFILAALSLS
ID116	MHLLIFILTVHHTPS
ID117	MLSSSLMVQLISQVYS
ID118-	MFSYILCMLFCLFS
ID119	MLFLYYVTLAFSLLVLSES
ID120	MLLSGLWLSSVKEC
ID121	MVAFSVFCFSWLMSSSSP
ID122	MVPLALGIGPPGCLQG
ID123	MNLCMGVLLKVGTSRRCLCLLWFCTAMRPGGA
ID124	MSLAKSLFLRVARG
ID125	MRLPPFLPSATLLLSAES
ID126	MSDRKRTKFSYVQLPCPISLLPRSFKRGQIPGPSAPPLLLLLREELVTG
ID127	MTPLGSGPPREASIAQVRGFSRTFFRVAFCFFPAFLVXVXS
ID128	MRCSALFPLLSLLSC
ID129	MLYDQYYLIISLLKLCSFCFI
ID130	MANCFLSHKSQTILISKPALTQSHFTSPAGLFLTVEKSHLLTRLFFHWLSLVLCSFLSLRFCTLS
ID131	MHGAGLTYLLFLPDWAAV
ID132	MCCLSATLAFSGSFL
ID133	MAELDLMAPGPLPRATAQPPAPLSPDSGLRGLLLQEALG
ID134	MTLTHGNNILHLANFFLVACPLFGVCLX
ID135	MVLRWLPWPRGSHS
ID136	MKARLSGNLICFSFLGTLFHKSNS

SEQ. ID NO.	SIGNAL PEPTIDE
ID137	MSHVCLVPQTPSLCLG
ID138	MYPASFVFKIPSTAYVVLTSVNLFIGING
ID139	MSSSRKDHLGAXAQSPSRSSLWVTAPLVSA
ID140	MASPAAATYLVQSSACCPA
ID141	MNAAINTGPAPAVTKTETEVQNPDVLWDLDIPEARSHADQDSNPXAEALLPCNLHXSWLHS
ID142	MINLLVGNCIYLLGAIRASCMCRXMSFAKFGIFLVIFCSESFS
ID143	MLCCGPLRFLLRDPGCLLA
ID144	MRKTSFILLRMTVLPTLWT
ID145	MWWKPAPEEGVRVGLVLVXRALC
ID146	MFNFLLGNSSCVYQ
ID147	MKRGAFSNLNDSQLSASFLQPSLQANCPALDPAVSLSAPAFA
ID148	MKSAKLGFLLRFFIFCSLNTLLLG
ID149	MDILFPLHSVIGSHP
ID150	MLKVFRAXHPKICHFGILILLSQRQWS
ID151	MLVRNARRGSRGRSPWWRAGCLXWRKLAASWTLS
ID152	MTKGHHHQHPLHPHPLFTLGLGYPIPTRL
ID153	MTYHXIQFSERLHILFIVCLARG
ID154	MSQFPLCSPPWKPLVKVSRNLKIRMSIPWPLSVLIYCGLSQPLTLG
ID155	MFRSLTTAFFRDAMGFLLMFDLTSQ
ID156	MVLTTLPLPSANSPVNMPTTGPNSLSYASSALSPCLX
ID157	MQRNATFIHLQLAIRPSLLPTLPWLPSTRL
ID158	MNILFCFHSFHPLFQ
ID159	MLTNRNYFNFLFLVQLCILA
ID160	MKLNPGQVPTWWEALCRFVGMQPCTA
ID161	MLAGFRRSAPASQSLCLNLCPCSSSLL
ID162	MKEGASFYLLFFLNDVPP
ID163	MGLECCCPPHNLRVYIETLLLKLSSQSRT
ID164	MQLCPFTSVLSIAASLLQCRL
ID165	MDVTCCFDAVEGSDFRVCCHGCVSWLCLQMLQLLFKLNSTWCRA
ID166	MRQGPGAPLHCFCFTLFSYSSS
ID167	MHITLLGIWLTXRLQ
ID168	MLYGSWVCLLSAGTAFE
ID169	MLFFPLLSFRFLPSESLLKXXXXFLLGRRVVG
ID170	MPVWAILGCWGTLSRG
ID171	MGMSGKKHFPLSWDHIQGSTEATSQGILCGSLPGPSLC
ID172	MASKILLNVQEEVTCPICLELLTEPLSLDCGHSLCRA
ID173	MYYMVCLFFRLIFS
ID174	MGAGGXREIRAAAASWLRAAEHSKLAGLWSPGLVPA
ID175	MGSKCCKGGPDEDAVERQRRQKLLLAQLHHRKRVKAAGQIQAWWRGVLVRRTLLVAA LRA
ID176	MQQGHPHLSAGTLSIHSWQLLTSAQP
ID177	MSRYEXGSSLLPFPDHFSVYSFKXXSFFEAYSISDYATCCLSLFQWCAV
ID178	MIYFIKINNKLLLLHHYLLLFITT
ID179	MELLYLKVKRGQKDLSWALCLSQSGYY
ID180	MTLAVTLSALGATG
ID181	MLGPPLQPGSHGKVLAPQGSSGLTPPFPCRCLITLPRSCRP
ID182	MGNVCSCCLRARYQQLXLILVHFPAYS
ID183	MLYGLGSGPRCVISCIHGVWC
ID184	MHRIMTLLHLKALQQLQNKIHVPRMLPGPVTPLDSCPPSAHS
ID185	MLFLVLFYSAIFL
ID186	MVSLCVAALFPLQA
ID187	MSSNLFYIPSILTLLLA
ID188	MGLLRKCFPVMLGGNTHIQITCIKQFILCLGTCRG

SEQ. ID NO.	SIGNAL PEPTIDE
ID189	MMLPLFCSPWESGG
ID190	MAKLLSDLSVDSARC
ID191	MCGYWVCWGHLLPARVST
ID192	MKLSCAGCADTAILGLSTFLNLLS
ID193	MIPFSGTVFSLGSCPAGPLSA
ID194	MIPSSQPRFXNPACKQTVLLXDPAVSLSAPAFASA
ID195	MAPTFLLISDSFLTS
ID196	MISLIVLSLLGIKIQWCLS
ID197	MACDSFLKDALPQELSQLXFLFPLVDMREDLLYFNTFLPRKVA
ID198	MLLLNENLKAEIQKNEAQGSCILFLFCFESQNMRSKSIFPFLILHFFPQQIRK
ID199	MISKYVHYSLTDLLLPFTFLSLKAFL
ID200	MARTMGVPRACKAFCSLLSSFCALHFG
ID201	MILCFLLPHHRLQEA
ID202	MQDYVSHAVRRHCQCFFVCFSPKIYG
ID203	MEFAHAAECVSFALNETHVLLNLALSHFNNC
ID204	MGNQGFPYLSPSLSVQDLLAASWLPRDAPC
ID205	MKYQMVSGSAQLASPLLPGATP
ID206	MGPSTPLLILFLLSWSGPLQG
ID207	MASLGHILVFCVGLLTMAKA
ID208	MSGSSLPSALALSLLLVSGSLLP
ID209	MMEVVVGNGVVALRGIPPRTSRKSSRKTRFCGERGSKQSGKCSPVGLAVVSLGGSRG
ID210	MARCFSLVLLLTSIWT
ID211	MGSRKCGGCLSCLLIPLALWS
ID212	MGSRKCGGCLSCLLIPLALWS
ID213	MMVMILFGVSFVFLTHC
ID214	MSNTHTVLVSLPHPHPALT
ID215	MXVYRLQTQEKPNTTVQVPAFLQELVDRDNSKFEEWCIEMAEMRXKVWIKEKQNTKRLRS CTKGYLLELSPMSLSLWNGCKSGWMNQQXPNLLITLACVPMTSFT
ID216	MFPVLGWILIAVVIIILLIFT
ID217	MFSCCISVCLCPCLNKGQS
ID218	MRLCLIMYCSFGTLSHLTYLLLLSPIKYP
ID219	MGKGMVAMLILGLLLLALLLPVQVSS
ID220	MGSSGLLSLLVLFVLLANVQG
ID221	MVLGGCPVSYLLLCGQAALLLGNLLLLHCVSRSHS
ID222	METGRLLSLSSLPLVLLG
ID223	MAASLGQVLALVLVAALWG
ID224	MHIKSIILEGFKSYAQRTEVNGFDPLFNAITGLNGSGKSNILDSICFLLGISNLSQVRA
ID225	MSPSPRWGFLCVLFTAVHP
ID226	MCSLLYPLVTFFLLCLCIAYWAST
ID227	MLPFLFFSTLFSSIFT
ID228	MVALNLILVPCCAA
ID229	MAARGVIAPVGESLRYAEYLQPSAKRPDADVDQQRLVRSLIAVGLGVAALAFA
ID230	MIKLKLLSLLRPSLC
ID231	MPSVNSAGLCVLQLTTAVTS
ID232	MMLGLHFALFLLVSXYMIRS
ID233	MALLLSVLRVLLG
ID234	MLKSLWLSLVAWHWGEA
ID235	MGIVTWLLXSFMSSA
ID236	MAGIKALISLSFGGAIGLMFLMLGCALP
ID237	MKKQKHQKLWCISVKLVTLSVPTSLA
ID238	MDGIPMSMKNEMPISQLLMIIAPSLGFVLFALFVAFLLRG
ID239	MGGFLHLPALSSSCLWTFPPMCVRIFSYVPLPILTPKTINLIPVLAICSCLPGPGPA
ID240	MSPSPRWGFLCVLFTAVHP

SEQ. ID NO.	SIGNAL PEPTIDE
ID241	MTSQPVPNETIIVLPSNVINFSQAEKPEPTNQGQDSLKKHLHAEXKVIGTIQILCGMMVL SLGIILASASFSPNFT
ID242	MRALENDFFNSPPRKTVRFGGTVTEVLLKYKKGETNDFELLKNQLLDPDIKDDQIINWLL EFRSSVMYLTKDFEQLISIILRLPWLNRSQT
ID243	MVFPAKRFCLVPSMEGVRWAFSCGTWLPSRA
ID244	MNCFQGTNASALEKDIGPEQFPINEHYFGLVNFGNTCYCNSVLQALYSCRPFRENVLAYK AQQKKKENLLTCLADLFHSIAT
ID245	MAAALRVRXXXFGTRA
ID246	MKLLTHNLLSSHVRG
ID247	MGXFSRRTFCGRSGRSCRGQLVQVSRPEVSAGSLLLPAPQA
ID248	MEGGVRLDLSACGETSGVAVSELPASETAALVPEGHGPGLRACALSLPDAPGASG
ID249	MTLLSFAALTAAFS
ID250	MAAATGDPGLSKLQFAPFSSA
ID251	MFTSTGSSGLYKAPLSKSLLLVPSXLS
ID252	MTSMTQSLREVIKAMTKARNFERVLGKITLVSAAPGKVIC
ID253	MADFGISAGQFVAVVWDKSSPVEALKGLVDKLQALTGNEGRVSVENIKQLLQSAHKESSX DIILSGLVPGSTT
ID254	MGILLGLLLLGHLT
ID255	MFLTVKLLLGQRCSLKVSG
ID256	MNVIDHVRDMAAAGLHSNVRLLSSLLLTMSNN
ID257	MGTPSLSILLIGAPESPIPYFPYHSGTGRVLCPLLXAAAAP
ID258	MVYHALDSPDDDYHALFVLCLLYAMS
ID259	MFIVLSMWLCCGFE
ID260	MVVVILSSXVPLAAM
ID261	MLAECSSLLHPSVRG
ID262	MQMARLLGLCAWARK
ID263	MTPQYLPHGGKYQVLGDYSLAVVFPLHFSDLISVLYLIPKTLT
ID264	MVVLRAGKKTFLPPLXRAFACRG
ID265	MKREGGAAHLCSDSLPESQQ
ID266	MVTCPGPSSGQPLSSMYTAGDRRGAPSLPYSLAACPCGSQG
ID267	MQRQLALEVIVTLSETAA
ID268	MGDYLLRGYRMLGETCADCGTILLQDKQRKIYCVACQELDSDVDKDNPALNAQAALSQAR EHQLASASELPLGSRP
ID269	MWLLYLLVPALFCRA
ID270	MKLEFTEKNXXSFVLQNLNRQRKRKEYWDMALSVDNHVFFAHRNVLAAVSPLVRSLIS

Minimum signal peptide score	false positive rate	false negative rate	proba(0.1)	proba(0.2)
3.5	0.121	0.036	0.467	0.664
4	0.096	0.06	0.519	0.708
4.5	0.078	0.079	0.565	0.745
5	0.062	0.098	0.615	0.782
5.5	0.05	0.127	0.659	0.813
6	0.04	0.163	0.694	0.836
6.5	0.033	0.202	0.725	0.855
7	0.025	0.248	0.763	0.878
7.5	0.021	0.304	0.78	0.889
8	0.015	0.368	0.816	0.909
8.5	0.012	0.418	0.836	0.92
9	0.009	0.512	0.856	0.93
9.5	0.007	0.581	0.863	0.934
10	0.006	0.679	0.835	0.919

TABLE IV

Minimum signal peptide score	All ESTs	New ESTs	ESTs matching public EST closer than 40 bp from beginning	ESTs extending known mRNA more than 40 bp	ESTs extending public EST more than 40 bp
3.5	2674	947	599	23	150
4	2278	784	499	23	126
4.5	1943	647	425	22	112
5	1657	523	353	21	96
5.5	1417	419	307	19	80
6	1190	340	238	18	68
6.5	1035	280	186	18	60
7	893	219	161	15	48
7.5	753	173	132	12	36
8	636	133	101	11	29
8.5	543	104	83	8	26
9	456	81	63	6	24
9.5	364	57	48	6	18
10	303	47	35	6	15

TABLE V

Tissue	All ESTs	New ESTs	ESTs matching public EST closer than 40 bp from beginning	ESTs extending known mRNA more than 40 bp	ESTs extending public EST more than 40 bp
Brain	329	131	75	3	24
Cancerous prostate	134	40	37	1	6
Cerebellum	17	9	1	0	6
Colon	21	11	4	0	0
Dystrophic muscle	41	18	8	0	1
Fetal brain	70	37	16	0	1
Fetal kidney	227	116	46	1	19
Fetal liver	13	7	2	0	0
Heart	30	15	7	0	1
Hypertrophic prostate	86	23	22	2	2
Kidney	10	7	3	0	0
Large intestine	21	8	4	0	1
Liver	23	9	6	0	0
Lung	24	12	4	0	1
Lung (cells)	57	38	6	0	4
Lymph ganglia	163	60	23	2	12
Lymphocytes	23	6	4	0	2
Muscle	33	16	6	0	4
Normal prostate	181	61	45	7	11
Ovary	90	57	12	1	2
Pancreas	48	11	6	0	1
Placenta	24	5	1	0	0
Prostate	34	16	4	0	2
Spleen	56	28	10	0	1
Substantia nigra	108	47	27	1	6
Surrenals	15	3	3	1	0
Testis	131	68	25	1	8
Thyroid	17	8	2	0	2
Umbilical cord	55	17	12	1	3
Uterus	28	15	3	0	2
Non tissue-specific	568	48	177	2	28
Total	2677	947	601	23	150

TABLE VI

Description of Transcription Factor Binding Sites present on promoters isolated from SignalTag sequences

Promoter sequence P13H2 (546 bp):

Matrix	Position	Orientation	Score	Length	Sequence
CMYB_01	-502	+	0.983	9	TGTCAGTTG
MYOD_Q6	-501	-	0.961	10	CCCAACTGAC
S8_01	-444	-	0.960	11	AATAGAATTAG
S8_01	-425	+	0.966	11	AACTAAATTAG
DELTAEF1_01	-390	-	0.960	11	GCACACCTCAG
GATA_C	-364	-	0.964	11	AGATAAATCCA
CMYB_01	-349	+	0.958	9	CTTCAGTTG
GATA1_02	-343	+	0.959	14	TTGTAGATAGGACA
GATA_C	-339	+	0.953	11	AGATAGGACAT
TAL1ALPHAE47_01	-235	+	0.973	16	CATAACAGATGGTAAG
TAL1BETAE47_01	-235	+	0.983	16	CATAACAGATGGTAAG
TAL1BETAITF2_01	-235	+	0.978	16	CATAACAGATGGTAAG
MYOD_Q6	-232	-	0.954	10	ACCATCTGTT
GATA1_04	-217	-	0.953	13	TCAAGATAAAGTA
IK1_01	-126	+	0.963	13	AGTTGGGAATTCC
IK2_01	-126	+	0.985	12	AGTTGGGAATTC
CREL_01	-123	+	0.962	10	TGGGAATTCC
GATA1_02	-96	+	0.950	14	TCAGTGATATGGCA
SRY_02	-41	-	0.951	12	TAAAACAAAACA
E2F_02	-33	+	0.957	8	TTTAGCGC
MZF1_01	-5	-	0.975	8	TGAGGGGA

Promoter sequence P15B4 (861bp) :

Matrix	Position	Orientation	Score	Length	Sequence
NFY_Q6	-748	-	0.956	11	GGACCAATCAT
MZF1_01	-738	+	0.962	8	CCTGGGGA
CMYB_01	-684	+	0.994	9	TGACCGTTG
VMYB_02	-682	-	0.985	9	TCCAACGGT
STAT_01	-673	+	0.968	9	TTCCTGGAA
STAT_01	-673	-	0.951	9	TTCCAGGAA
MZF1_01	-556	-	0.956	8	TTGGGGGA
IK2_01	-451	+	0.965	12	GAATGGGATTTC
MZF1_01	-424	+	0.986	8	AGAGGGGA
SRY_02	-398	-	0.955	12	GAAAACAAAACA
MZF1_01	-216	+	0.960	8	GAAGGGGA
MYOD_Q6	-190	+	0.981	10	AGCATCTGCC
DELTAEF1_01	-176	+	0.958	11	TCCCACCTTCC
S8_01	5	-	0.992	11	GAGGCAATTAT
MZF1_01	16	-	0.986	8	AGAGGGGA

Promoter sequence P29B6 (555 bp) :

Matrix	Position	Orientation	Score	Length	Sequence
ARNT_01	-311	+	0.964	16	GGACTCACGTGCTGCT
NMYC_01	-309	+	0.965	12	ACTCACGTGCTG
USF_01	-309	+	0.985	12	ACTCACGTGCTG
USF_01	-309	-	0.985	12	CAGCACGTGAGT
NMYC_01	-309	-	0.956	12	CAGCACGTGAGT
MYCMAX_02	-309	-	0.972	12	CAGCACGTGAGT
USF_C	-307	+	0.997	8	TCACGTGC
USF_C	-307	-	0.991	8	GCACGTGA
MZF1_01	-292	-	0.968	8	CATGGGGA
ELK1_02	-105	+	0.963	14	CTCTCCGGAAGCCT
CETS1P54_01	-102	+	0.974	10	TCCGGAAGCC
AP1_Q4	-42	-	0.963	11	AGTGACTGAAC
AP1FJ_Q2	-42	-	0.961	11	AGTGACTGAAC
PADS_C	45	+	1.000	9	TGTGGTCTC

TABLE VII

CLAIMS

1. A purified or isolated nucleic acid comprising the sequence of one of SEQ ID NOs: 38-270 or comprising a sequence complementary thereto.

2. The nucleic acid of Claim 1, wherein said nucleic acid is recombinant.

3. A purified or isolated nucleic acid comprising at least 10 consecutive bases of the sequence of one of SEQ ID NOs: 38-270 or one of the sequences complementary thereto.

4. A purified or isolated nucleic acid comprising at least 15 consecutive bases of one of the sequences of SEQ ID NOs: 38-270 or one of the sequences complementary thereto.

5. The nucleic acid of Claim 4, wherein said nucleic acid is recombinant.

6. A purified or isolated nucleic acid of at least 15 bases capable of hybridizing under stringent conditions to the sequence of one of SEQ ID NOs: 38-270 or one of the sequences complementary to the sequences of SEQ ID NOs: 38-270.

7. The nucleic acid of Claim 6, wherein said nucleic acid is recombinant.

8. A purified or isolated nucleic acid encoding a human gene product, said human gene product having a sequence partially encoded by one of the sequences of SEQ ID NO: 38-270.

9. A purified or isolated nucleic acid having the sequence of one of SEQ ID NOs: 38-270 or having a sequence complementary thereto.

10. A purified or isolated nucleic acid comprising the nucleotides of one of SEQ ID NOs: 38-270 which encode a signal peptide.

11. A purified or isolated polypeptides comprising a signal peptide encoded by one of the sequences of SEQ ID NOs: 38-270.

12. A vector encoding a fusion protein comprising a polypeptide and a signal peptide, said vector comprising a first nucleic acid encoding a signal peptide encoded by one of the sequences of SEQ ID NOs: 38-270 operably linked to a second nucleic acid encoding a polypeptide.

13. A method of directing the extracellular secretion of a polypeptide or the insertion of a polypetide into the membrane comprising the steps of:

obtaining a vector according to Claim 12; and

introducing said vector into a host cell such that said fusion protein is secreted into the extracellular environment of said host cell or inserted into the membrane of said host cell.

14. A method of importing a polypeptide into a cell comprising contacting said cell with a fusion protein comprising a signal peptide encoded by one of the sequences of SEQ ID NOs: 38-270 operably linked to said polypeptide.

15. A method of making a cDNA encoding a human secretory protein that is partially encoded by one of SEQ ID NOs 38-270, comprising the steps of:

obtaining a cDNA comprising one of the sequences of SEQ ID NOs: 38-270;

contacting said cDNA with a detectable probe comprising at least 15 consecutive nucleotides of said sequence of SEQ ID NO: 38-270 or a sequence complementary thereto under conditions which permit said probe to hybridize to said cDNA;

identifying a cDNA which hybridizes to said detectable probe; and

isolating said cDNA which hybridizes to said probe.

16. An isolated or purified cDNA encoding a human secretory protein, said human secretory protein comprising the protein encoded by one of SEQ ID NOs 38-270 or a fragment thereof of at least 10 amino acids, said cDNA being obtainable by the method of Claim 15.

17. The cDNA of Claim 16 wherein said cDNA comprises the full protein coding sequence partially included in one of the sequences of SEQ ID NOs: 38-270.

18. A method of making a cDNA comprising one of the sequences of SEQ ID NOs: 38-270, comprising the steps of:

contacting a collection of mRNA molecules from human cells with a first primer capable of hybridizing to the polyA tail of said mRNA;

hybridizing said first primer to said polyA tail;

reverse transcribing said mRNA to make a first cDNA strand;

making a second cDNA strand complementary to said first cDNA strand using at least one primer comprising at least 15 nucleotides of one of the sequences of SEQ ID NOs 38-270; and

isolating the resulting cDNA comprising said first cDNA strand and said second cDNA strand.

19. An isolated or purified cDNA encoding a human secretory protein, said human secretory protein comprising the protein encoded by one of SEQ ID NOs 38-270 or a fragment thereof of at least 10 amino acids, said cDNA being obtainable by the method of Claim 18.

20. The cDNA of Claim 19 wherein said cDNA comprises the full protein coding sequence partially included in one of the sequences of SEQ ID NOs: 38-270.

21. The method of Claim 18, wherein the second cDNA strand is made by:

contacting said first cDNA strand with a first pair of primers, said first pair of primers comprising a second primer comprising at least 15 consecutive nucleotides of one of the sequences of SEQ ID NOs 38-270 and a third primer having a sequence therein which is included within the sequence of said first primer;

performing a first polymerase chain reaction with said first pair of nested primers to generate a first PCR product;

contacting said first PCR product with a second pair of primers, said second pair of primers comprising a fourth primer, said fourth primer comprising at least 15 consecutive nucleotides of said sequence of one of SEQ ID NO:s 38-270 , and a fifth primer, said fourth and fifth primers being capable of hybridizing to sequences within said first PCR product; and

performing a second polymerase chain reaction, thereby generating a second PCR product.

22. An isolated or purified cDNA encoding a human secretory protein, said human secretory protein comprising the protein encoded by one of SEQ ID NOs 38-270, or a fragment thereof of at least 10 amino acids, said cDNA being obtainable by the method of Claim 21.

23. The cDNA of Claim 22 wherein said cDNA comprises the full protein coding sequence partially included in one of the sequences of SEQ ID NOs: 38-270.

24. The method of Claim 18 wherein the second cDNA strand is made by:

contacting said first cDNA strand with a second primer comprising at least 15 consecutive nucleotides of the sequences of SEQ ID NOs: 38-270;

hybridizing said second primer to said first strand cDNA; and

extending said hybridized second primer to generate said second cDNA strand.

25. An isolated or purified cDNA encoding a human secretory protein, said human secretory protein comprising the protein partially encoded by one of SEQ ID NOs 38-270 or comprising a fragment thereof of at least 10 amino acids, said cDNA being obtainable by the method of Claim 24.

26. The cDNA of Claim 25, wherein said cDNA comprises the full protein coding sequence partially included in of one of the sequences of SEQ ID NOs: 38-270.

27. A method of making a protein comprising one of the sequences of SEQ ID NO: 271-503, comprising the steps of:

obtaining a cDNA encoding the full protein sequence partially included in one of the sequences of sequence of SEQ ID NO: 38-270;

inserting said cDNA in an expression vector such that said cDNA is operably linked to a promoter;

introducing said expression vector into a host cell whereby said host cell produces the protein encoded by said cDNA; and

isolating said protein.

28. An isolated protein obtainable by the method of Claim 27.

29. A method of obtaining a promoter DNA comprising the steps of:

obtaining DNAs located upstream of the nucleic acids of SEQ ID NO: 38-270 or the sequences complementary thereto;

screening said upstream DNAs to identify a promoter capable of directing transcription initiation; and

isolating said DNA comprising said identified promoter.

30. The method of Claim 29, wherein said obtaining step comprises chromosome walking from said nucleic acids of SEQ ID NO: 38-270 or sequences complementary thereto.

31. The method of Claim 30, wherein said screening step comprises inserting said upstream sequences into a promoter reporter vector.

32. The method of Claim 30, wherein said screening step comprises identifying motifs in said upstream DNAs which are transcription factor binding sites or transcription start sites.

33. An isolated promoter obtainable by the method of Claim 32.

34. An isolated or purified protein comprising one of the sequences of SEQ ID NO: 271-503.

35. In an array of discrete ESTs or fragments thereof of at least 15 nucleotides in length, the improvement comprising inclusion in said array of at least one of the sequences of SEQ ID NOs: 38-270, or one of the sequences complementary to the sequences of SEQ ID NOs: 38-270, or a fragment thereof of at least 15 consecutive nucleotides.

36. The array of Claim 35 including therein at least two of the sequences of SEQ ID NOs: 38-270, the sequences complementary to the sequences of SEQ ID NOs: 38-270, or fragments thereof of at least 15 consecutive nucleotides.

37. The array of Claim 35 including therein at least five of the sequences of SEQ ID NOs: 38-270, the sequences complementary to the sequences of SEQ ID NOs: 38-270, or fragments thereof of at least 15 consecutive nucleotides.

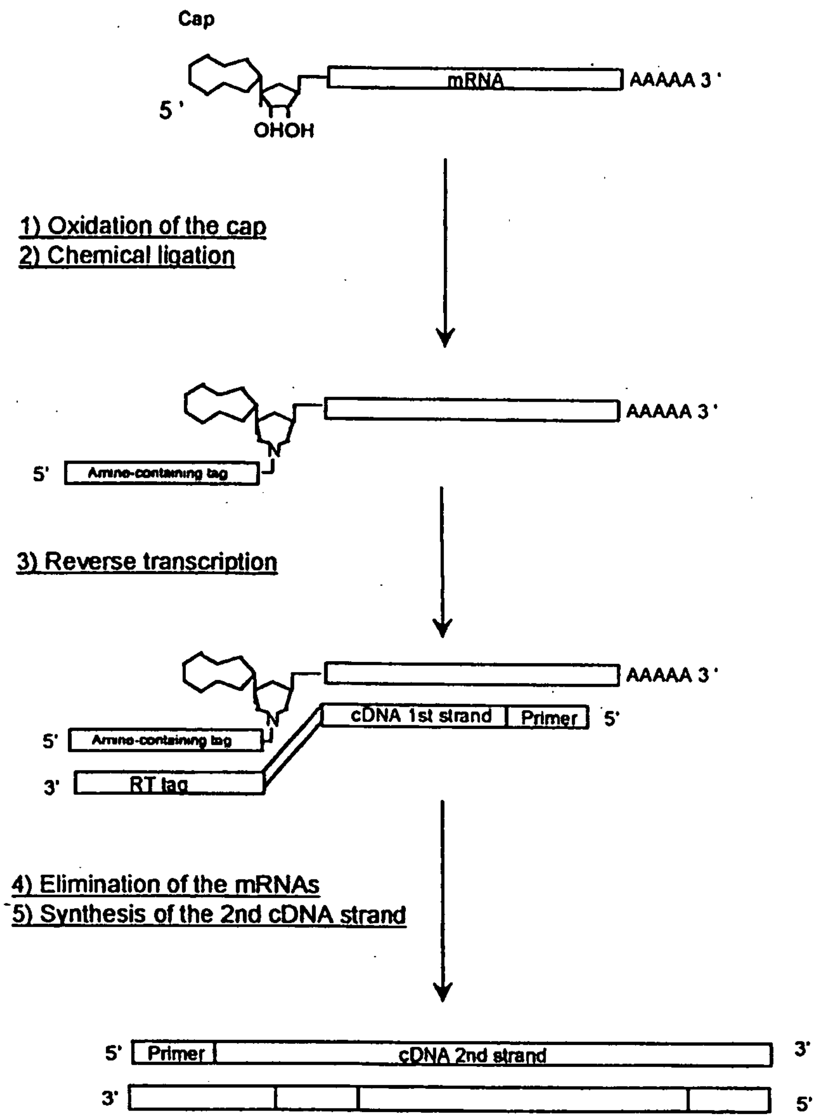
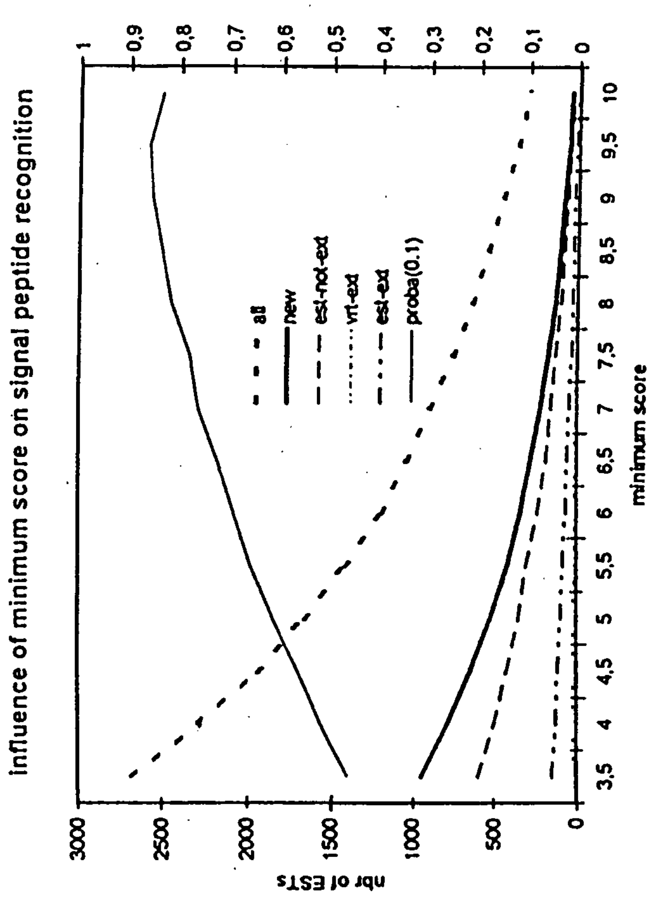

Cap
5'
mRNA
AAAAA 3'
OHOH
1) Oxidation of the cap
2) Chemical ligation
AAAAA 3'
5'
Amino-containing tag
3) Reverse transcription
AAAAA 3'
cDNA 1st strand
Primer
5'
5'
Amino-containing tag
3'
RT tag
4) Elimination of the mRNAs
5) Synthesis of the 2nd cDNA strand
5'
Primer
cDNA 2nd strand
3'
3'
5'

Figure 1



Influence of minimum score on signal peptide recognition
nbr of ESTs
minimum score
all
new
est-not-ext
vrf-ext
est-ext
proba(0.1)
3000
2500
2000
1500
1000
500
0
3,5
4
4,5
5
5,5
6
6,5
7
7,5
8
8,5
9
9,5
10
1
0,9
0,8
0,7
0,6
0,5
0,4
0,3
0,2
0,1
0

Figure 2

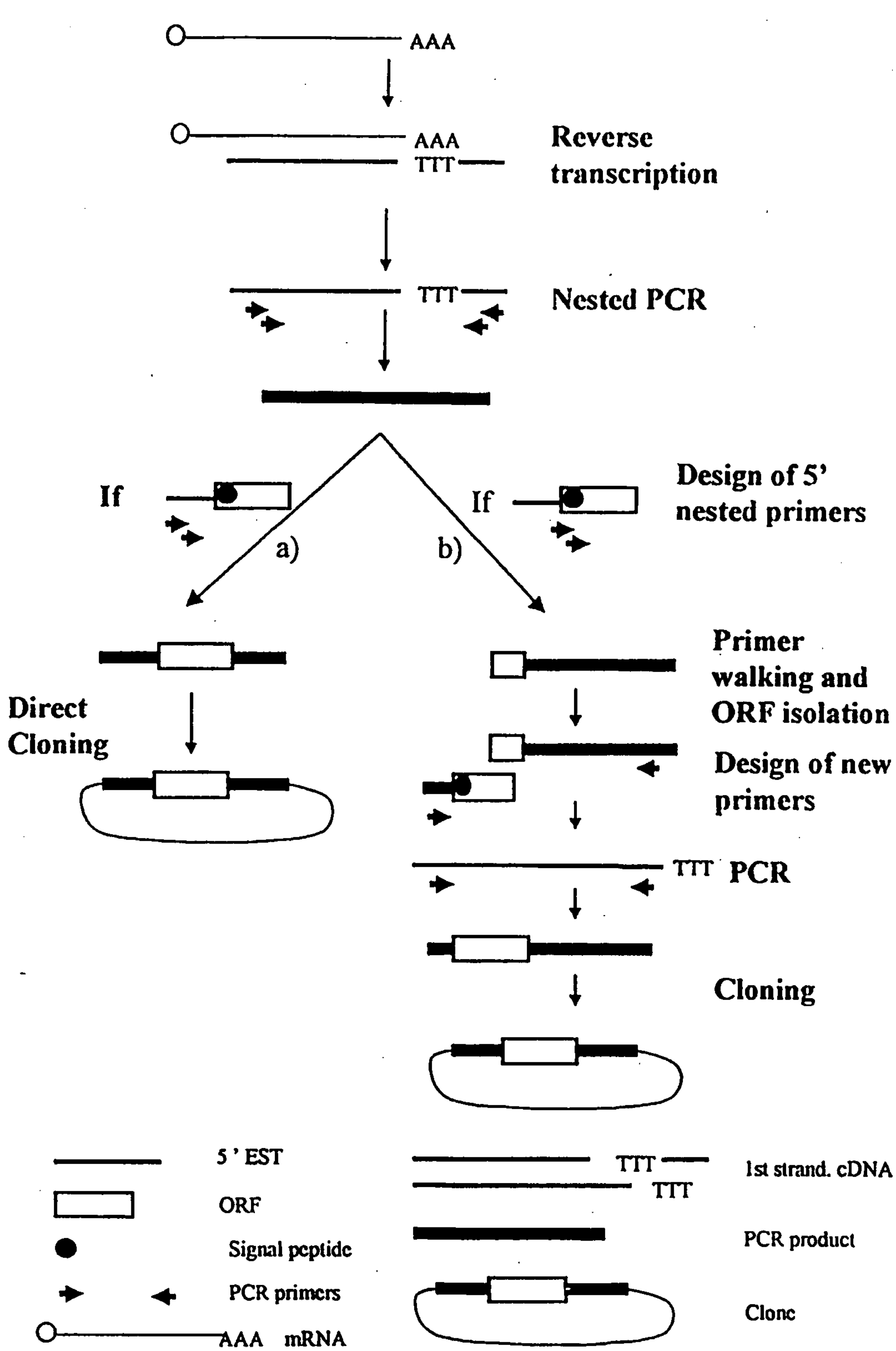

AAA
AAA
TTT
Reverse transcription
TTT
Nested PCR
If
If
Design of 5' nested primers
a)
b)
Primer walking and ORF isolation
Direct Cloning
Design of new primers
TTT
PCR
Cloning
5' EST
ORF
Signal peptide
PCR primers
AAA mRNA
TTT
TTT
1st strand. cDNA
PCR product
Clone

Figure 3

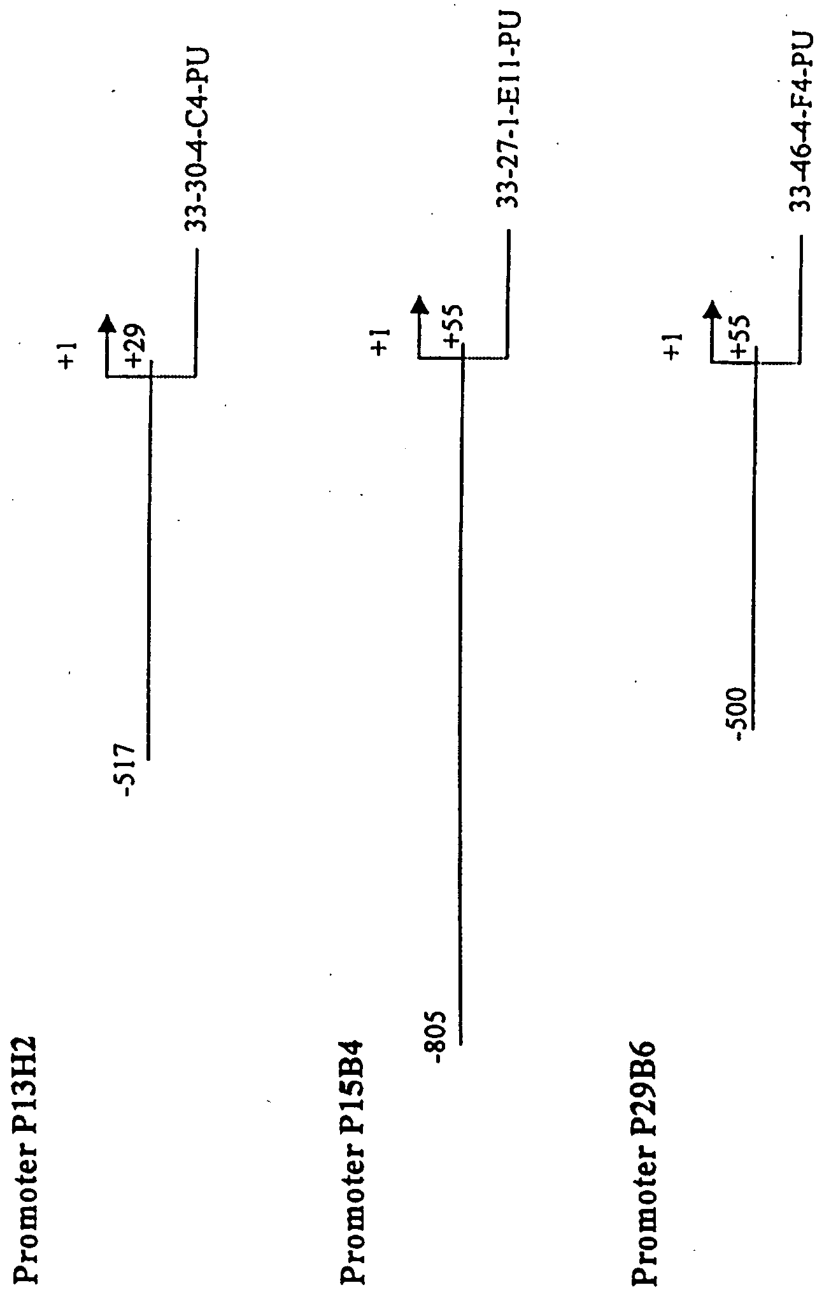

Promoter P13H2
-517
+1
+29
33-30-4-C4-PU
Promoter P15B4
-805
+1
+55
33-27-1-E11-PU
Promoter P29B6
-500
+1
+55
33-46-4-F4-PU

Figure 4

SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANT:
(A) NAME : GENSET SA
(B) STREET :24, RUE ROYALE
(C) CITY: PARIS
(E) COUNTRY : FRANCE
(F) POSTAL CODE (ZIP) : 75008

(ii) TITLE OF INVENTION: 5' ESTs FOR SECRETED PROTEINS EXPRESSED IN TESTIS AND OTHER TISSUES

(iii) NUMBER OF SEQUENCES: 503

(v) COMPUTER READABLE FORM:
(A) MEDIUM TYPE: Floppy Disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: Win95
(D) SOFTWARE: Word

(2) INFORMATION FOR SEQ ID NO: 1:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 47 base pairs
(B) TYPE: NUCLEIC ACID
(C) STRANDEDNESS: SINGLE
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: Other nucleic acid

(ix) FEATURE:
(A) NAME/KEY: Cap
(B) LOCATION: 1
(D) OTHER INFORMATION: m7Gppp added to 1

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

GGCAUCCUAC UCCCAUCCAA UUCCACCCUA ACUCCUCCCA UCUCCAC 47

(2) INFORMATION FOR SEQ ID NO: 2:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 46 base pairs
(B) TYPE: NUCLEIC ACID
(C) STRANDEDNESS: SINGLE
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: Other nucleic acid

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

GCAUCCUACU CCCAUCCAAU UCCACCCUAA CUCCUCCCAU CUCCAC 46

(2) INFORMATION FOR SEQ ID NO: 3:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 25 base pairs
(B) TYPE: NUCLEIC ACID
(C) STRANDEDNESS: SINGLE
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: Other nucleic acid

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:

ATCAAGAATT CGCACGAGAC CATTA 25

(2) INFORMATION FOR SEQ ID NO: 4:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 25 base pairs
(B) TYPE: NUCLEIC ACID
(C) STRANDEDNESS: SINGLE
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: Other nucleic acid

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:

TAATGGTCTC GTGCGAATTC TTGAT 25

(2) INFORMATION FOR SEQ ID NO: 5:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 25 base pairs
(B) TYPE: NUCLEIC ACID
(C) STRANDEDNESS: SINGLE
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: Other nucleic acid

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:

CCGACAAGAC CAACGTCAAG GCCGC 25

(2) INFORMATION FOR SEQ ID NO: 6:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 25 base pairs
(B) TYPE: NUCLEIC ACID
(C) STRANDEDNESS: SINGLE
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: Other nucleic acid

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:

TCACCAGCAG GCAGTGGCTT AGGAG 25

(2) INFORMATION FOR SEQ ID NO: 7:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 25 base pairs
(B) TYPE: NUCLEIC ACID
(C) STRANDEDNESS: SINGLE
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: Other nucleic acid

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:

AGTGATTCCT GCTACTTTGG ATGGC 25

(2) INFORMATION FOR SEQ ID NO: 8:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 25 base pairs
(B) TYPE: NUCLEIC ACID
(C) STRANDEDNESS: SINGLE
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: Other nucleic acid

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 8:

GCTTGGTCTT GTTCTGGAGT TTAGA 25

(2) INFORMATION FOR SEQ ID NO: 9:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 25 base pairs
(B) TYPE: NUCLEIC ACID
(C) STRANDEDNESS: SINGLE
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: Other nucleic acid

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 9:

TCCAGAATGG GAGACAAGCC AATTT 25

(2) INFORMATION FOR SEQ ID NO: 10:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 25 base pairs
(B) TYPE: NUCLEIC ACID
(C) STRANDEDNESS: SINGLE
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: Other nucleic acid

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 10:

AGGGAGGAGG AAACAGCGTG AGTCC 25

(2) INFORMATION FOR SEQ ID NO: 11:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 25 base pairs
(B) TYPE: NUCLEIC ACID
(C) STRANDEDNESS: SINGLE
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: Other nucleic acid

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 11:

ATGGGAAAGG AAAAGACTCA TATCA 25

(2) INFORMATION FOR SEQ ID NO: 12:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 25 base pairs
(B) TYPE: NUCLEIC ACID
(C) STRANDEDNESS: SINGLE
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: Other nucleic acid

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 12:

AGCAGCAACA ATCAGGACAG CACAG 25

(2) INFORMATION FOR SEQ ID NO: 13:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 25 base pairs
(B) TYPE: NUCLEIC ACID
(C) STRANDEDNESS: SINGLE
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: Other nucleic acid

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 13:

ATCAAGAATT CGCACGAGAC CATTA 25

(2) INFORMATION FOR SEQ ID NO: 14:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 67 base pairs
(B) TYPE: NUCLEIC ACID
(C) STRANDEDNESS: SINGLE
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: Other nucleic acid

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 14:

ATCGTTGAGA CTCGTACCAG CAGAGTCACG AGAGAGACTA CACGGTACTG GTTTTTTTTT 60

TTTTTVN 67

(2) INFORMATION FOR SEQ ID NO: 15:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 29 base pairs
(B) TYPE: NUCLEIC ACID
(C) STRANDEDNESS: SINGLE
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: Other nucleic acid

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 15:

CCAGCAGAGT CACGAGAGAG ACTACACGG 29

(2) INFORMATION FOR SEQ ID NO: 16:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 25 base pairs
(B) TYPE: NUCLEIC ACID
(C) STRANDEDNESS: SINGLE
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: Other nucleic acid

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 16:

CACGAGAGAG ACTACACGGT ACTGG 25

(2) INFORMATION FOR SEQ ID NO: 17:

(i) SEQUENCE CHARACTERISTICS:
    (A) LENGTH: 526 base pairs
    (B) TYPE: NUCLEIC ACID
    (C) STRANDEDNESS: DOUBLE
    (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:
    (A) ORGANISM: Homo Sapiens
    (F) TISSUE TYPE: Lymph ganglia

(ix) FEATURE:
    (A) NAME/KEY: other
    (B) LOCATION: complement(261..376)
    (C) IDENTIFICATION METHOD: blastn
    (D) OTHER INFORMATION: identity 96
        region 166..281
        id N70479
        est

(ix) FEATURE:
    (A) NAME/KEY: other
    (B) LOCATION: complement(380..486)
    (C) IDENTIFICATION METHOD: blastn
    (D) OTHER INFORMATION: identity 97
        region 54..160
        id N70479
        est

(ix) FEATURE:
    (A) NAME/KEY: other
    (B) LOCATION: complement(110..145)
    (C) IDENTIFICATION METHOD: blastn
    (D) OTHER INFORMATION: identity 94
        region 403..438
        id N70479
        est

(ix) FEATURE:
    (A) NAME/KEY: other
    (B) LOCATION: complement(196..229)
    (C) IDENTIFICATION METHOD: blastn
    (D) OTHER INFORMATION: identity 94
        region 315..348
        id N70479
        est

(ix) FEATURE:
    (A) NAME/KEY: sig_peptide
    (B) LOCATION: 90..140
    (C) IDENTIFICATION METHOD: Von Heijne matrix
    (D) OTHER INFORMATION: score 8.2
        seq LLLITAILAVAVG/FP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 17:

AATATRARAC AGCTACAATA TTCCAGGGCC ARTCACTTGC CATTTCTCAT AACAGCGTCA 60

GAGAGAAAGA ACTGACTGAR ACGTTTGAG ATG AAG AAA GTT CTC CTC CTG ATC 113

```
                                        Met Lys Lys Val Leu Leu Leu Ile
                                                -15                 -10

ACA GCC ATC TTG GCA GTG GCT GTW GGT TTC CCA GTC TCT CAA GAC CAG      161
Thr Ala Ile Leu Ala Val Ala Val Gly Phe Pro Val Ser Gln Asp Gln
                -5                  1               5

GAA CGA GAA AAA AGA AGT ATC AGT GAC AGC GAT GAA TTA GCT TCA GGR      209
Glu Arg Glu Lys Arg Ser Ile Ser Asp Ser Asp Glu Leu Ala Ser Gly
        10                  15                  20

WTT TTT GTG TTC CCT TAC CCA TAT CCA TTT CGC CCA CTT CCA CCA ATT      257
Xaa Phe Val Phe Pro Tyr Pro Tyr Pro Phe Arg Pro Leu Pro Pro Ile
    25                  30                  35

CCA TTT CCA AGA TTT CCA TGG TTT AGA CGT AAN TTT CCT ATT CCA ATA      305
Pro Phe Pro Arg Phe Pro Trp Phe Arg Arg Xaa Phe Pro Ile Pro Ile
40                  45                  50                  55

CCT GAA TCT GCC CCT ACA ACT CCC CTT CCT AGC GAA AAG TAAACAARAA       354
Pro Glu Ser Ala Pro Thr Thr Pro Leu Pro Ser Glu Lys
                60                  65

GGAAAAGTCA CRATAAACCT GGTCACCTGA AATTGAAATT GAGCCACTTC CTTGAARAAT    414

CAAAATTCCT GTTAATAAAA RAAAAACAAA TGTAATTGAA ATAGCACACA GCATTCTCTA    474

GTCAATATCT TTAGTGATCT TCTTTAATAA ACATGAAAGC AAAAAAAAAA AA            526
```

(2) INFORMATION FOR SEQ ID NO: 18:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 17 amino acids
(B) TYPE: AMINO ACID
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Homo Sapiens

(ix) FEATURE:
(A) NAME/KEY: sig_peptide
(B) LOCATION: 1..17
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 8.2
seq LLLITAILAVAVG/FP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 18:

```
Met Lys Lys Val Leu Leu Leu Ile Thr Ala Ile Leu Ala Val Ala Val
  1             5                  10                  15

Gly
```

(2) INFORMATION FOR SEQ ID NO: 19:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 822 base pairs
(B) TYPE: NUCLEIC ACID
(C) STRANDEDNESS: DOUBLE
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Homo Sapiens
(D) DEVELOPMENTAL STAGE: Fetal
(F) TISSUE TYPE: kidney

(ix) FEATURE:
(A) NAME/KEY: other
(B) LOCATION: 260..464
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 96
region 153..357
id H57434
est

(ix) FEATURE:
(A) NAME/KEY: other
(B) LOCATION: 118..184
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 98
region 98..164
id H57434
est

(ix) FEATURE:
(A) NAME/KEY: other
(B) LOCATION: 56..113
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 98
region 35..92
id H57434
est

(ix) FEATURE:
(A) NAME/KEY: other
(B) LOCATION: 454..485
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 100
region 348..379
id H57434
est

(ix) FEATURE:
(A) NAME/KEY: other
(B) LOCATION: 118..545
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 98
region 1..428
id N27248
est

(ix) FEATURE:
(A) NAME/KEY: other

(B) LOCATION: 65..369
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 98
region 41..345
id H94779
est

(ix) FEATURE:
(A) NAME/KEY: other
(B) LOCATION: 61..399
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 99
region 6..344
id H09880
est

(ix) FEATURE:
(A) NAME/KEY: other
(B) LOCATION: 408..458
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 92
region 355..405
id H09880
est

(ix) FEATURE:
(A) NAME/KEY: other
(B) LOCATION: 60..399
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 97
region 56..395
id H29351
est

(ix) FEATURE:
(A) NAME/KEY: other
(B) LOCATION: 393..432
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 90
region 391..430
id H29351
est

(ix) FEATURE:
(A) NAME/KEY: sig_peptide
(B) LOCATION: 346..408
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 5.5
seq SFLPSALVIWTSA/AF

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 19:

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ACTCCTTTTA GCATAGGGGC TTCGGCGCCA GCGGCCAGCG CTAGTCGGTC TGGTAAGTGC    60

CTGATGCCGA GTTCCGTCTC TCGCGTCTTT TCCTGGTCCC AGGCAAAGCG GASGNAGATC   120

CTCAAACGGC CTAGTGCTTC GCGCTTCCGG AGAAAATCAG CGGTCTAATT AATTCCTCTG   180

GTTTGTTGAA GCAGTTACCA AGAATCTTCA ACCCTTTCCC ACAAAAGCTA ATTGAGTACA   240
```

```
CGTTCCTGTT GAGTACACGT TCCTGTTGAT TTACAAAAGG TGCAGGTATG AGCAGGTCTG    300

AAGACTAACA TTTTGTGAAG TTGTAAAACA GAAAACCTGT TAGAA ATG TGG TGG TTT    357
                                                  Met Trp Trp Phe
                                                      -20

CAG CAA GGC CTC AGT TTC CTT CCT TCA GCC CTT GTA ATT TGG ACA TCT      405
Gln Gln Gly Leu Ser Phe Leu Pro Ser Ala Leu Val Ile Trp Thr Ser
        -15                 -10                 -5

GCT GCT TTC ATA TTT TCA TAC ATT ACT GCA GTA ACA CTC CAC CAT ATA      453
Ala Ala Phe Ile Phe Ser Tyr Ile Thr Ala Val Thr Leu His His Ile
    1               5                   10                  15

GAC CCG GCT TTA CCT TAT ATC AGT GAC ACT GGT ACA GTA GCT CCA RAA      501
Asp Pro Ala Leu Pro Tyr Ile Ser Asp Thr Gly Thr Val Ala Pro Xaa
                20                  25                  30

AAA TGC TTA TTT GGG GCA ATG CTA AAT ATT GCG GCA GTT TTA TGT CAA      549
Lys Cys Leu Phe Gly Ala Met Leu Asn Ile Ala Ala Val Leu Cys Gln
            35                  40                  45

AAA TAGAAATCAG GAARATAATT CAACTTAAAG AAKTTCATTT CATGACCAAA           602
Lys

CTCTTCARAA ACATGTCTTT ACAAGCATAT CTCTTGTATT GCTTTCTACA CTGTTGAATT    662

GTCTGGCAAT ATTTCTGCAG TGGAAAATTT GATTTARMTA GTTCTTGACT GATAAATATG    722

GTAAGGTGGG CTTTTCCCCC TGTGTAATTG GCTACTATGT CTTACTGAGC CAAGTTGTAW    782

TTTGAAATAA AATGATATGA GAGTGACACA AAAAAAAAAA                          822
```

(2) INFORMATION FOR SEQ ID NO: 20:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 21 amino acids
(B) TYPE: AMINO ACID
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Homo Sapiens

(ix) FEATURE:
(A) NAME/KEY: sig_peptide
(B) LOCATION: 1..21
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 5.5
seq SFLPSALVIWTSA/AF

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 20:

```
Met Trp Trp Phe Gln Gln Gly Leu Ser Phe Leu Pro Ser Ala Leu Val
  1               5                  10                  15
```

```
Ile Trp Thr Ser Ala
         20


(2) INFORMATION FOR SEQ ID NO: 21:

      (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 405 base pairs
            (B) TYPE: NUCLEIC ACID
            (C) STRANDEDNESS: DOUBLE
            (D) TOPOLOGY: LINEAR

      (ii) MOLECULE TYPE: CDNA

      (vi) ORIGINAL SOURCE:
            (A) ORGANISM: Homo Sapiens
            (F) TISSUE TYPE: Testis

      (ix) FEATURE:
            (A) NAME/KEY: other
            (B) LOCATION: complement(103..398)
            (C) IDENTIFICATION METHOD: blastn
            (D) OTHER INFORMATION:  identity 96
                                    region 1..296
                                    id AA442893
                                    est

      (ix) FEATURE:
            (A) NAME/KEY: sig_peptide
            (B) LOCATION: 185..295
            (C) IDENTIFICATION METHOD: Von Heijne matrix
            (D) OTHER INFORMATION:  score 5.9
                                    seq LSYASSALSPCLT/AP

      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 21:

ATCACCTTCT TCTCCATCCT TSTCTGGGCC AGTCCCCARC CCAGTCCCTC TCCTGACCTG      60

CCCAGCCCAA GTCAGCCTTC AGCACGCGCT TTTCTGCACA CAGATATTCC AGGCCTACCT     120

GGCATTCCAG GACCTCCGMA ATGATGCTCC AGTCCCTTAC AAGCGCTTCC TGGATGAGGG     180

TGGC ATG GTG CTG ACC ACC CTC CCC TTG CCC TCT GCC AAC AGC CCT GTG      229
     Met Val Leu Thr Thr Leu Pro Leu Pro Ser Ala Asn Ser Pro Val
             -35                 -30                 -25

AAC ATG CCC ACC ACT GGC CCC AAC AGC CTG AGT TAT GCT AGC TCT GCC       277
Asn Met Pro Thr Thr Gly Pro Asn Ser Leu Ser Tyr Ala Ser Ser Ala
        -20                 -15                 -10

CTG TCC CCC TGT CTG ACC GCT CCA AAK TCC CCC CGG CTT GCT ATG ATG       325
Leu Ser Pro Cys Leu Thr Ala Pro Xaa Ser Pro Arg Leu Ala Met Met
    -5                   1               5                  10

CCT GAC AAC TAAATATCCT TATCCAAATC AATAAARWRA RAATCCTCCC TCCARAAGGG    384
Pro Asp Asn

TTTCTAAAAA CAAAAAAAAA A                                                405
```

(2) INFORMATION FOR SEQ ID NO: 22:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 37 amino acids
(B) TYPE: AMINO ACID
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Homo Sapiens

(ix) FEATURE:
(A) NAME/KEY: sig_peptide
(B) LOCATION: 1..37
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 5.9
seq LSYASSALSPCLT/AP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 22:

```
Met Val Leu Thr Thr Leu Pro Leu Pro Ser Ala Asn Ser Pro Val Asn
  1               5                  10                  15

Met Pro Thr Thr Gly Pro Asn Ser Leu Ser Tyr Ala Ser Ser Ala Leu
             20                  25                  30

Ser Pro Cys Leu Thr
         35
```

(2) INFORMATION FOR SEQ ID NO: 23:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 496 base pairs
(B) TYPE: NUCLEIC ACID
(C) STRANDEDNESS: DOUBLE
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Cancerous prostate

(ix) FEATURE:
(A) NAME/KEY: other
(B) LOCATION: 149..331
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 98
region 1..183
id AA397994
est

(ix) FEATURE:
(A) NAME/KEY: other

(B) LOCATION: 328..485
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 96
region 179..336
id AA397994
est

(ix) FEATURE:
(A) NAME/KEY: other
(B) LOCATION: complement(182..496)
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 97
region 14..328
id AA399680
est

(ix) FEATURE:
(A) NAME/KEY: sig_peptide
(B) LOCATION: 196..240
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 5.5
seq ILSTVTALTFAXA/LD

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 23:

```
AAAAAATTGG TCCCAGTTTT CACCCTGCCG CAGGGCTGGC TGGGGAGGGC AGCGGTTTAG      60

ATTAGCCGTG GCCTAGGCCG TTTAACGGGG TGACACGAGC NTGCAGGGCC GAGTCCAAGG     120

CCCGGAGATA GGACCAACCG TCAGGAATGC GAGGAATGTT TTTCTTCGGA CTCTATCGAG     180

GCACACAGAC AGACC ATG GGG ATT CTG TCT ACA GTG ACA GCC TTA ACA TTT      231
                 Met Gly Ile Leu Ser Thr Val Thr Ala Leu Thr Phe
                 -15                 -10                 -5

GCC ARA GCC CTG GAC GGC TGC AGA AAT GGC ATT GCC CAC CCT GCA AGT       279
Ala Xaa Ala Leu Asp Gly Cys Arg Asn Gly Ile Ala His Pro Ala Ser
            1               5                  10

GAG AAG CAC AGA CTC GAG AAA TGT AGG GAA CTC GAG ASC ASC CAC TCG       327
Glu Lys His Arg Leu Glu Lys Cys Arg Glu Leu Glu Xaa Xaa His Ser
    15                  20                  25

GCC CCA GGA TCA ACC CAS CAC CGA AGA AAA ACA ACC AGA AGA AAT TAT       375
Ala Pro Gly Ser Thr Xaa His Arg Arg Lys Thr Thr Arg Arg Asn Tyr
30                  35                  40                  45

TCT TCA GCC TGAAATGAAK CCGGGATCAA ATGGTTGCTG ATCARAGCCC ATATTTAAAT     434
Ser Ser Ala

TGGAAAAGTC AAATTGASCA TTATTAAATA AAGCTTGTTT AATATGTCTC AAACAAAAAA     494

AA                                                                     496
```

(2) INFORMATION FOR SEQ ID NO: 24:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 15 amino acids
(B) TYPE: AMINO ACID
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Homo Sapiens

(ix) FEATURE:
(A) NAME/KEY: sig_peptide
(B) LOCATION: 1..15
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 5.5
seq ILSTVTALTFAXA/LD

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 24:

```
Met Gly Ile Leu Ser Thr Val Thr Ala Leu Thr Phe Ala Xaa Ala
  1               5                  10                  15
```

(2) INFORMATION FOR SEQ ID NO: 25:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 623 base pairs
(B) TYPE: NUCLEIC ACID
(C) STRANDEDNESS: DOUBLE
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Testis

(ix) FEATURE:
(A) NAME/KEY: sig_peptide
(B) LOCATION: 49..96
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 10.1
seq LVLTLCTLPLAVA/SA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 25:

```
AAAGATCCCT GCAGCCCGGC AGGAGAGAAG GCTGAGCCTT CTGGCGTC ATG GAG AGG      57
                                                     Met Glu Arg
                                                         -15

CTC GTC CTA ACC CTG TGC ACC CTC CCG CTG GCT GTG GCG TCT GCT GGC      105
Leu Val Leu Thr Leu Cys Thr Leu Pro Leu Ala Val Ala Ser Ala Gly
            -10                 -5                   1

TGC GCC ACG ACG CCA GCT CGC AAC CTG AGC TGC TAC CAG TGC TTC AAG      153
Cys Ala Thr Thr Pro Ala Arg Asn Leu Ser Cys Tyr Gln Cys Phe Lys
    5                   10                  15

GTC AGC AGC TGG ACG GAG TGC CCG CCC ACC TGG TGC AGC CCG CTG GAC      201
```

```
Val Ser Ser Trp Thr Glu Cys Pro Pro Thr Trp Cys Ser Pro Leu Asp
20                  25                  30                  35

CAA GTC TGC ATC TCC AAC GAG GTG GTC GTC TCT TTT AAA TGG AGT GTA     249
Gln Val Cys Ile Ser Asn Glu Val Val Val Ser Phe Lys Trp Ser Val
                40                  45                  50

CGC GTC CTG CTC AGC AAA CGC TGT GCT CCC AGA TGT CCC AAC GAC AAC     297
Arg Val Leu Leu Ser Lys Arg Cys Ala Pro Arg Cys Pro Asn Asp Asn
            55                  60                  65

ATG AAK TTC GAA TGG TCG CCG GCC CCC ATG GTG CAA GGC GTG ATC ACC     345
Met Xaa Phe Glu Trp Ser Pro Ala Pro Met Val Gln Gly Val Ile Thr
        70                  75                  80

AGG CGC TGC TGT TCC TGG GCT CTC TGC AAC AGG GCA CTG ACC CCA CAG     393
Arg Arg Cys Cys Ser Trp Ala Leu Cys Asn Arg Ala Leu Thr Pro Gln
    85                  90                  95

GAG GGG CGC TGG GCC CTG CRA GGG GGG CTC CTG CTC CAG GAC CCT TCG     441
Glu Gly Arg Trp Ala Leu Xaa Gly Gly Leu Leu Leu Gln Asp Pro Ser
100                 105                 110                 115

AGG GGC ARA AAA ACC TGG GTG CGG CCA CAG CTG GGG CTC CCA CTC TGC     489
Arg Gly Xaa Lys Thr Trp Val Arg Pro Gln Leu Gly Leu Pro Leu Cys
                120                 125                 130

CTT CCC AWT TCC AAC CCC CTC TGC CCA RGG GAA ACC CAG GAA GGA         534
Leu Pro Xaa Ser Asn Pro Leu Cys Pro Xaa Glu Thr Gln Glu Gly
            135                 140                 145

TAACACTGTG GGTGCCCCCA CCTGTGCATT GGGACCACRA CTTCACCCTC TTGGARACAA   594

TAAACTCTCA TGCCCCCAAA AAAAAAAAA                                     623
```

(2) INFORMATION FOR SEQ ID NO: 26:

(i) SEQUENCE CHARACTERISTICS:
  (A) LENGTH: 16 amino acids
  (B) TYPE: AMINO ACID
  (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:
  (A) ORGANISM: Homo Sapiens

(ix) FEATURE:
  (A) NAME/KEY: sig_peptide
  (B) LOCATION: 1..16
  (C) IDENTIFICATION METHOD: Von Heijne matrix
  (D) OTHER INFORMATION: score 10.1
      seq LVLTLCTLPLAVA/SA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 26:

```
Met Glu Arg Leu Val Leu Thr Leu Cys Thr Leu Pro Leu Ala Val Ala
 1              5                  10                  15
```

(2) INFORMATION FOR SEQ ID NO: 27:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 848 base pairs
(B) TYPE: NUCLEIC ACID
(C) STRANDEDNESS: DOUBLE
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Homo Sapiens
(D) DEVELOPMENTAL STAGE: Fetal
(F) TISSUE TYPE: kidney

(ix) FEATURE:
(A) NAME/KEY: sig_peptide
(B) LOCATION: 32..73
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 10.7
seq LWLLFFLVTAIHA/EL

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 27:

```
AACTTTGCCT TGTGTTTTCC ACCCTGAAAG A ATG TTG TGG CTG CTC TTT TTT CTG     55
                                   Met Leu Trp Leu Leu Phe Phe Leu
                                                   -10

GTG ACT GCC ATT CAT GCT GAA CTC TGT CAA CCA GGT GCA GAA AAT GCT       103
Val Thr Ala Ile His Ala Glu Leu Cys Gln Pro Gly Ala Glu Asn Ala
    -5                  1               5                  10

TTT AAA GTG AGA CTT AGT ATC AGA ACA GCT CTG GGA GAT AAA GCA TAT       151
Phe Lys Val Arg Leu Ser Ile Arg Thr Ala Leu Gly Asp Lys Ala Tyr
            15                  20                  25

GCC TGG GAT ACC AAT GAA GAA TAC CTC TTC AAA GCG ATG GTA GCT TTC       199
Ala Trp Asp Thr Asn Glu Glu Tyr Leu Phe Lys Ala Met Val Ala Phe
        30                  35                  40

TCC ATG AGA AAA GTT CCC AAC AGA GAA GCA ACA GAA ATT TCC CAT GTC       247
Ser Met Arg Lys Val Pro Asn Arg Glu Ala Thr Glu Ile Ser His Val
    45                  50                  55

CTA CTT TGC AAT GTA ACC CAG AGG GTA TCA TTC TGG TTT GTG GTT ACA       295
Leu Leu Cys Asn Val Thr Gln Arg Val Ser Phe Trp Phe Val Val Thr
    60                  65                  70

GAC CCT TCA AAA AAT CAC ACC CTT CCT GCT GTT GAG GTG CAA TCA GCC       343
Asp Pro Ser Lys Asn His Thr Leu Pro Ala Val Glu Val Gln Ser Ala
75                  80                  85                  90

ATA AGA ATG AAC AAG AAC CGG ATC AAC AAT GCC TTC TTT CTA AAT GAC       391
Ile Arg Met Asn Lys Asn Arg Ile Asn Asn Ala Phe Phe Leu Asn Asp
            95                  100                 105

CAA ACT CTG GAA TTT TTA AAA ATC CCT TCC ACA CTT GCA CCA CCC ATG       439
```

```
Gln Thr Leu Glu Phe Leu Lys Ile Pro Ser Thr Leu Ala Pro Pro Met
            110                 115                 120

GAC CCA TCT GTG CCC ATC TGG ATT ATT ATA TTT GGT GTG ATA TTT TGC      487
Asp Pro Ser Val Pro Ile Trp Ile Ile Ile Phe Gly Val Ile Phe Cys
        125                 130                 135

ATC ATC ATA GTT GCA ATT GCA CTA CTG ATT TTA TCA GGG ATC TGG CAA      535
Ile Ile Ile Val Ala Ile Ala Leu Leu Ile Leu Ser Gly Ile Trp Gln
    140                 145                 150

CGT ADA ARA AAG AAC AAA GAA CCA TCT GAA GTG GAT GAC GCT GAA RAT      583
Arg Xaa Xaa Lys Asn Lys Glu Pro Ser Glu Val Asp Asp Ala Glu Xaa
155                 160                 165                 170

AAK TGT GAA AAC ATG ATC ACA ATT GAA AAT GGC ATC CCC TCT GAT CCC      631
Xaa Cys Glu Asn Met Ile Thr Ile Glu Asn Gly Ile Pro Ser Asp Pro
                175                 180                 185

CTG GAC ATG AAG GGA GGG CAT ATT AAT GAT GCC TTC ATG ACA GAG GAT      679
Leu Asp Met Lys Gly Gly His Ile Asn Asp Ala Phe Met Thr Glu Asp
            190                 195                 200

GAG AGG CTC ACC CCT CTC TGAAGGGCTG TTGTTCTGCT TCCTCAARAA             727
Glu Arg Leu Thr Pro Leu
        205

ATTAAACATT TGTTTCTGTG TGACTGCTGA GCATCCTGAA ATACCAAGAG CAGATCATAT    787

WTTTTGTTTC ACCATTCTTC TTTTGTAATA AATTTTGAAT GTGCTTGAAA AAAAAAAAAA    847

C                                                                    848
```

(2) INFORMATION FOR SEQ ID NO: 28:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 14 amino acids
(B) TYPE: AMINO ACID
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Homo Sapiens

(ix) FEATURE:
(A) NAME/KEY: sig_peptide
(B) LOCATION: 1..14
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 10.7
seq LWLLFFLVTAIHA/EL

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 28:

```
Met Leu Trp Leu Leu Phe Phe Leu Val Thr Ala Ile His Ala
 1               5                  10
```

(2) INFORMATION FOR SEQ ID NO: 29:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 25 base pairs
(B) TYPE: NUCLEIC ACID
(C) STRANDEDNESS: SINGLE
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: Other nucleic acid

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 29:

GGGAAGATGG AGATAGTATT GCCTG 25

(2) INFORMATION FOR SEQ ID NO: 30:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 26 base pairs
(B) TYPE: NUCLEIC ACID
(C) STRANDEDNESS: SINGLE
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: Other nucleic acid

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 30:

CTGCCATGTA CATGATAGAG AGATTC 26

(2) INFORMATION FOR SEQ ID NO: 31:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 546 base pairs
(B) TYPE: NUCLEIC ACID
(C) STRANDEDNESS: DOUBLE
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:
(A) NAME/KEY: promoter
(B) LOCATION: 1..517

(ix) FEATURE:
(A) NAME/KEY: transcription start site
(B) LOCATION: 518

(ix) FEATURE:
(A) NAME/KEY: TF binding-site
(B) LOCATION: 17..25
(C) IDENTIFICATION METHOD: matinspector prediction
(D) OTHER INFORMATION: name CMYB_01
score 0.983
sequence TGTCAGTTG

```
(ix) FEATURE:
      (A) NAME/KEY: TF binding-site
      (B) LOCATION: complement(18..27)
      (C) IDENTIFICATION METHOD: matinspector prediction
      (D) OTHER INFORMATION:  name MYOD_Q6
                              score 0.961
                              sequence CCCAACTGAC

(ix) FEATURE:
      (A) NAME/KEY: TF binding-site
      (B) LOCATION: complement(75..85)
      (C) IDENTIFICATION METHOD: matinspector prediction
      (D) OTHER INFORMATION:  name S8_01
                              score 0.960
                              sequence AATAGAATTAG

(ix) FEATURE:
      (A) NAME/KEY: TF binding-site
      (B) LOCATION: 94..104
      (C) IDENTIFICATION METHOD: matinspector prediction
      (D) OTHER INFORMATION:  name S8_01
                              score 0.966
                              sequence AACTAAATTAG

(ix) FEATURE:
      (A) NAME/KEY: TF binding-site
      (B) LOCATION: complement(129..139)
      (C) IDENTIFICATION METHOD: matinspector prediction
      (D) OTHER INFORMATION:  name DELTAEF1_01
                              score 0.960
                              sequence GCACACCTCAG

(ix) FEATURE:
      (A) NAME/KEY: TF binding-site
      (B) LOCATION: complement(155..165)
      (C) IDENTIFICATION METHOD: matinspector prediction
      (D) OTHER INFORMATION:  name GATA_C
                              score 0.964
                              sequence AGATAAATCCA

(ix) FEATURE:
      (A) NAME/KEY: TF binding-site
      (B) LOCATION: 170..178
      (C) IDENTIFICATION METHOD: matinspector prediction
      (D) OTHER INFORMATION:  name CMYB_01
                              score 0.958
                              sequence CTTCAGTTG

(ix) FEATURE:
      (A) NAME/KEY: TF binding-site
      (B) LOCATION: 176..189
      (C) IDENTIFICATION METHOD: matinspector prediction
      (D) OTHER INFORMATION:  name GATA1_02
                              score 0.959
                              sequence TTGTAGATAGGACA

(ix) FEATURE:
      (A) NAME/KEY: TF binding-site
      (B) LOCATION: 180..190
      (C) IDENTIFICATION METHOD: matinspector prediction
      (D) OTHER INFORMATION:  name GATA_C
```

score 0.953
sequence AGATAGGACAT

(ix) FEATURE:
(A) NAME/KEY: TF binding-site
(B) LOCATION: 284..299
(C) IDENTIFICATION METHOD: matinspector prediction
(D) OTHER INFORMATION: name TAL1ALPHAE47_01
score 0.973
sequence CATAACAGATGGTAAG

(ix) FEATURE:
(A) NAME/KEY: TF binding-site
(B) LOCATION: 284..299
(C) IDENTIFICATION METHOD: matinspector prediction
(D) OTHER INFORMATION: name TAL1BETAE47_01
score 0.983
sequence CATAACAGATGGTAAG

(ix) FEATURE:
(A) NAME/KEY: TF binding-site
(B) LOCATION: 284..299
(C) IDENTIFICATION METHOD: matinspector prediction
(D) OTHER INFORMATION: name TAL1BETAITF2_01
score 0.978
sequence CATAACAGATGGTAAG

(ix) FEATURE:
(A) NAME/KEY: TF binding-site
(B) LOCATION: complement(287..296)
(C) IDENTIFICATION METHOD: matinspector prediction
(D) OTHER INFORMATION: name MYOD_Q6
score 0.954
sequence ACCATCTGTT

(ix) FEATURE:
(A) NAME/KEY: TF binding-site
(B) LOCATION: complement(302..314)
(C) IDENTIFICATION METHOD: matinspector prediction
(D) OTHER INFORMATION: name GATA1_04
score 0.953
sequence TCAAGATAAAGTA

(ix) FEATURE:
(A) NAME/KEY: TF binding-site
(B) LOCATION: 393..405
(C) IDENTIFICATION METHOD: matinspector prediction
(D) OTHER INFORMATION: name IK1_01
score 0.963
sequence AGTTGGGAATTCC

(ix) FEATURE:
(A) NAME/KEY: TF binding-site
(B) LOCATION: 393..404
(C) IDENTIFICATION METHOD: matinspector prediction
(D) OTHER INFORMATION: name IK2_01
score 0.985
sequence AGTTGGGAATTC

(ix) FEATURE:
(A) NAME/KEY: TF binding-site

(B) LOCATION: 396..405
(C) IDENTIFICATION METHOD: matinspector prediction
(D) OTHER INFORMATION: name CREL_01
score 0.962
sequence TGGGAATTCC

(ix) FEATURE:
(A) NAME/KEY: TF binding-site
(B) LOCATION: 423..436
(C) IDENTIFICATION METHOD: matinspector prediction
(D) OTHER INFORMATION: name GATA1_02
score 0.950
sequence TCAGTGATATGGCA

(ix) FEATURE:
(A) NAME/KEY: TF binding-site
(B) LOCATION: complement(478..489)
(C) IDENTIFICATION METHOD: matinspector prediction
(D) OTHER INFORMATION: name SRY_02
score 0.951
sequence TAAAACAAAACA

(ix) FEATURE:
(A) NAME/KEY: TF binding-site
(B) LOCATION: 486..493
(C) IDENTIFICATION METHOD: matinspector prediction
(D) OTHER INFORMATION: name E2F_02
score 0.957
sequence TTTAGCGC

(ix) FEATURE:
(A) NAME/KEY: TF binding-site
(B) LOCATION: complement(514..521)
(C) IDENTIFICATION METHOD: matinspector prediction
(D) OTHER INFORMATION: name MZF1_01
score 0.975
sequence TGAGGGGA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 31:

TGAGTGCAGT GTTACATGTC AGTTGGGTTA AGTTTGTTAA TGTCATTCAA ATCTTCTATG 60

TCTTGATTTG CCTGCTAATT CTATTATTTC TGGAACTAAA TTAGTTTGAT GGTTCTATTA 120

GTTATTGACT GAGGTGTGCT AATCTCCCAT TATGTGGATT TATCTATTTC TTCAGTTGTA 180

GATAGGACAT TGATAGATAC ATAAGTACCA GGACAAAAGC AGGGAGATCT TTTTTCCAAA 240

ATCAGGAGAA AAAAATGACA TCTGGAAAAC CTATAGGGAA AGGCATAACA GATGGTAAGG 300

ATACTTTATC TTGAGTAGGA GAGCCTTCCT GTGGCAACGT GGAGAAGGGA AGAGGTCGTA 360

GAATTGAGGA GTCAGCTCAG TTAGAAGCAG GGAGTTGGGA ATTCCGTTCA TGTGATTTAG 420

CATCAGTGAT ATGGCAAATG TGGGACTAAG GGTAGTGATC AGAGGGTTAA AATTGTGTGT 480

TTTGTTTTAG CGCTGCTGGG GCATCGCCTT GGGTCCCCTC AAACAGATTC CCATGAATCT 540

CTTCAT 546

(2) INFORMATION FOR SEQ ID NO: 32:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 23 base pairs
(B) TYPE: NUCLEIC ACID
(C) STRANDEDNESS: SINGLE
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: Other nucleic acid

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 32:

GTACCAGGGA CTGTGACCAT TGC 23

(2) INFORMATION FOR SEQ ID NO: 33:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 24 base pairs
(B) TYPE: NUCLEIC ACID
(C) STRANDEDNESS: SINGLE
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: Other nucleic acid

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 33:

CTGTGACCAT TGCTCCCAAG AGAG 24

(2) INFORMATION FOR SEQ ID NO: 34:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 861 base pairs
(B) TYPE: NUCLEIC ACID
(C) STRANDEDNESS: DOUBLE
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:
(A) NAME/KEY: promoter
(B) LOCATION: 1..806

(ix) FEATURE:
(A) NAME/KEY: transcription start site
(B) LOCATION: 807

(ix) FEATURE:
(A) NAME/KEY: TF binding-site
(B) LOCATION: complement(60..70)
(C) IDENTIFICATION METHOD: matinspector prediction
(D) OTHER INFORMATION: name NFY_Q6
score 0.956
sequence GGACCAATCAT

(ix) FEATURE:
(A) NAME/KEY: TF binding-site
(B) LOCATION: 70..77
(C) IDENTIFICATION METHOD: matinspector prediction
(D) OTHER INFORMATION: name MZF1_01
score 0.962
sequence CCTGGGGA

(ix) FEATURE:
(A) NAME/KEY: TF binding-site
(B) LOCATION: 124..132
(C) IDENTIFICATION METHOD: matinspector prediction
(D) OTHER INFORMATION: name CMYB_01
score 0.994
sequence TGACCGTTG

(ix) FEATURE:
(A) NAME/KEY: TF binding-site
(B) LOCATION: complement(126..134)
(C) IDENTIFICATION METHOD: matinspector prediction
(D) OTHER INFORMATION: name VMYB_02
score 0.985
sequence TCCAACGGT

(ix) FEATURE:
(A) NAME/KEY: TF binding-site
(B) LOCATION: 135..143
(C) IDENTIFICATION METHOD: matinspector prediction
(D) OTHER INFORMATION: name STAT_01
score 0.968
sequence TTCCTGGAA

(ix) FEATURE:
(A) NAME/KEY: TF binding-site
(B) LOCATION: complement(135..143)
(C) IDENTIFICATION METHOD: matinspector prediction
(D) OTHER INFORMATION: name STAT_01
score 0.951
sequence TTCCAGGAA

(ix) FEATURE:
(A) NAME/KEY: TF binding-site
(B) LOCATION: complement(252..259)
(C) IDENTIFICATION METHOD: matinspector prediction
(D) OTHER INFORMATION: name MZF1_01
score 0.956
sequence TTGGGGGA

(ix) FEATURE:
(A) NAME/KEY: TF binding-site
(B) LOCATION: 357..368
(C) IDENTIFICATION METHOD: matinspector prediction
(D) OTHER INFORMATION: name IK2_01
score 0.965
sequence GAATGGGATTTC

(ix) FEATURE:
(A) NAME/KEY: TF binding-site
(B) LOCATION: 384..391
(C) IDENTIFICATION METHOD: matinspector prediction

(D) OTHER INFORMATION: name MZF1_01
score 0.986
sequence AGAGGGGA

(ix) FEATURE:
(A) NAME/KEY: TF binding-site
(B) LOCATION: complement(410..421)
(C) IDENTIFICATION METHOD: matinspector prediction
(D) OTHER INFORMATION: name SRY_02
score 0.955
sequence GAAAACAAAACA

(ix) FEATURE:
(A) NAME/KEY: TF binding-site
(B) LOCATION: 592..599
(C) IDENTIFICATION METHOD: matinspector prediction
(D) OTHER INFORMATION: name MZF1_01
score 0.960
sequence GAAGGGGA

(ix) FEATURE:
(A) NAME/KEY: TF binding-site
(B) LOCATION: 618..627
(C) IDENTIFICATION METHOD: matinspector prediction
(D) OTHER INFORMATION: name MYOD_Q6
score 0.981
sequence AGCATCTGCC

(ix) FEATURE:
(A) NAME/KEY: TF binding-site
(B) LOCATION: 632..642
(C) IDENTIFICATION METHOD: matinspector prediction
(D) OTHER INFORMATION: name DELTAEF1_01
score 0.958
sequence TCCCACCTTCC

(ix) FEATURE:
(A) NAME/KEY: TF binding-site
(B) LOCATION: complement(813..823)
(C) IDENTIFICATION METHOD: matinspector prediction
(D) OTHER INFORMATION: name S8_01
score 0.992
sequence GAGGCAATTAT

(ix) FEATURE:
(A) NAME/KEY: TF binding-site
(B) LOCATION: complement(824..831)
(C) IDENTIFICATION METHOD: matinspector prediction
(D) OTHER INFORMATION: name MZF1_01
score 0.986
sequence AGAGGGGA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 34:

TACTATAGGG CACGCGTGGT CGACGGCCGG GCTGTTCTGG AGCAGAGGGC ATGTCAGTAA 60

TGATTGGTCC CTGGGGAAGG TCTGGCTGGC TCCAGCACAG TGAGGCATTT AGGTATCTCT 120

CGGTGACCGT TGGATTCCTG GAAGCAGTAG CTGTTCTGTT TGGATCTGGT AGGGACAGGG 180

CTCAGAGGGC TAGGCACGAG GGAAGGTCAG AGGAGAAGGS AGGSARGGCC CAGTGAGARG 240

GGAGCATGCC TTCCCCCAAC CCTGGCTTSC YCTTGGYMAM AGGGCGKTTY TGGGMACTTR 300

AAYTCAGGGC CCAASCAGAA SCACAGGCCC AKTCNTGGCT SMAAGCACAA TAGCCTGAAT 360

GGGATTTCAG GTTAGNCAGG GTGAGAGGGG AGGCTCTCTG GCTTAGTTTT GTTTTGTTTT 420

CCAAATCAAG GTAACTTGCT CCCTTCTGCT ACGGGCCTTG GTCTTGGCTT GTCCTCACCC 480

AGTCGGAACT CCCTACCACT TTCAGGAGAG TGGTTTTAGG CCCGTGGGGC TGTTCTGTTC 540

CAAGCAGTGT GAGAACATGG CTGGTAGAGG CTCTAGCTGT GTGCGGGGCC TGAAGGGGAG 600

TGGGTTCTCG CCCAAAGAGC ATCTGCCCAT TTCCCACCTT CCCTTCTCCC ACCAGAAGCT 660

TGCCTGAGCT GTTTGGACAA AAATCCAAAC CCCACTTGGC TACTCTGGCC TGGCTTCAGC 720

TTGGAACCCA ATACCTAGGC TTACAGGCCA TCCTGAGCCA GGGGCCTCTG GAAATTCTCT 780

TCCTGATGGT CCTTTAGGTT TGGGCACAAA ATATAATTGC CTCTCCCCTC TCCCATTTTC 840

TCTCTTGGGA GCAATGGTCA C 861

(2) INFORMATION FOR SEQ ID NO: 35:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: NUCLEIC ACID
(C) STRANDEDNESS: SINGLE
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: Other nucleic acid

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 35:

CTGGGATGGA AGGCACGGTA 20

(2) INFORMATION FOR SEQ ID NO: 36:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: NUCLEIC ACID
(C) STRANDEDNESS: SINGLE
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: Other nucleic acid

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 36:

GAGACCACAC AGCTAGACAA 20

(2) INFORMATION FOR SEQ ID NO: 37:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 555 base pairs
(B) TYPE: NUCLEIC ACID
(C) STRANDEDNESS: DOUBLE
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:
(A) NAME/KEY: promoter
(B) LOCATION: 1..500

(ix) FEATURE:
(A) NAME/KEY: transcription start site
(B) LOCATION: 501

(ix) FEATURE:
(A) NAME/KEY: TF binding-site
(B) LOCATION: 191..206
(C) IDENTIFICATION METHOD: matinspector prediction
(D) OTHER INFORMATION: name ARNT_01
score 0.964
sequence GGACTCACGTGCTGCT

(ix) FEATURE:
(A) NAME/KEY: TF binding-site
(B) LOCATION: 193..204
(C) IDENTIFICATION METHOD: matinspector prediction
(D) OTHER INFORMATION: name NMYC_01
score 0.965
sequence ACTCACGTGCTG

(ix) FEATURE:
(A) NAME/KEY: TF binding-site
(B) LOCATION: 193..204
(C) IDENTIFICATION METHOD: matinspector prediction
(D) OTHER INFORMATION: name USF_01
score 0.985
sequence ACTCACGTGCTG

(ix) FEATURE:
(A) NAME/KEY: TF binding-site
(B) LOCATION: complement(193..204)
(C) IDENTIFICATION METHOD: matinspector prediction
(D) OTHER INFORMATION: name USF_01
score 0.985
sequence CAGCACGTGAGT

(ix) FEATURE:
(A) NAME/KEY: TF binding-site
(B) LOCATION: complement(193..204)
(C) IDENTIFICATION METHOD: matinspector prediction
(D) OTHER INFORMATION: name NMYC_01
score 0.956
sequence CAGCACGTGAGT

(ix) FEATURE:
(A) NAME/KEY: TF binding-site
(B) LOCATION: complement(193..204)
(C) IDENTIFICATION METHOD: matinspector prediction

(D) OTHER INFORMATION: name MYCMAX_02
score 0.972
sequence CAGCACGTGAGT

(ix) FEATURE:
(A) NAME/KEY: TF binding-site
(B) LOCATION: 195..202
(C) IDENTIFICATION METHOD: matinspector prediction
(D) OTHER INFORMATION: name USF_C
score 0.997
sequence TCACGTGC

(ix) FEATURE:
(A) NAME/KEY: TF binding-site
(B) LOCATION: complement(195..202)
(C) IDENTIFICATION METHOD: matinspector prediction
(D) OTHER INFORMATION: name USF_C
score 0.991
sequence GCACGTGA

(ix) FEATURE:
(A) NAME/KEY: TF binding-site
(B) LOCATION: complement(210..217)
(C) IDENTIFICATION METHOD: matinspector prediction
(D) OTHER INFORMATION: name MZF1_01
score 0.968
sequence CATGGGGA

(ix) FEATURE:
(A) NAME/KEY: TF binding-site
(B) LOCATION: 397..410
(C) IDENTIFICATION METHOD: matinspector prediction
(D) OTHER INFORMATION: name ELK1_02
score 0.963
sequence CTCTCCGGAAGCCT

(ix) FEATURE:
(A) NAME/KEY: TF binding-site
(B) LOCATION: 400..409
(C) IDENTIFICATION METHOD: matinspector prediction
(D) OTHER INFORMATION: name CETS1P54_01
score 0.974
sequence TCCGGAAGCC

(ix) FEATURE:
(A) NAME/KEY: TF binding-site
(B) LOCATION: complement(460..470)
(C) IDENTIFICATION METHOD: matinspector prediction
(D) OTHER INFORMATION: name AP1_Q4
score 0.963
sequence AGTGACTGAAC

(ix) FEATURE:
(A) NAME/KEY: TF binding-site
(B) LOCATION: complement(460..470)
(C) IDENTIFICATION METHOD: matinspector prediction
(D) OTHER INFORMATION: name AP1FJ_Q2
score 0.961
sequence AGTGACTGAAC

(ix) FEATURE:

(A) NAME/KEY: TF binding-site
(B) LOCATION: 547..555
(C) IDENTIFICATION METHOD: matinspector prediction
(D) OTHER INFORMATION: name PADS_C
score 1.000
sequence TGTGGTCTC

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 37:

```
CTATAGGGCA CGCKTGGTCG ACGGCCCGGG CTGGTCTGGT CTGTKGTGGA GTCGGGTTGA   60
AGGACAGCAT TTGTKACATC TGGTCTACTG CACCTTCCCT CTGCCGTGCA CTTGGCCTTT  120
KAWAAGCTCA GCACCGGTGC CCATCACAGG GCCGGCAGCA CACACATCCC ATTACTCAGA  180
AGGAACTGAC GGACTCACGT GCTGCTCCGT CCCCATGAGC TCAGTGGACC TGTCTATGTA  240
GAGCAGTCAG ACAGTGCCTG GGATAGAGTG AGAGTTCAGC CAGTAAATCC AAGTGATTGT  300
CATTCCTGTC TGCATTAGTA ACTCCCAACC TAGATGTGAA AACTTAGTTC TTTCTCATAG  360
GTTGCTCTGC CCATGGTCCC ACTGCAGACC CAGGCACTCT CCGGAAGCCT GGAAATCACC  420
CGTGTCTTCT GCCTGCTCCC GCTCACATCC CACACTTGTG TTCAGTCACT GAGTTACAGA  480
TTTTGCCTCC TCAATTTCTC TTGTCTTAGT CCCATCCTCT GTTCCCCTGG CCAGTTTGTC  540
TAGCTGTGTG GTCTC                                                  555
```

(2) INFORMATION FOR SEQ ID NO: 38:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 464 base pairs
(B) TYPE: NUCLEIC ACID
(C) STRANDEDNESS: DOUBLE
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Testis

(ix) FEATURE:
(A) NAME/KEY: sig_peptide
(B) LOCATION: 90..179
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 13.2
seq LLLLSTLVIPSAA/AP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 38:

```
AAAACAGTAC GTGGGCGGCC GGAATCCGGG AGTCCGGTGA CCCGGGCTGT GGTCTAGCAT    60
AAAGGCGGAG CCAGAAGAAG GGGCGGGGT ATG GGA GAA GCC TCC CCA CCT GCC    113
                                Met Gly Glu Ala Ser Pro Pro Ala
                                -30                 -25
```

```
CCC GCA AGG CGG CAT CTG CTG GTC CTG CTG CTG CTC CTC TCT ACC CTG      161
Pro Ala Arg Arg His Leu Leu Val Leu Leu Leu Leu Leu Ser Thr Leu
        -20                 -15                 -10

GTG ATC CCC TCC GCT GCA GCT CCT ATC CAT GAT GCT GAC GCC CAA GAG      209
Val Ile Pro Ser Ala Ala Ala Pro Ile His Asp Ala Asp Ala Gln Glu
     -5                   1               5                  10

AGC TCC TTG GGT CTC ACA GGC CTC CAG AGC CTA CTC CAA GGC TTC AGC      257
Ser Ser Leu Gly Leu Thr Gly Leu Gln Ser Leu Leu Gln Gly Phe Ser
                15                  20                  25

CGA CTT TTC CTG AAA GGT AAC CTG CTT CGG GGC ATA GAC AGC TTA TTC      305
Arg Leu Phe Leu Lys Gly Asn Leu Leu Arg Gly Ile Asp Ser Leu Phe
            30                  35                  40

TCT GCC CCC ATG GAC TTC CGG GGC CTC CCT GGG AAC TAC CAC AAA GAG      353
Ser Ala Pro Met Asp Phe Arg Gly Leu Pro Gly Asn Tyr His Lys Glu
        45                  50                  55

GAG AAC CAG GAG CAC CAG CTG GGG AAC AAC ACC CTC TCC AGC MAC CTC      401
Glu Asn Gln Glu His Gln Leu Gly Asn Asn Thr Leu Ser Ser Xaa Leu
    60                  65                  70

CAG ATC GAC NNG ATG ACC GAC AAC AAG ACA GGA GAG GTG CTG ATC TCC      449
Gln Ile Asp Xaa Met Thr Asp Asn Lys Thr Gly Glu Val Leu Ile Ser
 75                  80                  85                  90

GAG AAT GTG GTG GCA                                                  464
Glu Asn Val Val Ala
                 95
```

(2) INFORMATION FOR SEQ ID NO: 39:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 199 base pairs
(B) TYPE: NUCLEIC ACID
(C) STRANDEDNESS: DOUBLE
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Testis

(ix) FEATURE:
(A) NAME/KEY: sig_peptide
(B) LOCATION: 56..118
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 12
seq VLVLCVLLLQAQG/GY

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 39:

```
AAGGGAAGTC TGTGACTGCC TGGCCAGACT TAGGGCTCAC GCTCTGGTCA GAGTT ATG      58
                                                             Met
```

```
GCA CCC CAG ACT CTG CTG CCT GTC CTG GTT CTC TGT GTG CTG CTG CTG     106
Ala Pro Gln Thr Leu Leu Pro Val Leu Val Leu Cys Val Leu Leu Leu
-20                 -15                 -10                  -5

CAG GCC CAG GGA GGA TAC CGT GAC AAG ATG AGG ATG CAG AGA ATC AAG     154
Gln Ala Gln Gly Gly Tyr Arg Asp Lys Met Arg Met Gln Arg Ile Lys
                      1               5                  10

GTC TGT GAG AAG CGA CCC AGC ATA GAT CTA TGC ATC CAC CAC AGG         199
Val Cys Glu Lys Arg Pro Ser Ile Asp Leu Cys Ile His His Arg
         15                  20                  25
```

(2) INFORMATION FOR SEQ ID NO: 40:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 349 base pairs
(B) TYPE: NUCLEIC ACID
(C) STRANDEDNESS: DOUBLE
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Testis

(ix) FEATURE:
(A) NAME/KEY: sig_peptide
(B) LOCATION: 47..103
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 11
seq SLVLLLCLTCSYA/FM

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 40:

```
AAAGCAAACC CGTCATGAGC AACTCCCTTC CCCATCTCTG TTCACC ATG TGG ACG      55
                                                   Met Trp Thr

CTG AAA TCG TCC CTG GTC CTG CTT CTG TGC CTC ACC TGC AGC TAT GCC     103
Leu Lys Ser Ser Leu Val Leu Leu Leu Cys Leu Thr Cys Ser Tyr Ala
    -15                 -10                     -5

TTT ATG TTC TCT TCT CTG AGA CAG AAA ACT AGC GAA CCC CAG GGG AAG     151
Phe Met Phe Ser Ser Leu Arg Gln Lys Thr Ser Glu Pro Gln Gly Lys
  1               5                  10                  15

GTG CAA TAC GGA GAG CAC TTT CGG ATT CGG CAG AAT CTA CCA GAG CAC     199
Val Gln Tyr Gly Glu His Phe Arg Ile Arg Gln Asn Leu Pro Glu His
             20                  25                  30

ACC CAA GGC TGG CTT GGG AGC AAA TGG CTC TGG CTT CTT KTT GTT GTT     247
Thr Gln Gly Trp Leu Gly Ser Lys Trp Leu Trp Leu Leu Xaa Val Val
         35                  40                  45

GTG CCG TTT GTG ATA CTG CAG TGT CAA AGA GAC AGT GAG AAG AAT AAG     295
Val Pro Phe Val Ile Leu Gln Cys Gln Arg Asp Ser Glu Lys Asn Lys
     50                  55                  60
```

```
GAG CAG AGT CCT CCT GGC CTT CGA GGC GGC CAA CTT CAC TCT CCA TTA     343
Glu Gln Ser Pro Pro Gly Leu Arg Gly Gly Gln Leu His Ser Pro Leu
 65                  70                  75                  80

AAG AAA                                                             349
Lys Lys
```

(2) INFORMATION FOR SEQ ID NO: 41:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 414 base pairs
(B) TYPE: NUCLEIC ACID
(C) STRANDEDNESS: DOUBLE
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Testis

(ix) FEATURE:
(A) NAME/KEY: sig_peptide
(B) LOCATION: 70..117
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 10.6
seq LLLLPLLWGGSLQ/EK

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 41:

```
AAATTTTGGA GCATTTCCTT CCCTGACAGC CGGACCTGGG ACTGGGCTGG GGCCCTGGCG    60

GATGGAGAC ATG CTG CCC CTG CTG CTG CTG CCC CTG CTG TGG GGG GGG TCC   111
          Met Leu Pro Leu Leu Leu Leu Pro Leu Leu Trp Gly Gly Ser
              -15                 -10                  -5

CTG CAG GAG AAG CCA GTG TAC GAG CTG CAA GTG CAG AAG TCG GTG ACG     159
Leu Gln Glu Lys Pro Val Tyr Glu Leu Gln Val Gln Lys Ser Val Thr
          1               5                  10

GTG CAG GAG GGC CTG TGC GTC CTT GTG CCC TGC TCC TTC TCT TAC CCC     207
Val Gln Glu Gly Leu Cys Val Leu Val Pro Cys Ser Phe Ser Tyr Pro
 15                  20                  25                  30

TGG AGA TCC TGG TAT TCC TCT CCC CCA CTC TAC GTC TAC TGG TTC CGG     255
Trp Arg Ser Trp Tyr Ser Ser Pro Pro Leu Tyr Val Tyr Trp Phe Arg
                 35                  40                  45

GAC GGG GAG ATC CCA TAC TAC GCT GAG GTT GTG GCC ACA AAC AAC CCA     303
Asp Gly Glu Ile Pro Tyr Tyr Ala Glu Val Val Ala Thr Asn Asn Pro
             50                  55                  60

GAC AGA AGA GTG AAG CCA GAG ACC CAG GGC CGA TTC CGC CTC CTT GGG     351
Asp Arg Arg Val Lys Pro Glu Thr Gln Gly Arg Phe Arg Leu Leu Gly
         65                  70                  75

GAT GTC CAG AAG AAG AAC TGC TCC CTG AGC ATC GGA GAT SCC AGA ATG     399
```

```
Asp Val Gln Lys Lys Asn Cys Ser Leu Ser Ile Gly Asp Xaa Arg Met
     80                  85                  90

GAG GAC ACG GGC GGG                                                 414
Glu Asp Thr Gly Gly
 95
```

(2) INFORMATION FOR SEQ ID NO: 42:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 215 base pairs
(B) TYPE: NUCLEIC ACID
(C) STRANDEDNESS: DOUBLE
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Ovary

(ix) FEATURE:
(A) NAME/KEY: sig_peptide
(B) LOCATION: 24..101
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 10.4
seq LLLLLCGPSQDQC/RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 42:

```
AANCCAGCTG CSGCCGGCCA GCC ATG GAG ACT GGA GCG CTG CGG CGC CCG CAA    53
                          Met Glu Thr Gly Ala Leu Arg Arg Pro Gln
                              -25                 -20

CTT CTC CCG TTG CTG CTG CTG CTC TGC GGC CCT TCC CAG GAT CAA TGC     101
Leu Leu Pro Leu Leu Leu Leu Leu Cys Gly Pro Ser Gln Asp Gln Cys
    -15                 -10                  -5

CGA CCT GTA CTC CAG AAT CTG TTG CAG AGC CCA GGC TTG ACA TGG AGC     149
Arg Pro Val Leu Gln Asn Leu Leu Gln Ser Pro Gly Leu Thr Trp Ser
  1               5                  10                  15

TTG GAA GTG CCC ACT GGG AGA GAA GGA AAG GAA GGT ACT ATG AGA GTT     197
Leu Glu Val Pro Thr Gly Arg Glu Gly Lys Glu Gly Thr Met Arg Val
             20                  25                  30

TCA CCA ACT GCA CCA AGG                                             215
Ser Pro Thr Ala Pro Arg
         35
```

(2) INFORMATION FOR SEQ ID NO: 43:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 297 base pairs
(B) TYPE: NUCLEIC ACID
(C) STRANDEDNESS: DOUBLE

(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Testis

(ix) FEATURE:
(A) NAME/KEY: sig_peptide
(B) LOCATION: 49..96
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 10.1
seq LVLTLCTLPLAVA/SA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 43:

```
AAAGATCCCT GCAGCCCGGC AGGAGAGAAG GCTGAGCCTT CTGGCGTC ATG GAG AGG      57
                                                     Met Glu Arg
                                                         -15

CTC GTC CTA ACC CTG TGC ACC CTC CCG CTG GCT GTG GCG TCT GCT GGC      105
Leu Val Leu Thr Leu Cys Thr Leu Pro Leu Ala Val Ala Ser Ala Gly
            -10                 -5                   1

TGC GCC ACG ACG CCA GCT CGC AAC CTG AGC TGC TAC CAG TGC TTC AAG      153
Cys Ala Thr Thr Pro Ala Arg Asn Leu Ser Cys Tyr Gln Cys Phe Lys
        5                  10                  15

GTC AGC AGC TGG ACG GAG TGC CCG CCC ACC TGG TGC AGC CCG CTG GAC      201
Val Ser Ser Trp Thr Glu Cys Pro Pro Thr Trp Cys Ser Pro Leu Asp
 20                 25                  30                  35

CAA GTC TGC ATC TCC AAC GAG GTG GTC GTC TCT TTT AAA TGG AGT GTA      249
Gln Val Cys Ile Ser Asn Glu Val Val Val Ser Phe Lys Trp Ser Val
                40                  45                  50

CGC GTC CTG CTC AGC AAA CGC TGT GCT CCC AGA TGT CCC AAC TCA GGG      297
Arg Val Leu Leu Ser Lys Arg Cys Ala Pro Arg Cys Pro Asn Ser Gly
            55                  60                  65
```

(2) INFORMATION FOR SEQ ID NO: 44:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 421 base pairs
(B) TYPE: NUCLEIC ACID
(C) STRANDEDNESS: DOUBLE
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Testis

(ix) FEATURE:
(A) NAME/KEY: sig_peptide
(B) LOCATION: 62..130

(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 9.8
seq FLLFFFLFLLTRG/SL

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 44:

```
ACATGGTCGG YGTGCAGGAT ATTTCGCTGG ACCCTAGAAA AGCCACCACG ACCTGTGGGC    60

C ATG ATG CTA CCC CAA TGG CTG CTG CTG CTG TTC CTT CTC TTC TTC TTT  109
  Met Met Leu Pro Gln Trp Leu Leu Leu Leu Phe Leu Leu Phe Phe Phe
          -20                 -15                 -10

CTC TTC CTC CTC ACC AGG GGC TCA CTT TCT CCA ACA AAA TAC AAC CTT    157
Leu Phe Leu Leu Thr Arg Gly Ser Leu Ser Pro Thr Lys Tyr Asn Leu
     -5                   1               5

TTG GAG CTC AAG GAG KSK KGC ATS GGG AAC CAG GAC TGC GAG ACT GGC    205
Leu Glu Leu Lys Glu Xaa Xaa Xaa Gly Asn Gln Asp Cys Glu Thr Gly
 10                  15                  20                  25

TGC TGC CAA CGT GCT CCA GAC AAT TGC GAG TCG CAC TGC GCG GAG AAG    253
Cys Cys Gln Arg Ala Pro Asp Asn Cys Glu Ser His Cys Ala Glu Lys
                 30                  35                  40

GGG TCC GAG GGC AGT CTG TGT CAA ACG CAG GTG TTC TTT GGC CAA TAT    301
Gly Ser Glu Gly Ser Leu Cys Gln Thr Gln Val Phe Phe Gly Gln Tyr
             45                  50                  55

AGA GCG TGT CCC TGC CTG CGG AAC CTG ACT TGT ATA TAT TCA AAG AAT    349
Arg Ala Cys Pro Cys Leu Arg Asn Leu Thr Cys Ile Tyr Ser Lys Asn
         60                  65                  70

GAG AAA TGG CTT AGC ATC GCC TAT GGC CGT TGT CAG AAA ATT GGA AGG    397
Glu Lys Trp Leu Ser Ile Ala Tyr Gly Arg Cys Gln Lys Ile Gly Arg
     75                  80                  85

CAG AAG TTG GCT AGR AAA TGT TCT                                    421
Gln Lys Leu Ala Arg Lys Cys Ser
 90                  95
```

(2) INFORMATION FOR SEQ ID NO: 45:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 151 base pairs
(B) TYPE: NUCLEIC ACID
(C) STRANDEDNESS: DOUBLE
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Testis

(ix) FEATURE:
(A) NAME/KEY: sig_peptide
(B) LOCATION: 68..133
(C) IDENTIFICATION METHOD: Von Heijne matrix

(D) OTHER INFORMATION: score 9.8
seq LVVFCLALQLVPG/SP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 45:

```
AAACAGCAGT GCCTGGTCAA ACCCAGCAAC CCTTGGCCAG AACTTACTCA CCCATCCCAC   60

TGACACC ATG AAG CCT GTG CTG CCT CTC CAG TWC CTG GTG GTG TTC TGC    109
        Met Lys Pro Val Leu Pro Leu Gln Xaa Leu Val Val Phe Cys
                -20                 -15                 -10

CTA GCA CTG CAG CTG GTG CCT GGG AGT CCC AAG CAG CTA GGG            151
Leu Ala Leu Gln Leu Val Pro Gly Ser Pro Lys Gln Leu Gly
            -5                  1               5
```

(2) INFORMATION FOR SEQ ID NO: 46:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 253 base pairs
(B) TYPE: NUCLEIC ACID
(C) STRANDEDNESS: DOUBLE
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Spleen

(ix) FEATURE:
(A) NAME/KEY: sig_peptide
(B) LOCATION: 134..238
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 9.5
seq LFFSLFSAPLASA/VR

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 46:

```
AAACAGATAC TCCCAGCACA TGTTCCAWAG CAGCCCCCTG ATCCAATTTT CCTTAGCACG   60

TAGGCTCAAG ACAATGCCCC ACTTCCCAAA GGCCTTGTGG CAATGTCCTC TTTTTCTTTC  120

ACATATATGA TTT ATG TTC CGT CAA CGA CAG GAA ACT GCT CAA AGA TCC     169
               Met Phe Arg Gln Arg Gln Glu Thr Ala Gln Arg Ser
               -35                 -30                 -25

ACC CAG TCC TGC CGC TGC CCC CGT GAT GGT TTG TTT TTC TCA TTG TTT    217
Thr Gln Ser Cys Arg Cys Pro Arg Asp Gly Leu Phe Phe Ser Leu Phe
            -20                 -15                 -10

AGC GCT CCA TTA GCT TCC GCA GTG AGA GCC GCC ASG                    253
Ser Ala Pro Leu Ala Ser Ala Val Arg Ala Ala Xaa
        -5                      1               5
```

(2) INFORMATION FOR SEQ ID NO: 47:

(i) SEQUENCE CHARACTERISTICS:
    (A) LENGTH: 124 base pairs
    (B) TYPE: NUCLEIC ACID
    (C) STRANDEDNESS: DOUBLE
    (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:
    (A) ORGANISM: Homo Sapiens
    (F) TISSUE TYPE: Ovary

(ix) FEATURE:
    (A) NAME/KEY: sig_peptide
    (B) LOCATION: 14..91
    (C) IDENTIFICATION METHOD: Von Heijne matrix
    (D) OTHER INFORMATION: score 9.4
        seq RLLLALPLALVLG/FE

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 47:

```
AGTACCACAG GCA ATG GGG TCA AGT GCC TGT GAA ATA GCT GTC GGG ACT       49
               Met Gly Ser Ser Ala Cys Glu Ile Ala Val Gly Thr
                   -25                 -20                 -15

AAA AGG TTA TTA TTA GCT CTG CCT CTC GCT CTT GTT CTG GGC TTT GAA      97
Lys Arg Leu Leu Leu Ala Leu Pro Leu Ala Leu Val Leu Gly Phe Glu
                -10                 -5                   1

GGC TCA TCA GTT CCC CCA AGA AAT TTT                                  124
Gly Ser Ser Val Pro Pro Arg Asn Phe
        5                  10
```

(2) INFORMATION FOR SEQ ID NO: 48:

(i) SEQUENCE CHARACTERISTICS:
    (A) LENGTH: 353 base pairs
    (B) TYPE: NUCLEIC ACID
    (C) STRANDEDNESS: DOUBLE
    (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:
    (A) ORGANISM: Homo Sapiens
    (F) TISSUE TYPE: Testis

(ix) FEATURE:
    (A) NAME/KEY: sig_peptide
    (B) LOCATION: 186..254
    (C) IDENTIFICATION METHOD: Von Heijne matrix
    (D) OTHER INFORMATION: score 9.4
        seq SLLFICFFGESFC/IC

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 48:

```
AATATTTTGC TGACTGGCAA GGTTATATGA AGTGCTTTTA TTGAAGCACC ATTTTAACTA   60

ATAGCTCCTG GTATTTTCTG CTTCCCTTCG TAGGGAATTT AGTTATTTTA TTTTATTATT  120

TAGCTAATTT AGCTATTTTA AAATAGCTAA ATTTAGCTA CTTTTTTTTC AATTGACAAA  180

GAAGG ATG TCT AAT CAA AGA CTA CCG CTG ATT TTT TCT CTG TTG TTT ATC  230
      Met Ser Asn Gln Arg Leu Pro Leu Ile Phe Ser Leu Leu Phe Ile
                  -20                 -15                 -10

TGC TTC TTC GGG GAG AGT TTC TGC ATT TGT GAT GGA ACT GTC TGG ACA    278
Cys Phe Phe Gly Glu Ser Phe Cys Ile Cys Asp Gly Thr Val Trp Thr
            -5                  1               5

WWG GTT KRA TGG GAG ATT CTT CCA GAA GAA GTA CAT TAT TGG AAA GTT    326
Xaa Val Xaa Trp Glu Ile Leu Pro Glu Glu Val His Tyr Trp Lys Val
     10                  15                  20

AAG GGT TCT CCA TCT CAC TGC CTG CGG                                353
Lys Gly Ser Pro Ser His Cys Leu Arg
 25                  30
```

(2) INFORMATION FOR SEQ ID NO: 49:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 167 base pairs
(B) TYPE: NUCLEIC ACID
(C) STRANDEDNESS: DOUBLE
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Ovary

(ix) FEATURE:
(A) NAME/KEY: sig_peptide
(B) LOCATION: 108..155
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 9.2
seq FLSFLLALLSLNC/IP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 49:

```
ACATGGAGTT TACAAAATTT ATATTATCAT GAAATACTTC AATAGAGGGT TGGGAAATCT   60

AACTCTGGAG GAAATGCCAC AAATTTCCAC TGCTGGGGTT TTTGAAG ATG CTC TGG    116
                                                    Met Leu Trp
                                                        -15

TTC CTA TCT TTT CTT CTA GCT CTC CTT TCC CTC AAT TGT ATC CCC ATC    164
Phe Leu Ser Phe Leu Leu Ala Leu Leu Ser Leu Asn Cys Ile Pro Ile
            -10                 -5                  1

GGG                                                                167
Gly
```

(2) INFORMATION FOR SEQ ID NO: 50:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 203 base pairs
(B) TYPE: NUCLEIC ACID
(C) STRANDEDNESS: DOUBLE
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Testis

(ix) FEATURE:
(A) NAME/KEY: sig_peptide
(B) LOCATION: 84..155
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 9.2
seq ICCVIVLISLSWT/SP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 50:

```
ATGTKCGAAT TTATTGCTGA GACTTTCCAG TGCATTTTGC ATCTCTCTGA GTGTGTCCTT   60

GATTTCCAAA AGTTGTTTTA TTT ATG CTG TKT ATT TCA CTC GAG ATT KTT TCC  113
                          Met Leu Xaa Ile Ser Leu Glu Ile Xaa Ser
                                          -20                 -15

TTC ATA TGC TGT GTC ATT GTT TTG ATT TCT TTA AGT TGG ACT TCA CCT    161
Phe Ile Cys Cys Val Ile Val Leu Ile Ser Leu Ser Trp Thr Ser Pro
                -10                 -5                  1

TTC ACT GGT GTG TAC TTG ATT GGT TTA ATA ATC GAG CCA GGG            203
Phe Thr Gly Val Tyr Leu Ile Gly Leu Ile Ile Glu Pro Gly
        5                   10                  15
```

(2) INFORMATION FOR SEQ ID NO: 51:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 266 base pairs
(B) TYPE: NUCLEIC ACID
(C) STRANDEDNESS: DOUBLE
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Ovary

(ix) FEATURE:
(A) NAME/KEY: sig_peptide
(B) LOCATION: 183..239
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 9.2

seq ILFILTFFSHTFC/SR

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 51:

```
AATTTCACTG ATGTCTAGCT GTGGCTCTCT TTTTATACCT CCTATTTAAT ACCACATGGT    60

CTTTGAAACC TGGAGACTTA CTGATTTCTT GAGCTCTAGT AAATGTTCTT TTCTCATTTA   120

ATTGATCATT TTCTCCCATT TGTTGTCTCC TTACATCCCC AGGGCATTAC TATTTTGTAG   180

CT ATG GTA TTC AGG AAC TGC ATT TTA TTT ATT TTA ACT TTT TTT TCT      227
   Met Val Phe Arg Asn Cys Ile Leu Phe Ile Leu Thr Phe Phe Ser
                   -15                 -10                 -5

CAT ACT TTC TGT AGT AGG CAG AAT AAA GCC CAG CCC TGG                 266
His Thr Phe Cys Ser Arg Gln Asn Lys Ala Gln Pro Trp
                1               5
```

(2) INFORMATION FOR SEQ ID NO: 52:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 159 base pairs
(B) TYPE: NUCLEIC ACID
(C) STRANDEDNESS: DOUBLE
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Ovary

(ix) FEATURE:
(A) NAME/KEY: sig_peptide
(B) LOCATION: 7..45
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 9.1
seq MLAACPLSPGCQS/AP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 52:

```
GACGGC ATG CTG GCT GCG TGT CCC CTC TCA CCA GGT TGC CAA AGC GCT       48
       Met Leu Ala Ala Cys Pro Leu Ser Pro Gly Cys Gln Ser Ala
                   -10                 -5                   1

CCA TCA ACG TGG AAT CAT TTT CCT CCT GAA AGA ATA ACC ACT GGA GCC      96
Pro Ser Thr Trp Asn His Phe Pro Pro Glu Arg Ile Thr Thr Gly Ala
            5                  10                  15

GGC AGC CTT CTG AAA CCA GGG GGT GGC CTC TGG CCA CGC ACA GTC TCT     144
Gly Ser Leu Leu Lys Pro Gly Gly Gly Leu Trp Pro Arg Thr Val Ser
        20                  25                  30

CTG CCC TCC CCT GCG                                                 159
Leu Pro Ser Pro Ala
    35
```

(2) INFORMATION FOR SEQ ID NO: 53:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 270 base pairs
(B) TYPE: NUCLEIC ACID
(C) STRANDEDNESS: DOUBLE
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Spleen

(ix) FEATURE:
(A) NAME/KEY: sig_peptide
(B) LOCATION: 43..99
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 9.1
seq FLTLITHCTVSWA/QS

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 53:

```
AAGCTGCGGG TAGAGAAGAC AGGACTCAGG ACAATCTCCA GC ATG GCC TGG TCC       54
                                               Met Ala Trp Ser

CCT CTC TTC CTC ACC CTC ATC ACT CAC TGT ACA GTG TCC TGG GCC CAG     102
Pro Leu Phe Leu Thr Leu Ile Thr His Cys Thr Val Ser Trp Ala Gln
-15                 -10                 -5                   1

TCT GTT CTG ACT CAG CCA CCC TCG GTG TCT GAA GCC CCC AGA CAG AGG     150
Ser Val Leu Thr Gln Pro Pro Ser Val Ser Glu Ala Pro Arg Gln Arg
             5                  10                  15

GTC ACC ATC TCC TGT TTT GGA AGC AGC TCC AAT ATC GGA CGA AAT GCT     198
Val Thr Ile Ser Cys Phe Gly Ser Ser Ser Asn Ile Gly Arg Asn Ala
         20                  25                  30

GTA AAC TGG TAT CAG CAA CTC CCA GGA AGG TCT CCC AGA CTT CTC ATT     246
Val Asn Trp Tyr Gln Gln Leu Pro Gly Arg Ser Pro Arg Leu Leu Ile
     35                  40                  45

TTT TAT AAT AAT CTC CCG GCA TCG                                     270
Phe Tyr Asn Asn Leu Pro Ala Ser
 50                  55
```

(2) INFORMATION FOR SEQ ID NO: 54:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 111 base pairs
(B) TYPE: NUCLEIC ACID
(C) STRANDEDNESS: DOUBLE
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Testis

(ix) FEATURE:
(A) NAME/KEY: sig_peptide
(B) LOCATION: 49..102
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 9.1
seq LVSLCSWSPPLTS/SP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 54:

```
ACAGGCATAG ATCTAGCCCC ACCATCAAGA CAAACAACAT TTTCTATT ATG TTA AAA    57
                                                     Met Leu Lys

AGT GTC CTT GTA AGC CTT TGC AGT TGG TCT CCT CCC CTG ACT TCC AGC    105
Ser Val Leu Val Ser Leu Cys Ser Trp Ser Pro Pro Leu Thr Ser Ser
-15                 -10                 -5                   1

CCC AGG                                                            111
Pro Arg
```

(2) INFORMATION FOR SEQ ID NO: 55:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 285 base pairs
(B) TYPE: NUCLEIC ACID
(C) STRANDEDNESS: DOUBLE
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Testis

(ix) FEATURE:
(A) NAME/KEY: sig_peptide
(B) LOCATION: 154..219
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 9
seq FILAALSLSTTFS/LQ

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 55:

```
AAKACCCTCC CTCCCGTTGC TCCAAACTAA TACGGACTGA ACGGATCGCT GCGAGGGTGG   60

GAGAGAAAAT TAGGGGGAGA AAGGACAGAK AGAKCAACTA CCATCCATAG CCAGATAGAT  120

TATCTTACAC TGAACTGATC AAGTACTKTG AAA ATG ACT TCG AAA TTN ATC TTG  174
                                     Met Thr Ser Lys Xaa Ile Leu
                                             -20

GTG TCC TTC ATA CTT GCT GCA CTG AGT CTT TCA ACC ACC TTT TCT CTC    222
Val Ser Phe Ile Leu Ala Ala Leu Ser Leu Ser Thr Thr Phe Ser Leu
-15                 -10                 -5                   1
```

```
CAA CCA TAC CAG CAR AAG GTT CTA CTA GTT TCT TTT GAT GGA TTC CGT     270
Gln Pro Tyr Gln Gln Lys Val Leu Leu Val Ser Phe Asp Gly Phe Arg
            5                   10                  15

TGG GAT TAC TTA TAT                                                 285
Trp Asp Tyr Leu Tyr
        20
```

(2) INFORMATION FOR SEQ ID NO: 56:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 123 base pairs
(B) TYPE: NUCLEIC ACID
(C) STRANDEDNESS: DOUBLE
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Ovary

(ix) FEATURE:
(A) NAME/KEY: other
(B) LOCATION: 85..120
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 100
region 44..79
id AA280744
est

(ix) FEATURE:
(A) NAME/KEY: sig_peptide
(B) LOCATION: 52..111
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 8.9
seq LAVXLGLATAVSA/GP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 56:

```
GAAAGTGAAA GGAGGAAGAG GAGGCTAAAT GGCTGAGGAG GTCGCAGCGC C ATG AAG     57
                                                         Met Lys
                                                         -20

TCC CTG TCT CTV MTC CTM GCT GTG GMT TTG GGC CTG GCG ACC GCC GTC     105
Ser Leu Ser Leu Xaa Leu Ala Val Xaa Leu Gly Leu Ala Thr Ala Val
            -15                 -10                 -5

TCA GCA GGA CCC GCG TGG                                             123
Ser Ala Gly Pro Ala Trp
        1
```

(2) INFORMATION FOR SEQ ID NO: 57:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 345 base pairs
(B) TYPE: NUCLEIC ACID
(C) STRANDEDNESS: DOUBLE
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Ovary

(ix) FEATURE:
(A) NAME/KEY: sig_peptide
(B) LOCATION: 106..168
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 8.8
seq LLWALLFMQSLWP/QL

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 57:

```
AAAGATACTG ACTGAACATG GCTGGCGGAC TCAGGCTGGG GTCTGCAGTG CAGCATTAAT   60

GGGCCGCTGA CATGAATATG GAGTAGTTTT CTCTAGCAAA GAGTA ATG TGG GCC ATG  117
                                                  Met Trp Ala Met
                                                      -20

GAG TCA GGC CAC CTC CTC TGG GCT CTG CTG TTC ATG CAG TCC TTG TGG      165
Glu Ser Gly His Leu Leu Trp Ala Leu Leu Phe Met Gln Ser Leu Trp
        -15                 -10                 -5

CCT CAA CTG ACT GAT GGA GCC ACT CGA GTC TAC TAC CTG GGC ATC CGG      213
Pro Gln Leu Thr Asp Gly Ala Thr Arg Val Tyr Tyr Leu Gly Ile Arg
      1               5                  10                  15

GAT GTG CAG TGG AAC TAT GCT CCC AAG GGA AGA AAT GTC ATC ACG AAC      261
Asp Val Gln Trp Asn Tyr Ala Pro Lys Gly Arg Asn Val Ile Thr Asn
                20                  25                  30

CAG CCT CTG GAC AGT GAC ATA GTG GCT TCC AGC TTC TTA AAG TCT GAC      309
Gln Pro Leu Asp Ser Asp Ile Val Ala Ser Ser Phe Leu Lys Ser Asp
            35                  40                  45

AAG AAC CGG ATA GGG GGA ACT ACA AGA AGA CCA TGG                      345
Lys Asn Arg Ile Gly Gly Thr Thr Arg Arg Pro Trp
        50                  55
```

(2) INFORMATION FOR SEQ ID NO: 58:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 246 base pairs
(B) TYPE: NUCLEIC ACID
(C) STRANDEDNESS: DOUBLE
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Homo Sapiens

(F) TISSUE TYPE: Testis

(ix) FEATURE:
(A) NAME/KEY: sig_peptide
(B) LOCATION: 100..159
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 8.8
seq LLVMGSLPSASWS/LP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 58:

```
ACGGTGCAGG GCAGAGAAGG AGCAGCCTTG GACTGGGGAT CCTGAGTAGT CCTGTCTGGG    60

AATGGAGGGC ACTGAATTGG CACCCTCCTT GGAGGCCAC ATG GCC CAA ACA TGG      114
                                          Met Ala Gln Thr Trp
                                          -20

GCA TTD CTG CTG GTG ATG GGA TCT CTC CCT TCT GCC AGC TGG TCT CTG     162
Ala Xaa Leu Leu Val Met Gly Ser Leu Pro Ser Ala Ser Trp Ser Leu
-15                 -10                 -5                   1

CCC TGT TTG AGC TGG GAA AGT TTG CTG AAG GCT GCA GCC TGT TCT GAG     210
Pro Cys Leu Ser Trp Glu Ser Leu Leu Lys Ala Ala Ala Cys Ser Glu
            5                  10                  15

TTG GAT GGT AGA AAT GTA GGA AAT ACA CCA ACT CGG                     246
Leu Asp Gly Arg Asn Val Gly Asn Thr Pro Thr Arg
        20                  25
```

(2) INFORMATION FOR SEQ ID NO: 59:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 201 base pairs
(B) TYPE: NUCLEIC ACID
(C) STRANDEDNESS: DOUBLE
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Ovary

(ix) FEATURE:
(A) NAME/KEY: sig_peptide
(B) LOCATION: 130..195
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 8.7
seq LITLLYVWPVINA/CQ

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 59:

```
ATGAATGAGT GTTAATAGGC AATTTTAAAG GACAGAACCT CTGGGGAACC ATCCTGCAGT    60

TCTCCATGTG TACTTAAGTT GATTTTGGAA ACCAGAAACA TATACKACTT CCTTAGAAGT   120

TCTACATTG ATG AAA TGT GGG TTT CTG GCT TAC TTG CTA ATC ACA CTC TTG   171
```

```
        Met Lys Cys Gly Phe Leu Ala Tyr Leu Leu Ile Thr Leu Leu
                -20                     -15                     -10

TAT GTT TGG CCA GTT ATT AAT GCT TGC CAG                                  201
Tyr Val Trp Pro Val Ile Asn Ala Cys Gln
         -5                      1
```

(2) INFORMATION FOR SEQ ID NO: 60:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 128 base pairs
(B) TYPE: NUCLEIC ACID
(C) STRANDEDNESS: DOUBLE
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Testis

(ix) FEATURE:
(A) NAME/KEY: sig_peptide
(B) LOCATION: 21..95
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 8.5
seq LKVLLLPLAPAAA/QD

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 60:

```
AGGGCGGATC TTCTCCGGCC ATG AGG AAG CCA GCC GCT GGC TTC CTT CCC TCA    53
                      Met Arg Lys Pro Ala Ala Gly Phe Leu Pro Ser
                      -25                 -20                 -15

CTC CTG AAG GTG CTG CTC CTG CCT CTG GCA CCT GCC GCA GCC CAG GAT     101
Leu Leu Lys Val Leu Leu Leu Pro Leu Ala Pro Ala Ala Ala Gln Asp
             -10                 -5                  1

TCG ACT CAG GCC TCC ACT CCA GGC AGG                                 128
Ser Thr Gln Ala Ser Thr Pro Gly Arg
         5                   10
```

(2) INFORMATION FOR SEQ ID NO: 61:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 313 base pairs
(B) TYPE: NUCLEIC ACID
(C) STRANDEDNESS: DOUBLE
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Spleen

(ix) FEATURE:
(A) NAME/KEY: sig_peptide
(B) LOCATION: 152..202
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 8.4
seq LLFLTSVVPFVLA/PR

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 61:

```
AAGAATCTTC CCAGTAGGCG GCGCGGGAGG GAAAAGAGGA TTGAGGGGCT AGGCCGGGCG    60

GATCCCGTCC TCCCCCGATG TGAGCAGTTT TCCGAAACCC CGTCAGGCGA AGGCTGCCCA   120

GAGAGGTGGA GTCGGTAGCG GGGCCGGGAA C ATG AGG CAG TCT CTC CTA TTC     172
                                   Met Arg Gln Ser Leu Leu Phe
                                           -15

CTG ACC AGC GTG GTT CCT TTC GTG CTG GCG CCG CGA CCT CCG GAT GAC    220
Leu Thr Ser Val Val Pro Phe Val Leu Ala Pro Arg Pro Pro Asp Asp
-10                 -5                   1               5

CCG GGC TTC GGC CCC CAC CAG AGA CTC GAG AAG CTT GAT TCT TTG CTC    268
Pro Gly Phe Gly Pro His Gln Arg Leu Glu Lys Leu Asp Ser Leu Leu
            10                  15                  20

TCA GAC TAC GAT ATT CTC TCT TTA TCT AAT ATC CAG CAG CAG CSG        313
Ser Asp Tyr Asp Ile Leu Ser Leu Ser Asn Ile Gln Gln Gln Xaa
        25                  30                  35
```

(2) INFORMATION FOR SEQ ID NO: 62:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 142 base pairs
(B) TYPE: NUCLEIC ACID
(C) STRANDEDNESS: DOUBLE
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Ovary

(ix) FEATURE:
(A) NAME/KEY: sig_peptide
(B) LOCATION: 29..103
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 8.1
seq SVLLGLLALMATA/AV

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 62:

```
AAGCTGAGGT GGCAGTGGTT CCACCAAC ATG GAG CTC TCG CAG ATG TCG GAG      52
                               Met Glu Leu Ser Gln Met Ser Glu
                               -25                 -20

CTC ATG GGG CTG TCG GTG TTG CTT GGG CTG CTG GCC CTG ATG GCG ACG    100
```

```
Leu Met Gly Leu Ser Val Leu Leu Gly Leu Leu Ala Leu Met Ala Thr
        -15                 -10                     -5

GCG GCG GTA GCG CGG GGG TGG CTG CGC GCG GGG GAG GTG AGG              142
Ala Ala Val Ala Arg Gly Trp Leu Arg Ala Gly Glu Val Arg
    1               5                   10
```

(2) INFORMATION FOR SEQ ID NO: 63:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 358 base pairs
(B) TYPE: NUCLEIC ACID
(C) STRANDEDNESS: DOUBLE
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Testis

(ix) FEATURE:
(A) NAME/KEY: sig_peptide
(B) LOCATION: 50..244
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 8
seq LTLIGCLVTGVES/KI

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 63:

```
AAGGAAAGGA TTACTCGAGC CTTGTTAGAA TCAGACATGG CTTCAGGGG ATG CAG GAC     58
                                                      Met Gln Asp
                                                      -65

GCT CCC CTG AGC TGC CTG TCA CCG ACT AAG TGG AGC AGT GTT TCT TCC     106
Ala Pro Leu Ser Cys Leu Ser Pro Thr Lys Trp Ser Ser Val Ser Ser
        -60                 -55                 -50

GCA GAC TCA ACT GAG AAG TCA GCC TCT GCG GCA GGC ACC AGG AAT CTG     154
Ala Asp Ser Thr Glu Lys Ser Ala Ser Ala Ala Gly Thr Arg Asn Leu
    -45                 -40                 -35

CCT TTT CAG TTC TGT CTC CGG CAG GCT TTG AGG ATG AAG GCT GCG GGC     202
Pro Phe Gln Phe Cys Leu Arg Gln Ala Leu Arg Met Lys Ala Ala Gly
-30                 -25                 -20                 -15

ATT CTG ACC CTC ATT GGC TGC CTG GTC ACA GGC GTC GAG TCC AAA ATC     250
Ile Leu Thr Leu Ile Gly Cys Leu Val Thr Gly Val Glu Ser Lys Ile
            -10                 -5                      1

TAC ACT CGT TGC AAA CTG GCA AAA ATA TTC TCG AGG GCT GGC CTG GAC     298
Tyr Thr Arg Cys Lys Leu Ala Lys Ile Phe Ser Arg Ala Gly Leu Asp
        5                   10                  15

AAT CYG AGG GGC TTC AGC CTT GGA AAS TGG ATC TGC ATG GCG TAT TAT     346
Asn Xaa Arg Gly Phe Ser Leu Gly Xaa Trp Ile Cys Met Ala Tyr Tyr
    20                  25                  30
```

GAG AGC GGC TGG 358
Glu Ser Gly Trp
35

(2) INFORMATION FOR SEQ ID NO: 64:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 419 base pairs
(B) TYPE: NUCLEIC ACID
(C) STRANDEDNESS: DOUBLE
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Spleen

(ix) FEATURE:
(A) NAME/KEY: sig_peptide
(B) LOCATION: 24..311
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 7.6
seq ALCGLCLLCPRAA/RV

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 64:

ATTTCTCCTG GCACCCTGTA TTC ATG GCC TTG GCG TTC TGC CTC TGC ATG GCT 53
Met Ala Leu Ala Phe Cys Leu Cys Met Ala
-95 -90

GAA GCC ATC CTA CTC TTC TCA CCT GAA CAC TCC CTG TTC TTC TTC TGC 101
Glu Ala Ile Leu Leu Phe Ser Pro Glu His Ser Leu Phe Phe Phe Cys
-85 -80 -75

TCC CGA AAA GCA CGG ATC CGG CTC CAC TGG GCA GGG CAG ACC CTA GCC 149
Ser Arg Lys Ala Arg Ile Arg Leu His Trp Ala Gly Gln Thr Leu Ala
-70 -65 -60 -55

ATC CTC TGT GCA GCT CTG GGC CTG GGC TTC ATC ATC TCC AGC AGG ACC 197
Ile Leu Cys Ala Ala Leu Gly Leu Gly Phe Ile Ile Ser Ser Arg Thr
-50 -45 -40

CGC AGT GAG CTG CCT CAT CTG GTG TCC TGG CAC AGC TGG GTG GGA GCC 245
Arg Ser Glu Leu Pro His Leu Val Ser Trp His Ser Trp Val Gly Ala
-35 -30 -25

CTG ACA CTG CTG GCC ACT GCT GTC CAG GCA CTG TGT GGG CTC TGC CTC 293
Leu Thr Leu Leu Ala Thr Ala Val Gln Ala Leu Cys Gly Leu Cys Leu
-20 -15 -10

CTT TGT CCC CGG GCA GCC AGG GTC TCA AGG GTG GCT CGC CTC AAG CTC 341
Leu Cys Pro Arg Ala Ala Arg Val Ser Arg Val Ala Arg Leu Lys Leu
-5 1 5 10

TAC CAT CTG ACA TGT GGA CTG GTG GTC TAC CTG ATG GCT ACA GTA ACG 389
Tyr His Leu Thr Cys Gly Leu Val Val Tyr Leu Met Ala Thr Val Thr
15 20 25

```
GTG CTT CTG GGC ATG TAC TCA GTA TGG TTC                               419
Val Leu Leu Gly Met Tyr Ser Val Trp Phe
            30                  35
```

(2) INFORMATION FOR SEQ ID NO: 65:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 336 base pairs
(B) TYPE: NUCLEIC ACID
(C) STRANDEDNESS: DOUBLE
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Spleen

(ix) FEATURE:
(A) NAME/KEY: sig_peptide
(B) LOCATION: 37..207
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 7.5
seq LLHRLASFHRVWS/FP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 65:

```
AAGKCTGCCG GTGGGGACTC TTGCAGGGCC GTCCCC ATG TTR CGT TTT CCG ACC        54
                                        Met Leu Arg Phe Pro Thr
                                                -55

TGT TTC CCA TCC KTC CGG GTG RTG GGA GAK AAG CAG CTC CCG CAG GAG       102
Cys Phe Pro Ser Xaa Arg Val Xaa Gly Xaa Lys Gln Leu Pro Gln Glu
    -50                 -45                     -40

ATT ATT TWC CTG GTC TGG TCG CCC AAK CGG GAT CKC ATT GST TTG GCC       150
Ile Ile Xaa Leu Val Trp Ser Pro Xaa Arg Asp Xaa Ile Xaa Leu Ala
-35                 -30                 -25                 -20

AAC ACA GCT GGC GAG GTT TTA CTT CAT CGA CTG GCA AGT TTT CAT CGA       198
Asn Thr Ala Gly Glu Val Leu Leu His Arg Leu Ala Ser Phe His Arg
                -15                 -10                 -5

GTT TGG AGT TTT CCA CCA AAT GAA AAT ACA GGA AWK GAG GTG ACG TGT       246
Val Trp Ser Phe Pro Pro Asn Glu Asn Thr Gly Xaa Glu Val Thr Cys
            1                   5                   10

CTG GCA TGG AGA CCA GAT GGC AAA CTT TTG GCC TTT GCT CTT GCT GAT       294
Leu Ala Trp Arg Pro Asp Gly Lys Leu Leu Ala Phe Ala Leu Ala Asp
    15                  20                  25

ACC AAG AAA ATT GTT TTG TGT GAT GTA GAA AAA CCT GAG AGC               336
Thr Lys Lys Ile Val Leu Cys Asp Val Glu Lys Pro Glu Ser
30                  35                  40
```

(2) INFORMATION FOR SEQ ID NO: 66:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 398 base pairs
(B) TYPE: NUCLEIC ACID
(C) STRANDEDNESS: DOUBLE
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Spleen

(ix) FEATURE:
(A) NAME/KEY: sig_peptide
(B) LOCATION: 9..134
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 7.5
seq LALVVALVAERFA/RR

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 66:

```
AGACCTTC ATG TTC ATG GTG CTG GAG GTG GTG GTG AGC CGG GTG ACC TCG      50
         Met Phe Met Val Leu Glu Val Val Val Ser Arg Val Thr Ser
                 -40                 -35                 -30

TCG CTG GCG ATG CTC TCC GAC TCC TTC CAC ATG CTG TCG GAC GTG CTG      98
Ser Leu Ala Met Leu Ser Asp Ser Phe His Met Leu Ser Asp Val Leu
            -25                 -20                 -15

GCG CTG GTG GTG GCG CTG GTG GCC GAG CGC TTC GCC CGG CGG ACC CAC     146
Ala Leu Val Val Ala Leu Val Ala Glu Arg Phe Ala Arg Arg Thr His
        -10                  -5                   1

GCC ACC CAG AAG AAC ACG TTC GGC TGG ATC CGA GCC GAG GTA ATG GGG     194
Ala Thr Gln Lys Asn Thr Phe Gly Trp Ile Arg Ala Glu Val Met Gly
  5                  10                  15                  20

GCT CTG GTG AAC GCC ATC TTC CTG ACT GGC CTC TGT TTC GCG ATC CTG     242
Ala Leu Val Asn Ala Ile Phe Leu Thr Gly Leu Cys Phe Ala Ile Leu
                 25                  30                  35

CTG GAG GCC ATC GAG CGC TTC ATC GAG CCG CAC GAG ATG CAG CAG CCG     290
Leu Glu Ala Ile Glu Arg Phe Ile Glu Pro His Glu Met Gln Gln Pro
            40                  45                  50

CTG GTG GTS CNT TGG GGT CGG GCG TGG CSG GCT GCT GGT CAA CGT GCT     338
Leu Val Val Xaa Trp Gly Arg Ala Trp Xaa Ala Ala Gly Gln Arg Ala
        55                  60                  65

GGG GCT CTG CCT CTT CCA CCA TCA CAG CGG CTT CAG CCA GGA CTC CGG     386
Gly Ala Leu Pro Leu Pro Pro Ser Gln Arg Leu Gln Pro Gly Leu Arg
    70                  75                  80

CCG CGG CCA TGG                                                     398
Pro Arg Pro Trp
 85
```

(2) INFORMATION FOR SEQ ID NO: 67:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 306 base pairs
(B) TYPE: NUCLEIC ACID
(C) STRANDEDNESS: DOUBLE
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Testis

(ix) FEATURE:
(A) NAME/KEY: sig_peptide
(B) LOCATION: 70..186
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 7.5
seq LLLLLGLIVLVNI/GI

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 67:

```
AASTGTGSST TGGGGCCGGG GGTGGGGGGC AGAGGGGGGT GGCCCAGGTG GCCCTAGGAC   60

CCCCCCTCC ATG GAA AAC CAG CTA TGG CAT AAC ACC GTG AGA TGT TGC AAT  111
          Met Glu Asn Gln Leu Trp His Asn Thr Val Arg Cys Cys Asn
                          -35                 -30

CAA TAC CAA GAA AGC CCC CAC GAT GCC GAG GAC ATC TTA CTC CTG CTG    159
Gln Tyr Gln Glu Ser Pro His Asp Ala Glu Asp Ile Leu Leu Leu Leu
-25                 -20                 -15                 -10

CTG GGC CTC ATC GTT CTT GTC AAC ATT GGC ATC AAC GTG GCA ACT ATG    207
Leu Gly Leu Ile Val Leu Val Asn Ile Gly Ile Asn Val Ala Thr Met
                -5                   1                   5

ATG TGG CAT GGA CTC CAG AAC GCC TTA GAC AAG ATG ATT GAT TGG GCT    255
Met Trp His Gly Leu Gln Asn Ala Leu Asp Lys Met Ile Asp Trp Ala
    10                  15                  20

ACT CAG AAA ATA GCA GTC TTC TTC GCT GTG TTC GTC GCC GCC GCC GCC    303
Thr Gln Lys Ile Ala Val Phe Phe Ala Val Phe Val Ala Ala Ala Ala
    25                  30                  35

CGG                                                                306
Arg
 40
```

(2) INFORMATION FOR SEQ ID NO: 68:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 178 base pairs
(B) TYPE: NUCLEIC ACID
(C) STRANDEDNESS: DOUBLE
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Ovary

(ix) FEATURE:
(A) NAME/KEY: sig_peptide
(B) LOCATION: 23..76
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 7.5
seq ITLLTLSPNSVCC/CP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 68:

```
AATACTGAGG TATATTGCCA AA ATG CTC TCC AKW AAG ATC ACC CTC TTG ACA     52
                         Met Leu Ser Xaa Lys Ile Thr Leu Leu Thr
                                     -15                 -10

CTG TCA CCC AAT AGT GTG TGT TGC TGC CCC TCA GCA ACC CTG GGT GCC     100
Leu Ser Pro Asn Ser Val Cys Cys Cys Pro Ser Ala Thr Leu Gly Ala
            -5                   1               5

AGC AAT CAT TCT CAT CTT TGG AGA TCT ACT AGC AGA CAT GGC ATC TCC     148
Ser Asn His Ser His Leu Trp Arg Ser Thr Ser Arg His Gly Ile Ser
     10                  15                  20

TTC CCA TGG GCA TTC CTT TTA ATT AAC GGG                             178
Phe Pro Trp Ala Phe Leu Leu Ile Asn Gly
 25                  30
```

(2) INFORMATION FOR SEQ ID NO: 69:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 234 base pairs
(B) TYPE: NUCLEIC ACID
(C) STRANDEDNESS: DOUBLE
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Testis

(ix) FEATURE:
(A) NAME/KEY: sig_peptide
(B) LOCATION: 79..132
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 7.4
seq GWLVLCVLAISLA/SM

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 69:

```
CTGCTGGGCA GCCCACAGGG TCCCTGGGCG GAGGGCAGGA GCATCCMGTT GGAGTTGACA     60

ACAGGAGGCA GAGGCATC ATG GAG GGT CCC CGG GGA TGG CTG GTG CTC TGT     111
```

```
                    Met Glu Gly Pro Arg Gly Trp Leu Val Leu Cys
                                -15                 -10

GTG CTG GCC ATA TCG CTG GCC TCT ATG GTG ACC GAG GAC TTG TGC CGA     159
Val Leu Ala Ile Ser Leu Ala Ser Met Val Thr Glu Asp Leu Cys Arg
        -5                  1                   5

GCA CCA GAC GGG AAG AAA GGG GAG GCA GGV AVA CCT GGC AGA CGG GGG     207
Ala Pro Asp Gly Lys Lys Gly Glu Ala Gly Xaa Pro Gly Arg Arg Gly
 10                 15                  20                  25

CGG CCA GGC CTC AAG GGG GAG CAA CGG                                 234
Arg Pro Gly Leu Lys Gly Glu Gln Arg
                30
```

(2) INFORMATION FOR SEQ ID NO: 70:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 364 base pairs
(B) TYPE: NUCLEIC ACID
(C) STRANDEDNESS: DOUBLE
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Testis

(ix) FEATURE:
(A) NAME/KEY: sig_peptide
(B) LOCATION: 41..100
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 7.3
seq LAVFMLLAQLVSG/NW

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 70:

```
AATAGAGACT TCTGGACTCT ATAGAACCCA CTGCCTCCTG ATG AAG TCC CTA CTG      55
                                            Met Lys Ser Leu Leu
                                            -20

TTC ACC CTT GCA GTT TTT ATG CTC CTG GCC CAA TTG GTC TCA GGT AAT     103
Phe Thr Leu Ala Val Phe Met Leu Leu Ala Gln Leu Val Ser Gly Asn
-15                 -10                 -5                    1

TGG TAT GTG AAA AAG TGT CTA AAC GAC GTT GGA ATT TGC AAG AAG AAG     151
Trp Tyr Val Lys Lys Cys Leu Asn Asp Val Gly Ile Cys Lys Lys Lys
            5                   10                  15

TGC AAA CCT GAA GAG ATG CAT GTA AAG AAT GGT TGG GCA ATG TGC GGC     199
Cys Lys Pro Glu Glu Met His Val Lys Asn Gly Trp Ala Met Cys Gly
        20                  25                  30

AAA CAA AGG GAC TGC TGT GTT CCA GCT GAC AGA CGT GCT AAT TAT CCT     247
Lys Gln Arg Asp Cys Cys Val Pro Ala Asp Arg Arg Ala Asn Tyr Pro
    35                  40                  45
```

```
GTT TTC TGT GTC CAG ACA AAG ACT ACA AGA ATT TCA ACA GTC ACA GCA     295
Val Phe Cys Val Gln Thr Lys Thr Thr Arg Ile Ser Thr Val Thr Ala
 50                 55                  60                  65

ACA ACA GCA ACA ACA ACT TTG ATG ATG ACT ACT GCT TCG ATG TCT TCG     343
Thr Thr Ala Thr Thr Thr Leu Met Met Thr Thr Ala Ser Met Ser Ser
                70                  75                  80

ATG GCT CCT ACC CGT TTC TCC                                         364
Met Ala Pro Thr Arg Phe Ser
             85
```

(2) INFORMATION FOR SEQ ID NO: 71:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 62 base pairs
(B) TYPE: NUCLEIC ACID
(C) STRANDEDNESS: DOUBLE
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Ovary

(ix) FEATURE:
(A) NAME/KEY: sig_peptide
(B) LOCATION: 9..56
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 7.3
seq LILLFSLLISIVC/MI

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 71:

```
ATAGTAAA ATG TTA AAG TTG ATC TTA CTT TTT TCG CTC CTC ATC TCT ATT    50
         Met Leu Lys Leu Ile Leu Leu Phe Ser Leu Leu Ile Ser Ile
             -15                 -10                     -5

GTT TGT ATG ATT                                                      62
Val Cys Met Ile
         1
```

(2) INFORMATION FOR SEQ ID NO: 72:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 296 base pairs
(B) TYPE: NUCLEIC ACID
(C) STRANDEDNESS: DOUBLE
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Testis

(ix) FEATURE:
(A) NAME/KEY: sig_peptide
(B) LOCATION: 195..272
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 7.1
seq LASLQWSLTLAWC/GS

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 72:

```
AAAGTGTAGA ACACGGACCT CTGAGTTATG CTCTTGAGAG GTGCCAAAGC TGGGCTGTTT   60

ACCTACCTTA TCCACAGAGC TCTGAAAGTC AAGCCAGAAA GGAAGGATTC CAAATTCTTG  120

GAATTTTATC TAGAAAAGAA GACTAAGCAG CTTTTGTTCT TCTGTGACCC AGTTGCTGGC  180

CCAAGACATG GACA ATG ACC CCC TGG TGT TTG GCG TGT CTG GGG AGG AGG    230
                Met Thr Pro Trp Cys Leu Ala Cys Leu Gly Arg Arg
                    -25                 -20                 -15

CCT CTC GCT TCT TTG CAG TGG AGC CTG ACA CTG GCG TGG TGT GGC TCC    278
Pro Leu Ala Ser Leu Gln Trp Ser Leu Thr Leu Ala Trp Cys Gly Ser
                -10                 -5                   1

GGC AGC CAC TGG ACA GAG                                            296
Gly Ser His Trp Thr Glu
        5
```

(2) INFORMATION FOR SEQ ID NO: 73:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 315 base pairs
(B) TYPE: NUCLEIC ACID
(C) STRANDEDNESS: DOUBLE
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Spleen

(ix) FEATURE:
(A) NAME/KEY: sig_peptide
(B) LOCATION: 151..228
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 6.9
seq LWVLLLCAHVVTL/LV

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 73:

```
AACACGCAGC TAGACACAGC TAMCTTGAGT CTTGGAGCTC CTAGAGGGAM GCTTCTGGAM   60

AGGAAGGCTC TTCAGGACCT CTTAGGAGCC AGAGMMSMGG ACGTKSACAC AGATAAAGAG  120

CCAGGCTCAC CAGCTCCTGA CGCATGCAKS ATG ACC ATG AGA CAC AAC TGG ACA   174
                                 Met Thr Met Arg His Asn Trp Thr
```

```
                                         -25                 -20

CCA GAC CTC AGC CCT TTG TGG GTC CTG CTC CTG TGT GCC CAC GTC GTC      222
Pro Asp Leu Ser Pro Leu Trp Val Leu Leu Leu Cys Ala His Val Val
            -15                 -10                 -5

ACT CTC CTG GTC AGA GCC ACA CCT GTC TCG CAG ACC ACC ACA GCT GCC      270
Thr Leu Leu Val Arg Ala Thr Pro Val Ser Gln Thr Thr Thr Ala Ala
         1               5                  10

ACT GCC TCA GTT AGA AGC ACA AAG GAC CCC TGC CCC TCC CAG CGG          315
Thr Ala Ser Val Arg Ser Thr Lys Asp Pro Cys Pro Ser Gln Arg
 15                 20                  25
```

(2) INFORMATION FOR SEQ ID NO: 74:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 131 base pairs
(B) TYPE: NUCLEIC ACID
(C) STRANDEDNESS: DOUBLE
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Testis

(ix) FEATURE:
(A) NAME/KEY: sig_peptide
(B) LOCATION: 27..86
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 6.9
seq LFCATLSCMPATS/AP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 74:

```
AAGCCTACTT TGACACTCAT TTAAAG ATG ACA GGG AAC AAT AGA GAT TTG TTC      53
                             Met Thr Gly Asn Asn Arg Asp Leu Phe
                             -20                 -15

TGT GCA ACC CTT TCT TGT ATG CCG GCG ACA TCA GCT CCG CAC ATG AAA      101
Cys Ala Thr Leu Ser Cys Met Pro Ala Thr Ser Ala Pro His Met Lys
    -10                 -5                   1                   5

CTG CCC GAT ATT TCA TTC CAC CTG CCC GGG                              131
Leu Pro Asp Ile Ser Phe His Leu Pro Gly
                10                  15
```

(2) INFORMATION FOR SEQ ID NO: 75:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 224 base pairs
(B) TYPE: NUCLEIC ACID
(C) STRANDEDNESS: DOUBLE
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Ovary

(ix) FEATURE:
(A) NAME/KEY: sig_peptide
(B) LOCATION: 114..191
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 6.9
seq LWVLLLCAHVVTL/LV

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 75:

```
ACTTCCCAGA AGCAGCTCTG GTGCTGAAGA GAGCACTGCC TCCCTGTGTG ACTGGAGAAG    60

AGGACGTTGT CACAGATAAA GAGCCAGGCT CACCAGCTCC TGACGCATGC ATC ATG      116
                                                            Met

ACC ATG AGA CAC AAC TGG ACA CCA GAC CTC AGC CCT TTG TGG GTC CTG     164
Thr Met Arg His Asn Trp Thr Pro Asp Leu Ser Pro Leu Trp Val Leu
-25                 -20                 -15                 -10

CTC CTG TGT GCC CAC GTC GTC ACT CTC CTG GTC AGA GCC ACA CCT GTC     212
Leu Leu Cys Ala His Val Val Thr Leu Leu Val Arg Ala Thr Pro Val
                -5                   1               5

TCG CAG CCC ACG                                                     224
Ser Gln Pro Thr
        10
```

(2) INFORMATION FOR SEQ ID NO: 76:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 333 base pairs
(B) TYPE: NUCLEIC ACID
(C) STRANDEDNESS: DOUBLE
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Testis

(ix) FEATURE:
(A) NAME/KEY: sig_peptide
(B) LOCATION: 79..138
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 6.9
seq LYLLGMLVPGGLG/YD

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 76:

```
ACTTGATGCA TTCATTCTCA AGGACACTTG ATCCACTGCC AGAGAGGCCC AGAATTTTCT    60
```

```
AACTTACTGT GTGGCAGA ATG AAG CCT CTG CTT GAA ACC CTT TAT CTT TTG     111
                    Met Lys Pro Leu Leu Glu Thr Leu Tyr Leu Leu
                    -20             -15                 -10

GGG ATG CTG GTT CCT GGA GGG CTG GGA TAT GAT AGA TCC TTA GCC CAA     159
Gly Met Leu Val Pro Gly Gly Leu Gly Tyr Asp Arg Ser Leu Ala Gln
                -5                  1               5

CAC AGA CAA GAG ATT GTG GAC AAG TCA GTG AGT CCA TGG AGC CTG GAG     207
His Arg Gln Glu Ile Val Asp Lys Ser Val Ser Pro Trp Ser Leu Glu
        10                  15                  20

ACG TAT TCC TAT AAC ATA TAC CAC CCC ATG GGA GAG ATC TAT GAG TGG     255
Thr Tyr Ser Tyr Asn Ile Tyr His Pro Met Gly Glu Ile Tyr Glu Trp
    25                  30                  35

ATG AGA GAG ATC AGT GAG AAG TAC AAG GAA GTG GTG ACA CAG CAT TTC     303
Met Arg Glu Ile Ser Glu Lys Tyr Lys Glu Val Val Thr Gln His Phe
40                  45                  50                  55

CTA GGA GTG ACC TAT GAG ACC CAA CCC GCG                             333
Leu Gly Val Thr Tyr Glu Thr Gln Pro Ala
                60                  65
```

(2) INFORMATION FOR SEQ ID NO: 77:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 295 base pairs
(B) TYPE: NUCLEIC ACID
(C) STRANDEDNESS: DOUBLE
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Spleen

(ix) FEATURE:
(A) NAME/KEY: sig_peptide
(B) LOCATION: 80..274
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 6.8
seq LLFLISLAAHLSQ/WT

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 77:

```
AAAGTATTGG GGATGCTGAG CTGCGGGGTA CGGGCCTGAG GAGGGATGGG AGTAAGAAGT    60

GCTGTGGAAA CCGTCAGCC ATG AAC CAG GCT GAC CCT CGG CTC AGA GCA GTG     112
                     Met Asn Gln Ala Asp Pro Arg Leu Arg Ala Val
                     -65                 -60                 -55

TGC TTG TGG ACT CTC ACA TCT GCA GCC ATG AGC AGA GGC GAC AAC TGC     160
Cys Leu Trp Thr Leu Thr Ser Ala Ala Met Ser Arg Gly Asp Asn Cys
            -50                 -45                 -40
```

```
ACG GAT CTA CTC GCA CTG GGA ATC CCC TCC ATA ACC CAG GCC TGG GGA    208
Thr Asp Leu Leu Ala Leu Gly Ile Pro Ser Ile Thr Gln Ala Trp Gly
            -35                     -30                     -25

CTG TGG GTC CTC TTA GGG GCT GTG ACG CTG CTA TTT CTC ATC TCG CTG    256
Leu Trp Val Leu Leu Gly Ala Val Thr Leu Leu Phe Leu Ile Ser Leu
        -20                 -15                     -10

GCT GCA CAC TTG TCC CAG TGG ACC AGG GGT CGG AGC GGG                295
Ala Ala His Leu Ser Gln Trp Thr Arg Gly Arg Ser Gly
    -5                      1               5
```

(2) INFORMATION FOR SEQ ID NO: 78:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 451 base pairs
(B) TYPE: NUCLEIC ACID
(C) STRANDEDNESS: DOUBLE
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Spleen

(ix) FEATURE:
(A) NAME/KEY: sig_peptide
(B) LOCATION: 317..442
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 6.8
seq LLSILSSLTMVIC/RH

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 78:

```
ACTACACAGA GAGAAGCCAT CATTCTAGCT AGACAAGAAG CTCGGGAAGA ATTACTTTTA   60

CATCAGAGTG AATGGGAGGG AAGAATATCT CCCGAGCAGG TTGACACCTC TTCCTTACCC  120

CTAGTACCAC AGCATTCATT CGCCTCATTA CCTCTTAATG AATCTGAAAG AAACCAAGAA  180

CCATGTTCAA TTAACAGTGA TAATATAGTA TCCTCAGGTC ACTCAGAGAT ACCAACATTG  240

CCTGATGGGC TGTTGGGTTT ATCACATCTT GTTTTACCTC AACAAGATAA TTTGATTGCA  300

CTTGAAGAAC ACTTGC ATG CAC AGA CAG ATT TCC TTC CTT CTA TTG AGA AAA  352
                  Met His Arg Gln Ile Ser Phe Leu Leu Leu Arg Lys
                          -40                     -35

CCC AGA AAG AAT TGG TTT TGT CAA AAC CAT GTA AAT TTG AGG AAA AGG    400
Pro Arg Lys Asn Trp Phe Cys Gln Asn His Val Asn Leu Arg Lys Arg
-30                 -25                     -20                 -15

TAT CTT CTG AGC ATT TTA TCC AGT CTC ACC ATG GTG ATT TGC AGA CAC    448
Tyr Leu Leu Ser Ile Leu Ser Ser Leu Thr Met Val Ile Cys Arg His
            -10                     -5                      1

GGG                                                                451
```

Gly

(2) INFORMATION FOR SEQ ID NO: 79:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 317 base pairs
(B) TYPE: NUCLEIC ACID
(C) STRANDEDNESS: DOUBLE
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Testis

(ix) FEATURE:
(A) NAME/KEY: sig_peptide
(B) LOCATION: 162..290
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 6.8
seq ALSAXTFVSFLHA/AP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 79:

```
AGTACGGATC TCTTTAATAT TCTGTGTAAC AAAATAGAAA TGCTCATAAA GTACTTCTGC    60

GGCAAACCAA AGTATAGCAC CTGACTCAAG GAAAAGCAAG GAAAAGCACA TGTGGGATCC   120

CTTGAATGGC AAGTGAAACT AGCCACTAGT TTCATTTTTA C ATG AAA CAA TGG CTG   176
                                              Met Lys Gln Trp Leu
                                                              -40

TGT TGG GTG CTG AGG CTG GAA GGT AGA CAG GGG CTT GGG GTT GGA GAG      224
Cys Trp Val Leu Arg Leu Glu Gly Arg Gln Gly Leu Gly Val Gly Glu
            -35                 -30                 -25

CCT CGT GGG CTG CGT TTG TGC TTG GGG GCC TTG AGC GCA SCC ACC TTT      272
Pro Arg Gly Leu Arg Leu Cys Leu Gly Ala Leu Ser Ala Xaa Thr Phe
        -20                 -15                 -10

GTC AGC TTT CTA CAC GCT GCT CCC CAC TCC CAT CCA GCC CTT GGG          317
Val Ser Phe Leu His Ala Ala Pro His Ser His Pro Ala Leu Gly
     -5                   1               5
```

(2) INFORMATION FOR SEQ ID NO: 80:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 235 base pairs
(B) TYPE: NUCLEIC ACID
(C) STRANDEDNESS: DOUBLE
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

```
        (A) ORGANISM: Homo Sapiens
        (F) TISSUE TYPE: Ovary

   (ix) FEATURE:
        (A) NAME/KEY: sig_peptide
        (B) LOCATION: 29..226
        (C) IDENTIFICATION METHOD: Von Heijne matrix
        (D) OTHER INFORMATION:  score 6.8
                                seq LLFFLFPILFIRS/QH

   (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 80:

ACAATTTGGG TGTGTCTGGT GTYTTGCC ATG AGA CTG GGG TTA TGC TTC TGG      52
                               Met Arg Leu Gly Leu Cys Phe Trp
                                   -65                 -60

GTG CCA CAC AGA GGT GAA ATG TCC TTC TCA TCA CAT TAT TCG AGA GGT    100
Val Pro His Arg Gly Glu Met Ser Phe Ser Ser His Tyr Ser Arg Gly
            -55                 -50                 -45

ACA TGG TAC CAA TGG GAC TTA TCG CTG CTG ATG TTA ACC TTG ATC TCT    148
Thr Trp Tyr Gln Trp Asp Leu Ser Leu Leu Met Leu Thr Leu Ile Ser
        -40                 -35                 -30

TGG TTC AGG TGG TGC CTG CCA GCT GTC TCC ACT GTG GAG TTA CTA TTT    196
Trp Phe Arg Trp Cys Leu Pro Ala Val Ser Thr Val Glu Leu Leu Phe
    -25                 -20                 -15

TTC CTT TTC CCC ATT TTA TTC ATC AGA AGC CAG CAC CGG                235
Phe Leu Phe Pro Ile Leu Phe Ile Arg Ser Gln His Arg
-10                 -5                   1


(2) INFORMATION FOR SEQ ID NO: 81:

   (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 390 base pairs
        (B) TYPE: NUCLEIC ACID
        (C) STRANDEDNESS: DOUBLE
        (D) TOPOLOGY: LINEAR

   (ii) MOLECULE TYPE: CDNA

   (vi) ORIGINAL SOURCE:
        (A) ORGANISM: Homo Sapiens
        (F) TISSUE TYPE: Ovary

   (ix) FEATURE:
        (A) NAME/KEY: sig_peptide
        (B) LOCATION: 67..369
        (C) IDENTIFICATION METHOD: Von Heijne matrix
        (D) OTHER INFORMATION:  score 6.6
                                seq IIIVITITSACSA/CI

   (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 81:

ACTTTCTAAG AGTACTTGTT TAGATATTTT GTGTCCCTAG ATTTGTCTGA TGATTAGGCT   60
```

```
GCAGTT ATG GAT TTT TGG GAA GAA TAC CGC AGA GGT GAT GTG CCC TTC      108
       Met Asp Phe Trp Glu Glu Tyr Arg Arg Gly Asp Val Pro Phe
           -100                -95                 -90

TCA TGG TGT CCT ATC AGG AGC TAC CTG ATG TCA GTA TGT CCT GTT ACT     156
Ser Trp Cys Pro Ile Arg Ser Tyr Leu Met Ser Val Cys Pro Val Thr
        -85                 -80                 -75

GGC AAA GTT AAC CTT AAT CAT TTG GTT AAG GTA GCC TCT GCC AGG TTT     204
Gly Lys Val Asn Leu Asn His Leu Val Lys Val Ala Ser Ala Arg Phe
    -70                 -65                 -60

CTC CAC CAA GTT ACT ATT TTT CCT TTT CTG TAC TCT GTT AAG GCA AAT     252
Leu His Gln Val Thr Ile Phe Pro Phe Leu Tyr Ser Val Lys Ala Asn
-55                 -50                 -45                 -40

TAT TGC TTT TTA AAT TTT GAT GTA CCT CAA TAT GCA TGG GAG ATA CAT     300
Tyr Cys Phe Leu Asn Phe Asp Val Pro Gln Tyr Ala Trp Glu Ile His
                -35                 -30                 -25

AGC TTT GCA GCT CCC TCA ATC TTA ATT GTA ATA ATA ATA GTA ATA ACA     348
Ser Phe Ala Ala Pro Ser Ile Leu Ile Val Ile Ile Ile Val Ile Thr
            -20                 -15                 -10

ATA ACT AGC GCT TGC TCC GCC TGC ATA GTT CTA AAC ACA TGT             390
Ile Thr Ser Ala Cys Ser Ala Cys Ile Val Leu Asn Thr Cys
        -5                  1                   5
```

(2) INFORMATION FOR SEQ ID NO: 82:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 349 base pairs
(B) TYPE: NUCLEIC ACID
(C) STRANDEDNESS: DOUBLE
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Testis

(ix) FEATURE:
(A) NAME/KEY: sig_peptide
(B) LOCATION: 59..139
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 6.5
seq SLSLSTVWNWIQA/SF

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 82:

```
AATATTTAGA TTCCTGAAGC TTCTGCACAT GTAGTTCCTA GAGCTGCTGC TTATTAAA      58

ATG TCA ACA TCT TCA TCT TCT AGC TGG GAC AAC CTC TTA GAG TCT CTC     106
Met Ser Thr Ser Ser Ser Ser Ser Trp Asp Asn Leu Leu Glu Ser Leu
        -25                 -20                 -15

TCT CTC AGC ACA GTA TGG AAT TGG ATA CAA GCA AGT TTT TTG GGA GAG     154
```

```
Ser Leu Ser Thr Val Trp Asn Trp Ile Gln Ala Ser Phe Leu Gly Glu
    -10                 -5                  1               5

ACT AGT GCA CCT CAG CAA ACA AGT TTG GGA CTA TTA GAT AAT CTT GCT     202
Thr Ser Ala Pro Gln Gln Thr Ser Leu Gly Leu Leu Asp Asn Leu Ala
                10                  15                  20

CCA GCT GTG CAA ATC ATC TTG AGG ATT TCT TTC TTG ATT TTA TTG GGA     250
Pro Ala Val Gln Ile Ile Leu Arg Ile Ser Phe Leu Ile Leu Leu Gly
            25                  30                  35

ATA GGA ATA TAT GCC TTA TGG AAA CGA AGT ATT CAG TCA ATT CAG AAA     298
Ile Gly Ile Tyr Ala Leu Trp Lys Arg Ser Ile Gln Ser Ile Gln Lys
        40                  45                  50

ACA TTG TTG TTT GTA ATC ACA CTC TAC AAA CTT TAC AAG AAG GGC TCG     346
Thr Leu Leu Phe Val Ile Thr Leu Tyr Lys Leu Tyr Lys Lys Gly Ser
    55                  60                  65

GCG                                                                 349
Ala
 70
```

(2) INFORMATION FOR SEQ ID NO: 83:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 302 base pairs
(B) TYPE: NUCLEIC ACID
(C) STRANDEDNESS: DOUBLE
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Spleen

(ix) FEATURE:
(A) NAME/KEY: sig_peptide
(B) LOCATION: 27..104
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 6.5
seq LALGSAGLLWCLA/GF

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 83:

```
AGCAGACCGG CCGCCGCTTC ACCGGC ATG GTC TTC GCC ACC ATC GGT TTC TCG     53
                             Met Val Phe Ala Thr Ile Gly Phe Ser
                                 -25                 -20

CTG AAG TCG GGC CTG GCC CTT GGC TCG GCG GGC CTG CTG TGG TGC CTG     101
Leu Lys Ser Gly Leu Ala Leu Gly Ser Ala Gly Leu Leu Trp Cys Leu
        -15                 -10                 -5

GCC GGT TTC TTC GGC TAC GAC ACA CAG CAG CCC ACG GCA CCC AAC GCC     149
Ala Gly Phe Phe Gly Tyr Asp Thr Gln Gln Pro Thr Ala Pro Asn Ala
    1               5                   10                  15
```

```
ATC GAG GGC TAC CGC GTC ATG TCC AGC TTC GGC GTC GGC GCG CTG TTC     197
Ile Glu Gly Tyr Arg Val Met Ser Ser Phe Gly Val Gly Ala Leu Phe
                20                  25                  30

GCC GCC TGC ACG ATC TGC CTG CTG GCS RAC AAG CTG AAC AAG CAG ACG     245
Ala Ala Cys Thr Ile Cys Leu Leu Ala Xaa Lys Leu Asn Lys Gln Thr
            35                  40                  45

ACG CTG AAG ATG GCC GAC GAC CTC GCC CAA CGG CGC CAG CAG GCC GAC     293
Thr Leu Lys Met Ala Asp Asp Leu Ala Gln Arg Arg Gln Gln Ala Asp
        50                  55                  60

CTT GCG CCG                                                         302
Leu Ala Pro
    65
```

(2) INFORMATION FOR SEQ ID NO: 84:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 151 base pairs
(B) TYPE: NUCLEIC ACID
(C) STRANDEDNESS: DOUBLE
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Testis

(ix) FEATURE:
(A) NAME/KEY: sig_peptide
(B) LOCATION: 35..76
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 6.4
seq VLLLSGSVSVGVC/CA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 84:

```
ACAATCTCAC AGTCCGTGGC AGAGCCTTGT CCTG ATG GTT TTA TTG CTT TCT GGC    55
                                      Met Val Leu Leu Leu Ser Gly
                                                      -10

AGT GTG AGT GTG GGT GTG TGT TGT GCC TAC TTG TGC ATC TCC ATT TCT     103
Ser Val Ser Val Gly Val Cys Cys Ala Tyr Leu Cys Ile Ser Ile Ser
        -5                  1               5

AAA ACA CCA ACT GCT TGT GCA TTG TAT GGT CTT TAT TTA CCG TTT TTT     151
Lys Thr Pro Thr Ala Cys Ala Leu Tyr Gly Leu Tyr Leu Pro Phe Phe
 10                  15                  20                  25
```

(2) INFORMATION FOR SEQ ID NO: 85:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 169 base pairs
(B) TYPE: NUCLEIC ACID

(C) STRANDEDNESS: DOUBLE
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Uterus

(ix) FEATURE:
(A) NAME/KEY: sig_peptide
(B) LOCATION: 26..112
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 6.4
seq GLCXLCXVXNVFA/GS

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 85:

```
ATAATCTGTA ACTTTAGCCC CAACC ATG TGC TCG CAG AAA CGT GCT GTA TCA      52
                            Met Cys Ser Gln Lys Arg Ala Val Ser
                                            -25

AAT CAA GGT TTA ATG GAT TTA GGG CTG TGC ARG CTG TGC YTT GTT AMC     100
Asn Gln Gly Leu Met Asp Leu Gly Leu Cys Xaa Leu Cys Xaa Val Xaa
-20                 -15                 -10                  -5

AAT GTG TTT GCA GGC AGT ATG CCT GGT AAA AGT CAT TGC CAT TCT CCA     148
Asn Val Phe Ala Gly Ser Met Pro Gly Lys Ser His Cys His Ser Pro
                1               5                  10

TTC TCT ATT AAC CAG GGC AGG                                         169
Phe Ser Ile Asn Gln Gly Arg
        15
```

(2) INFORMATION FOR SEQ ID NO: 86:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 157 base pairs
(B) TYPE: NUCLEIC ACID
(C) STRANDEDNESS: DOUBLE
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Ovary

(ix) FEATURE:
(A) NAME/KEY: sig_peptide
(B) LOCATION: 29..70
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 6.4
seq LIVLTLHSPSCDT/AQ

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 86:

```
ATGGGGGTTT CTTTGTTGCT GCTGGGTG ATG CTA ATA GTC CTG ACT CTC CAC      52
                               Met Leu Ile Val Leu Thr Leu His
                                               -10

TCG CCC TCC TGT GAC ACT GCC CAG GAG GAG ATG GGG AGG GTG CCC ACT    100
Ser Pro Ser Cys Asp Thr Ala Gln Glu Glu Met Gly Arg Val Pro Thr
    -5              1               5                       10

ACT CCC AAG TGC AGG TGG AAG TTA GGG CTC TCC ATG TGT TCT TTG CTG    148
Thr Pro Lys Cys Arg Trp Lys Leu Gly Leu Ser Met Cys Ser Leu Leu
                15                  20                  25

ACA CCT GGG                                                        157
Thr Pro Gly
```

(2) INFORMATION FOR SEQ ID NO: 87:

(i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 437 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:
- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Testis

(ix) FEATURE:
- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 66..251
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 6.4
  seq SVLWLGALGLTIQ/AV

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 87:

```
AACTCCCAGA ATGCTGACCA AAGTGGGAGG AGCACTAGGT CTTCCCGTCA CCTCCACCTC   60

TCTCC ATG ACC CGG CTC TGC TTA CCC AGA CCC GAA GCA CGT GAG GAT CCG  110
      Met Thr Arg Leu Cys Leu Pro Arg Pro Glu Ala Arg Glu Asp Pro
              -60                 -55                 -50

ATC CCA GTT CCT CCA AGG GGC CTG GGT GCT GGG GAG GGG TCA GGT AGT    158
Ile Pro Val Pro Pro Arg Gly Leu Gly Ala Gly Glu Gly Ser Gly Ser
        -45                 -40                 -35

CCA GTG CGT CCA CCT GTA TCC ACC TGG GGC CCT AGC TGG GCC CAG CTC    206
Pro Val Arg Pro Pro Val Ser Thr Trp Gly Pro Ser Trp Ala Gln Leu
    -30                 -25                 -20

CTG GAC AGT GTC CTA TGG CTG GGG GCA CTA GGA CTG ACA ATC CAG GCA    254
Leu Asp Ser Val Leu Trp Leu Gly Ala Leu Gly Leu Thr Ile Gln Ala
-15                 -10                 -5                  1

GTC TTT TCC ACC ACT GGC CCA GCC CTG CTG CTG CTT CTG GTC AGC TTC    302
Val Phe Ser Thr Thr Gly Pro Ala Leu Leu Leu Leu Leu Val Ser Phe
```

```
              5                  10                  15

CTC ACC TTT GAC CTG CTC CAT AGG CCC GCA GTC ACA CTC TGC CAC AGC     350
Leu Thr Phe Asp Leu Leu His Arg Pro Ala Val Thr Leu Cys His Ser
         20                  25                  30

GCA AAC TTC TCA CCA GGG GCC AGA GTC AGG GGG CCG GTG AAG GTC CTG     398
Ala Asn Phe Ser Pro Gly Ala Arg Val Arg Gly Pro Val Lys Val Leu
     35                  40                  45

GAC AGC AGG AGG CTC TAC TCC TGC AAA TGG GTA CAG TCT                 437
Asp Ser Arg Arg Leu Tyr Ser Cys Lys Trp Val Gln Ser
 50                  55                  60
```

(2) INFORMATION FOR SEQ ID NO: 88:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 237 base pairs
(B) TYPE: NUCLEIC ACID
(C) STRANDEDNESS: DOUBLE
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Uterus

(ix) FEATURE:
(A) NAME/KEY: sig_peptide
(B) LOCATION: 133..177
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 6.4
seq LTCLFLSLISTYP/SC

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 88:

```
ATTTATGGTA GAGAGATATA TTTGTATTGG TTCCAGTTCC ATTGGTTTGT GAAATATTAA    60

TATGCCAACA CAGCCTAGCA TATTGGAGTC ACTGGAAATG CATCAGTGCT AGCCTTACAT   120

GCCTTTCACT CT ATG GTG TTA ACC TGC CTT TTT CTA AGT CTA ATC TCC ACT   171
              Met Val Leu Thr Cys Leu Phe Leu Ser Leu Ile Ser Thr
              -15                 -10                      -5

TAC CCC AGC TGT ATC ACA CTT TTT CTT TCC AAA ATT CCT AAT CCT CTG     219
Tyr Pro Ser Cys Ile Thr Leu Phe Leu Ser Lys Ile Pro Asn Pro Leu
         1               5                  10

TCT TCA CTC CCC TCA CTG                                             237
Ser Ser Leu Pro Ser Leu
 15                  20
```

(2) INFORMATION FOR SEQ ID NO: 89:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 281 base pairs
(B) TYPE: NUCLEIC ACID
(C) STRANDEDNESS: DOUBLE
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Testis

(ix) FEATURE:
(A) NAME/KEY: sig_peptide
(B) LOCATION: 171..224
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 6.3
seq FSFSLQLLSSSST/NP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 89:

```
ATCTGTCTCT TGTTTATTAA GATATGCACA GTTTCTGAAT CAACAAATAT ATCTGTGATT   60

CTTTTATACT ACTACATAAA AGAACAGGGR GTAATTCTTG CCTTATAAAT TAAATGTCAA  120

ACATTTCCTA TATGTAATCA TTTGTTCCTA AAATATGATT TAGTCCCAGC ATG CTT     176
                                                      Met Leu

ATC CCT GTT TTC TCT TTT TCT CTC CAG CTC CTA TCT AGT TCT TCA ACA    224
Ile Pro Val Phe Ser Phe Ser Leu Gln Leu Leu Ser Ser Ser Ser Thr
    -15                 -10                 -5

AAT CCT GTC AAC TCT ACC TTC CAA ATG CCT TTT GAA TCC AGC CAT STC    272
Asn Pro Val Asn Ser Thr Phe Gln Met Pro Phe Glu Ser Ser His Xaa
  1               5                  10                  15

ACC ACC AGA                                                        281
Thr Thr Arg
```

(2) INFORMATION FOR SEQ ID NO: 90:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 206 base pairs
(B) TYPE: NUCLEIC ACID
(C) STRANDEDNESS: DOUBLE
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Spleen

(ix) FEATURE:
(A) NAME/KEY: sig_peptide
(B) LOCATION: 15..155
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 6.3
seq LLLLESVSGLLQP/RT

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 90:

```
AAACCCGGGG GAAG ATG GCG GCA GCG TNT CTG AGT GGG CCC TCT GCG GGC     50
                Met Ala Ala Ala Xaa Leu Ser Gly Pro Ser Ala Gly
                        -45                 -40

TCC GCG GCT GGG GTT CCT GGC GGG ACC GGG GGT CTC TCG GCA GTR AGC     98
Ser Ala Ala Gly Val Pro Gly Gly Thr Gly Gly Leu Ser Ala Val Ser
-35                 -30                 -25                 -20

TCG GGC CCG CGG CTC CGC CTG CTG CTG CTG GAG AGT GTT TCT GGT TTG    146
Ser Gly Pro Arg Leu Arg Leu Leu Leu Leu Glu Ser Val Ser Gly Leu
                -15                 -10                  -5

CTG CAA CCT CGA ACG GGG TCT GCC GTT GCT CCG GTG CAT CCC CCA AAC    194
Leu Gln Pro Arg Thr Gly Ser Ala Val Ala Pro Val His Pro Pro Asn
              1               5                  10

CGC TCG GCA AGG                                                    206
Arg Ser Ala Arg
    15
```

(2) INFORMATION FOR SEQ ID NO: 91:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 140 base pairs
(B) TYPE: NUCLEIC ACID
(C) STRANDEDNESS: DOUBLE
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Ovary

(ix) FEATURE:
(A) NAME/KEY: sig_peptide
(B) LOCATION: 78..122
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 6.2
seq NWLFLFVFTFCNC/FF

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 91:

```
CATCTTGTAC ATCTGTKAGC ATGTATCTGT GAACATATCC ATAGGCTGGA TACCTAGCAG   60

GTCAAAATGA CGTGTGC ATG CAT AAT TGG CTT TTT TTG TTT GTW TTT ACT     110
                   Met His Asn Trp Leu Phe Leu Phe Val Phe Thr
                   -15                 -10                  -5

TTT TGT AAC TGC TTT TTT AAA AAT AAT GGC                            140
Phe Cys Asn Cys Phe Phe Lys Asn Asn Gly
                 1               5
```

(2) INFORMATION FOR SEQ ID NO: 92:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 352 base pairs
(B) TYPE: NUCLEIC ACID
(C) STRANDEDNESS: DOUBLE
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Uterus

(ix) FEATURE:
(A) NAME/KEY: sig_peptide
(B) LOCATION: 245..295
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 6.2
seq CFYFLSTALGSQA/DS

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 92:

```
ACTACCAATG GAAAATGCAG CTCTTGAGGA TGACGATTGC CAAACAAAGG CTCGGAGACG    60

AAGCAATCGG CGTGCGACAC TTTGCAGCCC ATGAGCGTGA AGACTTGGTG CAGCAGCTAG   120

AGCGAGCTAA GGAACAGGTT CTCACTAACA TCTATTCAGA GTGGGGGATG CATTTGCACA   180

GCTGGACACA ACACAAACAA GAGTGGACTG TGCCCCTCGT TTCTCAGAGT ATGGGGTGCC   240

TGGG ATG CAC GTT GAA TGC TTT TAC TTC CTC AGC ACT GCA CTA GGG TCC    289
     Met His Val Glu Cys Phe Tyr Phe Leu Ser Thr Ala Leu Gly Ser
         -15                     -10                      -5

CAA GCT GAC TCT TGG GTT TCT GGC CTC CAG CAG GCA GGT CTG CTC CCT     337
Gln Ala Asp Ser Trp Val Ser Gly Leu Gln Gln Ala Gly Leu Leu Pro
         1               5                  10

GCT ATT GGG TAC CGG                                                 352
Ala Ile Gly Tyr Arg
 15
```

(2) INFORMATION FOR SEQ ID NO: 93:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 353 base pairs
(B) TYPE: NUCLEIC ACID
(C) STRANDEDNESS: DOUBLE
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Ovary

(ix) FEATURE:
(A) NAME/KEY: sig_peptide
(B) LOCATION: 177..233
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 6.1
seq LALLWSLPASDLG/RS

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 93:

```
ATAAGTGAAC CAGACCACCC TGATGGCATC CACAGTGATG TCAAGGTTGG GGCTGGCCAG    60

GGGTGGGTGG ACTAGAAGCA TTTGGGAGTA GTGGCCAGGG GCCCTGGACG CTAGCCACGG   120

AGCTGCTGCA CAGAGCCTGG TGTCCACAAG CTTCCAGGTT GGGGTTGGAG CCTGGG ATG   179
                                                              Met

AGC CCC GGC AGC GCC TTG GCC CTT CTG TGG TCC CTG CCA GCC TCT GAC     227
Ser Pro Gly Ser Ala Leu Ala Leu Leu Trp Ser Leu Pro Ala Ser Asp
            -15                 -10                 -5

CTG GGC CGG TCA GTC ATT GCT GGA CTC TGG CCA CAC ACT GGC GTT CTC     275
Leu Gly Arg Ser Val Ile Ala Gly Leu Trp Pro His Thr Gly Val Leu
         1               5                  10

ATC CAC TTG GAA ACA AGC CAG TCT TTT CTG CAA GGT CAG TTG ACC AAG     323
Ile His Leu Glu Thr Ser Gln Ser Phe Leu Gln Gly Gln Leu Thr Lys
 15                  20                  25                  30

AGC ATA TTT CCC CTC TGT TGT ACA TCG TTG                             353
Ser Ile Phe Pro Leu Cys Cys Thr Ser Leu
                35                  40
```

(2) INFORMATION FOR SEQ ID NO: 94:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 290 base pairs
(B) TYPE: NUCLEIC ACID
(C) STRANDEDNESS: DOUBLE
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Spleen

(ix) FEATURE:
(A) NAME/KEY: sig_peptide
(B) LOCATION: 180..218
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 6.1
seq MALALGSIPSSIA/SS

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 94:

```
ACAAGGTCAT GAGGCTGAAT TAGGCTTTGT GTGCTCCTTC TAGGTTCTCA GCGTCTGTCT    60
```

```
GGTCCTTTAC TTGCTTTAGA TCTCTGCCCC AGCCACTGTA GGCAGGAACA GCTCTCTTCC  120

TTGAGAACTC AAGAGGTTCT CAAGGTAGTA AACTTCATGG TGCTCTTAGT TTAGTCTGA   179

ATG GCC TTG GCC TTG GGG TCC ATC CCA AGT TCC ATA GCC AGC AGT TGG     227
Met Ala Leu Ala Leu Gly Ser Ile Pro Ser Ser Ile Ala Ser Ser Trp
            -10                 -5                  1

GTC CAT GTC TCA CAT TTT TGT CCC TGT CTC CTC CAC ACA ACA TTG CCA     275
Val His Val Ser His Phe Cys Pro Cys Leu Leu His Thr Thr Leu Pro
     5                  10                  15

CAG TCC ACC CCG AAG                                                 290
Gln Ser Thr Pro Lys
 20
```

(2) INFORMATION FOR SEQ ID NO: 95:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 108 base pairs
(B) TYPE: NUCLEIC ACID
(C) STRANDEDNESS: DOUBLE
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Ovary

(ix) FEATURE:
(A) NAME/KEY: sig_peptide
(B) LOCATION: 31..78
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 6.1
seq FLFCTLFSLVVHP/SH

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 95:

```
AATAGTTCAC ATATTTATGT TTTTCCACAA ATG CTA GCA TTT TTG TTC TGC ACT     54
                                 Met Leu Ala Phe Leu Phe Cys Thr
                                     -15                 -10

CTG TTT TCT TTA GTA GTG CAT CCT TCA CAC ATA GAT TTA AAA TGC TCA     102
Leu Phe Ser Leu Val Val His Pro Ser His Ile Asp Leu Lys Cys Ser
            -5                  1                   5

TTT TAT                                                             108
Phe Tyr
    10
```

(2) INFORMATION FOR SEQ ID NO: 96:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 349 base pairs
(B) TYPE: NUCLEIC ACID

(C) STRANDEDNESS: DOUBLE
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Spleen

(ix) FEATURE:
(A) NAME/KEY: sig_peptide
(B) LOCATION: 32..139
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 6
seq LLYTLQTISSLSG/CF

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 96:

```
AGGTGCAGGG GAGGTAAGGT GGGAGCAGGT C ATG GCT CAA ATG CCA CTG ACA       52
                                   Met Ala Gln Met Pro Leu Thr
                                       -35                 -30

GGC TCT TAC CAA GAT TTA GAA TAT TTT CTT GAA TGC ATG TTT CTC CAT     100
Gly Ser Tyr Gln Asp Leu Glu Tyr Phe Leu Glu Cys Met Phe Leu His
            -25                 -20                 -15

TTA TTA TAT ACT CTT CAA ACA ATT TCC AGT TTA AGT GGT TGT TTT AAA     148
Leu Leu Tyr Thr Leu Gln Thr Ile Ser Ser Leu Ser Gly Cys Phe Lys
        -10                  -5                   1

CAA TTT TTT TTC CAG TTA AAT TGT TTT TGT TGG GGA GAA ATT CTA TGG     196
Gln Phe Phe Phe Gln Leu Asn Cys Phe Cys Trp Gly Glu Ile Leu Trp
      5                  10                  15

CAC TCT TCA TTC CTC CAT TCT GGA AGT TGT CTC TTG GTT TTG CTC ATT     244
His Ser Ser Phe Leu His Ser Gly Ser Cys Leu Leu Val Leu Leu Ile
 20                  25                  30                  35

AAA AAA AAA AAG ATA TAT CTT CAA TCT CYC TWA ATC TAT ACA GGT TAC     292
Lys Lys Lys Lys Ile Tyr Leu Gln Ser Xaa Xaa Ile Tyr Thr Gly Tyr
                 40                  45                  50

TTW ATA GAT YCT WAA YCT TTA SGT YCC TTC TCC ATC CCT TTA AGT TTC     340
Xaa Ile Asp Xaa Xaa Xaa Leu Xaa Xaa Phe Ser Ile Pro Leu Ser Phe
             55                  60                  65

ATA CAG TTT                                                         349
Ile Gln Phe
         70
```

(2) INFORMATION FOR SEQ ID NO: 97:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 150 base pairs
(B) TYPE: NUCLEIC ACID
(C) STRANDEDNESS: DOUBLE
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Ovary

(ix) FEATURE:
(A) NAME/KEY: sig_peptide
(B) LOCATION: 91..135
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 6
seq LLMGLWVRTVLQG/KE

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 97:

```
AATAAAGCAT ACAGAAACCC ACCTAAAATA GACTCAGGGA GGTAGGAGGT TTCCTAAGGG    60

CTGAGACTGA AAGATAATAG GGATTGCTTG ATG GCA TTG TTG ATG GGG CTG TGG   114
                                 Met Ala Leu Leu Met Gly Leu Trp
                                 -15                 -10

GTG AGA ACA GTG CTC CAG GGA AAA GAG GCC AGC GGG                     150
Val Arg Thr Val Leu Gln Gly Lys Glu Ala Ser Gly
        -5                   1               5
```

(2) INFORMATION FOR SEQ ID NO: 98:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 180 base pairs
(B) TYPE: NUCLEIC ACID
(C) STRANDEDNESS: DOUBLE
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Uterus

(ix) FEATURE:
(A) NAME/KEY: sig_peptide
(B) LOCATION: 100..156
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 6
seq LAILIXSLKLTIG/IQ

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 98:

```
ATTAAAGTTG GAGAGAGATT AGAGGCAGAA TTAACAGAAA GGAGATGTGA GAATCCAGTA    60

GTCATTTAAT TTTAAAAAAC AGGTATTCAA TAAAATTTT ATG ATT AAC CAT TTA      114
                                           Met Ile Asn His Leu
                                                           -15

TAT TTG GCT ATT CTT ATT KTT TCT TTA AAA TTA ACA ATA GGA ATC CAG    162
Tyr Leu Ala Ile Leu Ile Xaa Ser Leu Lys Leu Thr Ile Gly Ile Gln
                -10                 -5                   1
```

```
AAA CGT TTC GGA CCA CCG                                               180
Lys Arg Phe Gly Pro Pro
         5
```

(2) INFORMATION FOR SEQ ID NO: 99:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 218 base pairs
(B) TYPE: NUCLEIC ACID
(C) STRANDEDNESS: DOUBLE
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Ovary

(ix) FEATURE:
(A) NAME/KEY: sig_peptide
(B) LOCATION: 12..161
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 6
seq LLYLCSFPLPGTS/LF

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 99:

```
AAAACAAAAT T ATG GGT AGG CAA GGG ACT TTA GAA ATT GAG GGC ATT CTC     50
             Met Gly Arg Gln Gly Thr Leu Glu Ile Glu Gly Ile Leu
             -50                 -45                 -40

TGT GTC ATC ACT TGG TTA GAG GCA AAT CTA GGG AAA CAA AAA GAT GAG      98
Cys Val Ile Thr Trp Leu Glu Ala Asn Leu Gly Lys Gln Lys Asp Glu
        -35                 -30                 -25

AAT CAC TAC TAT AAG AAA TTA TCC CTT TTA TAC CTT TGC TCA TTT CCA     146
Asn His Tyr Tyr Lys Lys Leu Ser Leu Leu Tyr Leu Cys Ser Phe Pro
    -20                 -15                 -10

CTG CCT GGA ACG TCC CTT TTT CTT CTC TGC TCT TTC TCA TAT CTT ACT     194
Leu Pro Gly Thr Ser Leu Phe Leu Leu Cys Ser Phe Ser Tyr Leu Thr
 -5                  1               5                  10

CAA AGA CTT TCC CAA GGT GGA GGG                                     218
Gln Arg Leu Ser Gln Gly Gly Gly
            15
```

(2) INFORMATION FOR SEQ ID NO: 100:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 394 base pairs
(B) TYPE: NUCLEIC ACID
(C) STRANDEDNESS: DOUBLE
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Testis

(ix) FEATURE:
(A) NAME/KEY: sig_peptide
(B) LOCATION: 173..289
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 5.9
seq SAWWCVLLEWSQG/AS

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 100:

```
ACTGGGGAAA TTGAGCCTAA GAGAACAGAA AGTACTTGAG GTCCCACAAT GAATCTATGG   60

ATGAATGAGT GCTTATTCAT TCACTCATTT TTTAAAAAAA TCCATTCCAC AAGTATGTCT  120

TAATCACTGC AGTGTAAGGC ACATAGGGAC AAAATAGAAG ATTCCTGTCC TC ATG GAA  178
                                                          Met Glu

CTC ACA AAC AAG CAA ACA GGA ACT GAC AGA CAT GAA CAG GTA CTA CGG      226
Leu Thr Asn Lys Gln Thr Gly Thr Asp Arg His Glu Gln Val Leu Arg
        -35                 -30                 -25

AGG GTA AAG CAA GAC AAG AGG ATA AGT GCA TGG TGG TGC GTT TTA CTG      274
Arg Val Lys Gln Asp Lys Arg Ile Ser Ala Trp Trp Cys Val Leu Leu
    -20                 -15                 -10

GAG TGG TCA CAG GGG GCC TCT CTG AGG AGG CAA CAT CGA GGG GAG ACA      322
Glu Trp Ser Gln Gly Ala Ser Leu Arg Arg Gln His Arg Gly Glu Thr
 -5                   1               5                  10

AGC CCC AAA TCT GGG GAA AGA CTT TCC AGG CAG AGA GAA CAG CAA AAA      370
Ser Pro Lys Ser Gly Glu Arg Leu Ser Arg Gln Arg Glu Gln Gln Lys
             15                  20                  25

CCG CAG ATG AGT GAC AAG AGC CTG                                      394
Pro Gln Met Ser Asp Lys Ser Leu
         30                  35
```

(2) INFORMATION FOR SEQ ID NO: 101:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 213 base pairs
(B) TYPE: NUCLEIC ACID
(C) STRANDEDNESS: DOUBLE
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Testis

(ix) FEATURE:
(A) NAME/KEY: sig_peptide

(B) LOCATION: 4..69
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 5.9
seq VLGLLFSISDTWA/PA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 101:

```
ACA ATG GCC AAG CGT CAA AAT CCT ACG TCA GTG CTA GGA CTG CTT TTT      48
    Met Ala Lys Arg Gln Asn Pro Thr Ser Val Leu Gly Leu Leu Phe
            -20                 -15                 -10

TCT ATA TCA GAC ACG TGG GCT CCT GCT GTG TCT TCC TGG AAA GCA GAG      96
Ser Ile Ser Asp Thr Trp Ala Pro Ala Val Ser Ser Trp Lys Ala Glu
        -5                  1               5

GCC AAG GAT GGA GCA GAC CAA GAG GAT GCC AGG WWA WAA TCA CAA AGA     144
Ala Lys Asp Gly Ala Asp Gln Glu Asp Ala Arg Xaa Xaa Ser Gln Arg
 10                  15                  20                  25

AGC CCA GAW AGC ACA GCT GGA AGC CAA GAA CCC TAT TTT TGG TTT GTG     192
Ser Pro Xaa Ser Thr Ala Gly Ser Gln Glu Pro Tyr Phe Trp Phe Val
                30                  35                  40

TGG GTG GAA GGT GAG GGA CGG                                         213
Trp Val Glu Gly Glu Gly Arg
            45
```

(2) INFORMATION FOR SEQ ID NO: 102:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 375 base pairs
(B) TYPE: NUCLEIC ACID
(C) STRANDEDNESS: DOUBLE
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Testis

(ix) FEATURE:
(A) NAME/KEY: sig_peptide
(B) LOCATION: 250..324
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 5.9
seq FCLSLQIFRVSLA/LA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 102:

```
ATAAGGCTAG TTCTATTTTG AAGCCTATGT GTTTTGTGAA ACACAAAAAA AAGTACAGAG   60

AAAGATCGCA TCCTTTTCTG GTAGGGGTTT TCAGGAAAAA GTAAGAGTTC TGACTCATGT  120

TGGGATTTCT TGGGCCGTTA TTCTGCAGTG GTCAAAATGG GGGAAGCATG TCTGTAAAAG  180

TGTTACTGAT ATGACTAACA CTAACTGATC TACTTTCAAA CATTACCTTT TTCCTCTCCC  240
```

```
TCCCTGTTT ATG AAT GTT TTG CCC TTC TCT TAC TAT TAT ATC TTG TTT TGT  291
          Met Asn Val Leu Pro Phe Ser Tyr Tyr Tyr Ile Leu Phe Cys
          -25                 -20                 -15

TTG AGT TTA CAA ATT TTC AGA GTT TCC CTA GCT CTG GCA CAS ACT CAT    339
Leu Ser Leu Gln Ile Phe Arg Val Ser Leu Ala Leu Ala Xaa Thr His
    -10                 -5                  1                   5

GAG GTT CCT GTC TCT ACT CAT ACT AAC RAA TTG CAT                    375
Glu Val Pro Val Ser Thr His Thr Asn Xaa Leu His
                10                  15
```

(2) INFORMATION FOR SEQ ID NO: 103:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 190 base pairs
(B) TYPE: NUCLEIC ACID
(C) STRANDEDNESS: DOUBLE
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Ovary

(ix) FEATURE:
(A) NAME/KEY: sig_peptide
(B) LOCATION: 17..103
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 5.9
seq FSYISXFLSPVCG/CS

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 103:

```
ATCAAAATTC TCTTTG ATG AAA TGT TTA AAA GTG AAC CCT TTT TTA TTT CTG   52
                  Met Lys Cys Leu Lys Val Asn Pro Phe Leu Phe Leu
                                  -25                 -20

GTW TTT AAT TTC TTT TCC TAC ATC AGT KGC TTT TTG TCA CCA GTA TGT    100
Val Phe Asn Phe Phe Ser Tyr Ile Ser Xaa Phe Leu Ser Pro Val Cys
        -15                 -10                 -5

GGA TGT TCT GTC TGT AAT TTA AAA CAC TGG GAG AAT GAG CTT CTA TTT    148
Gly Cys Ser Val Cys Asn Leu Lys His Trp Glu Asn Glu Leu Leu Phe
    1               5                   10                  15

CCT TCT CCC CAC TTT TTG CCA TAT AAA TTT TTN TTT CTT TTT            190
Pro Ser Pro His Phe Leu Pro Tyr Lys Phe Xaa Phe Leu Phe
                20                  25
```

(2) INFORMATION FOR SEQ ID NO: 104:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 226 base pairs

(B) TYPE: NUCLEIC ACID
(C) STRANDEDNESS: DOUBLE
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Testis

(ix) FEATURE:
(A) NAME/KEY: sig_peptide
(B) LOCATION: 74..172
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 5.8
seq XLCLGMALCPRQA/TR

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 104:

```
ATCTCTTGGC GTCTCAACGT TCGGATCAGC AGCTTTTTTC CATTCTCTCT CTCCACTTCT    60

TCAGTGAGCA GCC ATG AGT TGG ACT GTG CCT GTT GTG CGG GCC AGC CAG      109
               Met Ser Trp Thr Val Pro Val Val Arg Ala Ser Gln
                           -30                 -25

AGA GTG AGC TCG GTG GGA GCG AAT KTC CTA TGC CTG GGG ATG GCC CTG     157
Arg Val Ser Ser Val Gly Ala Asn Xaa Leu Cys Leu Gly Met Ala Leu
    -20                 -15                 -10

TGT CCG CGT CAA GCA ACG CGC ATC CCG CTC AAC GGC ACC TGG CTC TTC     205
Cys Pro Arg Gln Ala Thr Arg Ile Pro Leu Asn Gly Thr Trp Leu Phe
 -5                  1               5                  10

ACC CCC GTG AGC AAG ATG GCG                                         226
Thr Pro Val Ser Lys Met Ala
            15
```

(2) INFORMATION FOR SEQ ID NO: 105:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 173 base pairs
(B) TYPE: NUCLEIC ACID
(C) STRANDEDNESS: DOUBLE
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Ovary

(ix) FEATURE:
(A) NAME/KEY: sig_peptide
(B) LOCATION: 111..155
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 5.8
seq FLXLMTLTTHVHS/SA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 105:

```
ATCCGATACA GAACATGCAG TAATGTGGAC TGCCCACCAG AAGCAGGTGA TTTCCGAGCT   60

CAGCAATGCT CAGCTCATAA TGATGTCAAG CACCATGGCC AGTTTTATGA ATG GGY     116
                                                       Met Gly
                                                       -15

TTC CTG WGT CTA ATG ACC CTG ACA ACC CAT GTT CAC TCA AGT GCC AAG     164
Phe Leu Xaa Leu Met Thr Leu Thr Thr His Val His Ser Ser Ala Lys
            -10                 -5                   1

CCA AAT GGG                                                         173
Pro Asn Gly
    5
```

(2) INFORMATION FOR SEQ ID NO: 106:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 98 base pairs
(B) TYPE: NUCLEIC ACID
(C) STRANDEDNESS: DOUBLE
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Ovary

(ix) FEATURE:
(A) NAME/KEY: sig_peptide
(B) LOCATION: 33..80
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 5.7
seq RVLLLAQLFLGSG/KT

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 106:

```
AAATTCTCTG GGCCTGCTTG TCATCACTCC AG ATG TTG TTT AGA GTT CTT CTG     53
                                    Met Leu Phe Arg Val Leu Leu
                                        -15                 -10

TTA GCA CAG CTG TTT CTA GGG TCT GGA AAA ACT CTA AGG ACC CCG         98
Leu Ala Gln Leu Phe Leu Gly Ser Gly Lys Thr Leu Arg Thr Pro
            -5                      1                   5
```

(2) INFORMATION FOR SEQ ID NO: 107:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 243 base pairs
(B) TYPE: NUCLEIC ACID
(C) STRANDEDNESS: DOUBLE
(D) TOPOLOGY: LINEAR

```
(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:
      (A) ORGANISM: Homo Sapiens
      (F) TISSUE TYPE: Ovary

(ix) FEATURE:
      (A) NAME/KEY: sig_peptide
      (B) LOCATION: 79..174
      (C) IDENTIFICATION METHOD: Von Heijne matrix
      (D) OTHER INFORMATION:  score 5.7
                              seq SLPLSTSAPPLRG/LR

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 107:

AACAGTCCTG CCGGCTGGCT TGGGTGGGTG GTGGGCTGCG GGTAGGGGAG GGGATGGACC   60

GAGTCCCGGC TTGTCGGG ATG AGG GTT CCG GAA GAT CTG GCC AGT AAG ATT    111
                    Met Arg Val Pro Glu Asp Leu Ala Ser Lys Ile
                            -30                 -25

CTA CTC CCT GGC TGT GCA CCG GGT TCC CTA CCC CTG TCT ACG TCG GCT    159
Leu Leu Pro Gly Cys Ala Pro Gly Ser Leu Pro Leu Ser Thr Ser Ala
    -20                 -15                 -10

CCG CCA CTT CGC GGC TTG AGA CTA AAA GAG CAT CCC GGC AGG GGG CCT    207
Pro Pro Leu Arg Gly Leu Arg Leu Lys Glu His Pro Gly Arg Gly Pro
 -5                  1               5                  10

TCC AGC CCC AAA GCA GCC TGT CCA GAG ACC CCC GCG                    243
Ser Ser Pro Lys Ala Ala Cys Pro Glu Thr Pro Ala
            15                  20


(2) INFORMATION FOR SEQ ID NO: 108:

(i) SEQUENCE CHARACTERISTICS:
      (A) LENGTH: 182 base pairs
      (B) TYPE: NUCLEIC ACID
      (C) STRANDEDNESS: DOUBLE
      (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:
      (A) ORGANISM: Homo Sapiens
      (F) TISSUE TYPE: Ovary

(ix) FEATURE:
      (A) NAME/KEY: sig_peptide
      (B) LOCATION: 63..155
      (C) IDENTIFICATION METHOD: Von Heijne matrix
      (D) OTHER INFORMATION:  score 5.7
                              seq SDLCLCQCILARA/HD

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 108:

ACATTTCTAA CGAGTACTGC CCAATCATTT GGTAGAATGC CCCTTAACTT TGGGTTWGTT   60
```

```
TG ATG TTT CCT CAC AGW GAR ACT CAG GTT AAG TGT TTT TGG CAG GGA      107
   Met Phe Pro His Xaa Glu Thr Gln Val Lys Cys Phe Trp Gln Gly
       -30                 -25                 -20

TTA CGC AGA AGC GAT CTG TGT CTG TGT CAA TGC ATC CTA GCA AGG GCA     155
Leu Arg Arg Ser Asp Leu Cys Leu Cys Gln Cys Ile Leu Ala Arg Ala
    -15                 -10                 -5

CAT GAT GGC GAT TTA TAC CTT TTT TTT                                 182
His Asp Gly Asp Leu Tyr Leu Phe Phe
  1               5
```

(2) INFORMATION FOR SEQ ID NO: 109:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 272 base pairs
(B) TYPE: NUCLEIC ACID
(C) STRANDEDNESS: DOUBLE
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Testis

(ix) FEATURE:
(A) NAME/KEY: sig_peptide
(B) LOCATION: 81..140
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 5.6
seq LAVFMXLAQLVSG/NW

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 109:

```
AAAAGAAGGA CAATAAAGAT CTGTGTTCAG AGTCATACTG AATAGAGACT TCTGGACTCT   60

ATAGAACCCA CTGCCTCCTG ATG AAG TCC CTA CTG TTC ACC CTT GCA GTT TTT  113
                      Met Lys Ser Leu Leu Phe Thr Leu Ala Val Phe
                      -20                 -15                 -10

ATG CKC CTG GCC CAA TTG GTC TCA GGT AAT TGG TAT GTG AAA AAG TGT    161
Met Xaa Leu Ala Gln Leu Val Ser Gly Asn Trp Tyr Val Lys Lys Cys
                -5                  1               5

CTA AAC GNN TTT GGA ATT TGC AAG ANG AAG TGC AAA CCT GAA GAG ATG    209
Leu Asn Xaa Phe Gly Ile Cys Lys Xaa Lys Cys Lys Pro Glu Glu Met
        10                  15                  20

CAT GTA AAG AAT GGT TGG SCA ATG TGC GGC AAA CAA AGG GAC TGC TGT    257
His Val Lys Asn Gly Trp Xaa Met Cys Gly Lys Gln Arg Asp Cys Cys
    25                  30                  35

GTT CCA GCT AAC GGG                                                272
Val Pro Ala Asn Gly
 40
```

(2) INFORMATION FOR SEQ ID NO: 110:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 161 base pairs
(B) TYPE: NUCLEIC ACID
(C) STRANDEDNESS: DOUBLE
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Testis

(ix) FEATURE:
(A) NAME/KEY: sig_peptide
(B) LOCATION: 18..86
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 5.6
seq LLNVACCIPFSSS/LF

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 110:

```
ATTTTCCAAA CATTGTG ATG CAC CTT TAT AGC TGT TCG TGT ATG CGC CTT        50
                   Met His Leu Tyr Ser Cys Ser Cys Met Arg Leu
                               -20                 -15

TTA AAC GTG GCA TGC TGC ATA CCC TTT TCG AGC AGC CTG TTT CCG CAC       98
Leu Asn Val Ala Cys Cys Ile Pro Phe Ser Ser Ser Leu Phe Pro His
        -10                 -5                  1

ATT CTT TTC AAG TCA TTA AAC TAT TCC TTG ACG TCC TTT CTC AAG GCT      146
Ile Leu Phe Lys Ser Leu Asn Tyr Ser Leu Thr Ser Phe Leu Lys Ala
  5                  10                  15                  20

GTG CGT GGC CGG TGG                                                  161
Val Arg Gly Arg Trp
                25
```

(2) INFORMATION FOR SEQ ID NO: 111:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 285 base pairs
(B) TYPE: NUCLEIC ACID
(C) STRANDEDNESS: DOUBLE
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Testis

(ix) FEATURE:
(A) NAME/KEY: sig_peptide
(B) LOCATION: 223..270

(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 5.5
seq PLVLSPLSYQCSS/QG

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 111:

```
AATGTTTAAG ATCTGTTTTA AATTTAAAAC AATGAATTGA ATGCTCTAAG AGGCTCCTAC    60

AGGCGCTCCA GGCCACTCTC AGAGACTCCC AGGAGTTGTT GAACTATATT TGGAGAAAAC   120

AGCCAMTGAA TATTATCATT TCTCCTTTAA AGAGAGTTTG TAAGGGGGGA ACATGCATTT   180

TATCAGACAA TTTATCCAAA GCATTTCAGA ACATGAGTGC TG ATG AGG GCA CCT      234
                                               Met Arg Ala Pro
                                                   -15

CTT GTG CTG AGT CCC CTC AGC TAT CAG TGT TCT TCT CAA GGA CAC ATT     282
Leu Val Leu Ser Pro Leu Ser Tyr Gln Cys Ser Ser Gln Gly His Ile
    -10                 -5                      1

TGG                                                                 285
Trp
  5
```

(2) INFORMATION FOR SEQ ID NO: 112:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 262 base pairs
(B) TYPE: NUCLEIC ACID
(C) STRANDEDNESS: DOUBLE
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Testis

(ix) FEATURE:
(A) NAME/KEY: sig_peptide
(B) LOCATION: 146..253
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 5.5
seq FTSMCILFHCLLS/FQ

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 112:

```
AACTTGGGAC AAGARATCAA ACTTTAAAGA TGGTCTAAAG CCCCTCTTAA AGGTCTGACT    60

GTGTCGGACC TCTAGAGCTA ATCTCACTAG ATGTGAGCCA TTGTTTATAT TCTAGCCATC   120

CTTTCATTTC ATTCTAGAAG ACCCC ATG CAA GTT CCC CAC CTA AGG GTC TGG     172
                            Met Gln Val Pro His Leu Arg Val Trp
                                -35                 -30

ACA CAG GTG AWA GAT ACC TTC ATT GGT TAT AGA AAT TTG GGA TTT ACA     220
Thr Gln Val Xaa Asp Thr Phe Ile Gly Tyr Arg Asn Leu Gly Phe Thr
```

```
        -25                    -20                    -15

AGT ATG TGC ATA TTG TTC CAC TGT CTT CTT AGC TTT CAG AGG          262
Ser Met Cys Ile Leu Phe His Cys Leu Leu Ser Phe Gln Arg
    -10                    -5                    1
```

(2) INFORMATION FOR SEQ ID NO: 113:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 183 base pairs
(B) TYPE: NUCLEIC ACID
(C) STRANDEDNESS: DOUBLE
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Testis

(ix) FEATURE:
(A) NAME/KEY: sig_peptide
(B) LOCATION: 46..153
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 5.4
seq LWLMHQSFQKSNS/SS

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 113:

```
ACTACGAATG CAGATGTGGA AACAACTTCT GTGCATCTCA TCGTT ATG CAG AAA CTC    57
                                                  Met Gln Lys Leu
                                                      -35

ATG GCT GTA CCT ATG ATT ACA AGA GCG CAG GGA GGA GAT ACT TGC ACG     105
Met Ala Val Pro Met Ile Thr Arg Ala Gln Gly Gly Asp Thr Cys Thr
        -30                 -25                 -20

AGG CAA ATC CTG TGG TTA ATG CAC CAA AGC TTC CAA AAA TCT AAC TCT     153
Arg Gln Ile Leu Trp Leu Met His Gln Ser Phe Gln Lys Ser Asn Ser
    -15                 -10                 -5

TCC TCT ACA TCT TAC TGT TCT GCC CAG GGG                             183
Ser Ser Thr Ser Tyr Cys Ser Ala Gln Gly
  1               5                  10
```

(2) INFORMATION FOR SEQ ID NO: 114:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 162 base pairs
(B) TYPE: NUCLEIC ACID
(C) STRANDEDNESS: DOUBLE
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Ovary

(ix) FEATURE:
(A) NAME/KEY: sig_peptide
(B) LOCATION: 1..135
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 5.4
seq AHRSLCLWPACLC/AR

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 114:

```
ATG TGT RTA GCT GGG TTT WAT GAC CAC CCT CGT GCG GCC CGG CAC GCC      48
Met Cys Xaa Ala Gly Phe Xaa Asp His Pro Arg Ala Ala Arg His Ala
-45                 -40                 -35                 -30

CGC ACG TCC CGC CAC CCC CTC CCT TGG GTG TGT GTC TCT CAG CYC CCT      96
Arg Thr Ser Arg His Pro Leu Pro Trp Val Cys Val Ser Gln Xaa Pro
                -25                 -20                 -15

GCA CAC CGT TCC CTA TGT CTG TGG CCC GCG TGC CTB TGT GCG CGT GTG     144
Ala His Arg Ser Leu Cys Leu Trp Pro Ala Cys Leu Cys Ala Arg Val
            -10                  -5                   1

CTC CCC CCA GCG CCA GGN                                             162
Leu Pro Pro Ala Pro Gly
    5
```

(2) INFORMATION FOR SEQ ID NO: 115:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 127 base pairs
(B) TYPE: NUCLEIC ACID
(C) STRANDEDNESS: DOUBLE
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Testis

(ix) FEATURE:
(A) NAME/KEY: sig_peptide
(B) LOCATION: 62..115
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 5.4
seq ILVSFILAALSLS/TT

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 115:

```
ATCGGACTGA ACGGATCGCT GCGAGGATTA TCTTACACTG AACTGATCAA GTACTTTGAA    60

A ATG ACT TCG AAA TTT ATC TTG GTG TCC TTC ATA CTT GCT GCA CTG AGT   109
  Met Thr Ser Lys Phe Ile Leu Val Ser Phe Ile Leu Ala Ala Leu Ser
          -15                 -10                  -5
```

```
CTT TCA ACC ACC ATA GGG                                       127
Leu Ser Thr Thr Ile Gly
          1
```

(2) INFORMATION FOR SEQ ID NO: 116:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 332 base pairs
(B) TYPE: NUCLEIC ACID
(C) STRANDEDNESS: DOUBLE
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Ovary

(ix) FEATURE:
(A) NAME/KEY: sig_peptide
(B) LOCATION: 279..323
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 5.4
seq LLIFILTVHHTPS/LP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 116:

```
ATCTTTTGTT TGAGTATCTT CAAGAAAAAT CTGTTGTGAG AAAGATCCTA AACATATGTA   60

TGTATAGATG CATATCTTTG AAAGCCTATG TGAATACCAA GGGAATCTGA ACTTTTTCTT  120

TGGAGATGTT TACATAATAA ATCTATTTTC ATCAATCTGG CATATTTTTC TCCTAGCACT  180

GACTTACTGA ATGCCGCTGA CCACGTGCTG CCTCTCATGC TAAATGCTTA CTTAATTCAT  240

CACCAAATTC TGTAGACTGT ACAGGCTAAA CACCTCTA ATG CAT TTA CTT ATT TTC  296
                                          Met His Leu Leu Ile Phe
                                          -15                 -10

ATC CTC ACT GTC CAT CAC ACT CCC TCC CTC CCC TCG                    332
Ile Leu Thr Val His His Thr Pro Ser Leu Pro Ser
                -5                  1
```

(2) INFORMATION FOR SEQ ID NO: 117:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 188 base pairs
(B) TYPE: NUCLEIC ACID
(C) STRANDEDNESS: DOUBLE
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Ovary

(ix) FEATURE:
(A) NAME/KEY: sig_peptide
(B) LOCATION: 129..176
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 5.3
seq SSLMVQLISQVYS/CM

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 117:

```
ACAGGAAGTT TGCCTAGAAG GAATAAATTA ACTCTTGTTA CTTGGTGAGA TCATGGAAGG   60

GAATGTAATT TGTTTTAGGT GGTGGTAATT GTGAGTTTGA GGCTGGCCCA GGAAATGAGT  120

TGTCAGAT ATG CTG TCA TCC TCA TTA ATG GTT CAG CTT ATT TCT CAG GTT   170
         Met Leu Ser Ser Ser Leu Met Val Gln Leu Ile Ser Gln Val
             -15                 -10                 -5

TAT AGT TGT ATG AGG AGG                                            188
Tyr Ser Cys Met Arg Arg
         1
```

(2) INFORMATION FOR SEQ ID NO: 118:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 146 base pairs
(B) TYPE: NUCLEIC ACID
(C) STRANDEDNESS: DOUBLE
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Testis

(ix) FEATURE:
(A) NAME/KEY: sig_peptide
(B) LOCATION: 57..98
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 5.3
seq FSYILCMLFCLFS/QD

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 118:

```
ACTAATCCCC TATTTAGGTT GTTTACTTTT AGGTATTCTG CATAGAGCTG TGATGG ATG   59
                                                              Met

TTC TCA TAT ATA CTT TGC ATG CTT TTC TGC TTA TTT TCT CAG GAT AAA    107
Phe Ser Tyr Ile Leu Cys Met Leu Phe Cys Leu Phe Ser Gln Asp Lys
        -10                 -5                  1

TTT CTG GAA GTG ACA TTG TTG TGT GAA AGG TAC ATG CTT                146
Phe Leu Glu Val Thr Leu Leu Cys Glu Arg Tyr Met Leu
    5                  10                  15
```

(2) INFORMATION FOR SEQ ID NO: 119:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 145 base pairs
(B) TYPE: NUCLEIC ACID
(C) STRANDEDNESS: DOUBLE
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Uterus

(ix) FEATURE:
(A) NAME/KEY: sig_peptide
(B) LOCATION: 11..67
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 5.2
seq VTLAFSLLVLSES/AV

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 119:

```
AYCWTCTTAA ATG TTA TTT TTA TAT TAT GTT ACA CTT GCA TTC TCT TTA       49
           Met Leu Phe Leu Tyr Tyr Val Thr Leu Ala Phe Ser Leu
                           -15                 -10

TTG GTG TTA TCA GAG TCA GCA GTA CTG AAA AGA AGA GAA ATC TTT TGR      97
Leu Val Leu Ser Glu Ser Ala Val Leu Lys Arg Arg Glu Ile Phe Xaa
    -5                  1               5                   10

ACA GGG TTA GGT TGT GTG ACA GGG TTA GGT TGT GTG ACA GGG TTA CGG     145
Thr Gly Leu Gly Cys Val Thr Gly Leu Gly Cys Val Thr Gly Leu Arg
                15                  20                  25
```

(2) INFORMATION FOR SEQ ID NO: 120:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 235 base pairs
(B) TYPE: NUCLEIC ACID
(C) STRANDEDNESS: DOUBLE
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Spleen

(ix) FEATURE:
(A) NAME/KEY: sig_peptide
(B) LOCATION: 143..184
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 5.2
seq LLSGLWLSSVKEC/DD

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 120:

```
AAGGAGTAGT GGCTTTGTTC CCAGCTCAGT GAAGGGTGGC ATGGTCTCTC CTGTCCACTT   60

CACTCTGGAT TCTTTAACCC TGTGAATTAC TAGACATGGA TTCCATCTCC AATGTGGATG  120

CCTCTCTTCA CCACAAGAAT AC ATG CTC CTT TCT GGG CTG TGG CTT AGC TCG   172
                         Met Leu Leu Ser Gly Leu Trp Leu Ser Ser
                                         -10                 -5

GTC AAG GAG TGT GAT GAC TGG CGA GCA GAT GGC TGC CTT CCA TCC ATC    220
Val Lys Glu Cys Asp Asp Trp Arg Ala Asp Gly Cys Leu Pro Ser Ile
                 1               5                  10

GTC CAC CCC CTA AGG                                                235
Val His Pro Leu Arg
         15
```

(2) INFORMATION FOR SEQ ID NO: 121:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 181 base pairs
(B) TYPE: NUCLEIC ACID
(C) STRANDEDNESS: DOUBLE
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Testis

(ix) FEATURE:
(A) NAME/KEY: sig_peptide
(B) LOCATION: 59..112
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 5.2
seq VFCFSWLMSSSSP/SI

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 121:

```
ATACAAAGGA AATTAGTATG TTCCTTGAGG TTCAGGGAAT CTATGTATAT TTCAGATC     58

ATG GTT GCA TTT TCA GTC TTC TGT TTT TCA TGG TTG ATG AGT TCA TCA    106
Met Val Ala Phe Ser Val Phe Cys Phe Ser Trp Leu Met Ser Ser Ser
            -15                 -10                 -5

AGT CCT TCC ATC TTT TGG AGT CAT TTC TAT TCA CCA TTC AAG GAT CTA    154
Ser Pro Ser Ile Phe Trp Ser His Phe Tyr Ser Pro Phe Lys Asp Leu
         1               5                  10

TCT AAA ATG TAT AAT TAT GTC TCC CCG                                181
Ser Lys Met Tyr Asn Tyr Val Ser Pro
 15                 20
```

(2) INFORMATION FOR SEQ ID NO: 122:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 248 base pairs
(B) TYPE: NUCLEIC ACID
(C) STRANDEDNESS: DOUBLE
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Spleen

(ix) FEATURE:
(A) NAME/KEY: sig_peptide
(B) LOCATION: 123..170
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 5.1
seq LALGIGPPGCLQG/SP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 122:

```
ATGTTTTCTT AAGATCCAGA AGTTTTTGCT TTAGCTTAAG GATGTGTGCA ATTTTCCATG   60

TGGCTTCATA ATTCATCCAT GACTTTGAAT TTTAAAATGG AGAGAAGTTG GCTTCCCAGG  120

AA ATG GTG CCC CTG GCC CTG GGC ATC GGC CCA CCT GGC TGT CTC CAA     167
   Met Val Pro Leu Ala Leu Gly Ile Gly Pro Pro Gly Cys Leu Gln
       -15                 -10                     -5

GGC TCT CCT TCC CAG TGG CTG GTG CGG GCT CCG GGA GCT CAG CTG AGT    215
Gly Ser Pro Ser Gln Trp Leu Val Arg Ala Pro Gly Ala Gln Leu Ser
  1               5                  10                  15

CCC ATT GGG GTG GCA ACG GAA AGG GAG CAG AGG                        248
Pro Ile Gly Val Ala Thr Glu Arg Glu Gln Arg
                 20                  25
```

(2) INFORMATION FOR SEQ ID NO: 123:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 186 base pairs
(B) TYPE: NUCLEIC ACID
(C) STRANDEDNESS: DOUBLE
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Uterus

(ix) FEATURE:
(A) NAME/KEY: sig_peptide
(B) LOCATION: 64..159
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 5.1
seq LLWFCTAMRPGGA/GL

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 123:

```
AGGATTAAGC AAGCACAGCC CTAGTTGATC ACCCAGCATG AAAAGTCCTG GAATCTCTCA   60

GAG ATG AAC CTG TGT ATG GGA GTT TTG CTT AAA GTK GGT ACT TCA AGA    108
    Met Asn Leu Cys Met Gly Val Leu Leu Lys Val Gly Thr Ser Arg
            -30                 -25                 -20

AGG TGC CTC TGT TTA CTT TGG TTT TGC ACT GCC ATG CGA CCA GGT GGT    156
Arg Cys Leu Cys Leu Leu Trp Phe Cys Thr Ala Met Arg Pro Gly Gly
        -15                 -10                  -5

GCA GGT CTC CCA AAT GCC ACC CCC GAA TGG                            186
Ala Gly Leu Pro Asn Ala Thr Pro Glu Trp
     1               5
```

(2) INFORMATION FOR SEQ ID NO: 124:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 159 base pairs
(B) TYPE: NUCLEIC ACID
(C) STRANDEDNESS: DOUBLE
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Uterus

(ix) FEATURE:
(A) NAME/KEY: sig_peptide
(B) LOCATION: 112..153
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 5.1
seq SLAKSLFLRVARG/LG

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 124:

```
ATTTTTAAGG GAAAGACCCG GAAACAGCAC ATTCTCTTTT TCCAGTAGCC GGAATTTGCA   60

ACTACATATA GTCGCAAAGA AGACTGGGAG GWWATCTTTA GTTGGGAAGC A ATG AGT   117
                                                         Met Ser

CTA GCA AAA TCT CTG TTT TTA AGG GTG GCA AGG GGA CTG GGG            159
Leu Ala Lys Ser Leu Phe Leu Arg Val Ala Arg Gly Leu Gly
        -10                  -5                   1
```

(2) INFORMATION FOR SEQ ID NO: 125:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 342 base pairs
(B) TYPE: NUCLEIC ACID
(C) STRANDEDNESS: DOUBLE

(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Ovary

(ix) FEATURE:
(A) NAME/KEY: sig_peptide
(B) LOCATION: 61..114
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 5.1
seq FLPSATLLLSAES/FF

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 125:

```
AAGGGCTCTG CCTCTTCCCT ATACCATGCT GTCTTCCATA GCCTTCCTCC TGTCCTACTC    60

ATG AGA CTG CCT CCA TTT CTT CCT TCT GCA ACC CTG CTC CTA TCA GCT     108
Met Arg Leu Pro Pro Phe Leu Pro Ser Ala Thr Leu Leu Leu Ser Ala
            -15                 -10                     -5

GAA TCC TTC TTT CGG AGT GTT AGT GAG TAC CCG TCT CTC CCC AGC CCC     156
Glu Ser Phe Phe Arg Ser Val Ser Glu Tyr Pro Ser Leu Pro Ser Pro
         1               5                  10

TCA GCT GGT GGG CCT GGG TGT GTC AGC GGC AAA TGG GGC TCT GGT TCC     204
Ser Ala Gly Gly Pro Gly Cys Val Ser Gly Lys Trp Gly Ser Gly Ser
 15                  20                  25                  30

AAT GGG CCA CTC TCA TCT CTC TCT TGT TCC TTG TGC AGA AAA CCT TTG     252
Asn Gly Pro Leu Ser Ser Leu Ser Cys Ser Leu Cys Arg Lys Pro Leu
                 35                  40                  45

CTT CAC TCC ACT GCC CTC TCT AGT TCC CGA CCC TTT TTC TCT CCT GGC     300
Leu His Ser Thr Ala Leu Ser Ser Ser Arg Pro Phe Phe Ser Pro Gly
             50                  55                  60

TTT CCC TGC CAA ATT TCT CCA AGG AGT GGT CTA CAY CCT CTG             342
Phe Pro Cys Gln Ile Ser Pro Arg Ser Gly Leu His Pro Leu
         65                  70                  75
```

(2) INFORMATION FOR SEQ ID NO: 126:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 354 base pairs
(B) TYPE: NUCLEIC ACID
(C) STRANDEDNESS: DOUBLE
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Ovary

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
(B) LOCATION: 202..348
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 5
seq PLLLLLREELVTG/AV

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 126:

```
ATATTTAGTT CCTTTATTTT TTTCTTTTCA AATGAATGGC TTTTAAAGTA CATGTTATGT    60

GAAGTATTCA CAAACACTGG TGCTTCCATG ATTATTGAGG AACATGTGAT TTATAAAATG   120

CCTCACTGTT TTCCAAGATA CACGATTGCG TCTGGGCACA GTTGATTTCT CCTTGCCTAC   180

TCCCCCTCGC CCCTCACCCC C ATG AGT GAC AGA AAA AGA ACT AAA TTC TCA     231
                        Met Ser Asp Arg Lys Arg Thr Lys Phe Ser
                                        -45                 -40

TAT GTC CAA CTC CCA TGC CCA ATC TCC CTT CTC CCA CGC AGT TTT AAA     279
Tyr Val Gln Leu Pro Cys Pro Ile Ser Leu Leu Pro Arg Ser Phe Lys
            -35                 -30                 -25

AGG GGA CAA ATC CCA GGT CCC TCG GCT CCA CCA CTT CTT CTT CTT CTG     327
Arg Gly Gln Ile Pro Gly Pro Ser Ala Pro Pro Leu Leu Leu Leu Leu
        -20                 -15                 -10

CGT GAG GAG TTG GTT ACC GGG GCC GTG                                 354
Arg Glu Glu Leu Val Thr Gly Ala Val
     -5                   1
```

(2) INFORMATION FOR SEQ ID NO: 127:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 248 base pairs
(B) TYPE: NUCLEIC ACID
(C) STRANDEDNESS: DOUBLE
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Ovary

(ix) FEATURE:
(A) NAME/KEY: sig_peptide
(B) LOCATION: 12..134
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 5
seq FCFFPAFLVXVXS/QP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 127:

```
ACTCTTCGTT T ATG ACT CCG TTG GGC TCC GGC CCT CCT AGA GAG GCC TCC     50
             Met Thr Pro Leu Gly Ser Gly Pro Pro Arg Glu Ala Ser
                 -40                 -35                 -30
```

```
ATA GCG CAG GTT CGT GGG TTC TCG CGG ACC TTT TTC CGT GTA GCT TTC      98
Ile Ala Gln Val Arg Gly Phe Ser Arg Thr Phe Phe Arg Val Ala Phe
            -25                 -20                 -15

TGC TTC TTC CCG GCA TTC CTT GTT WCG GTT TTM TCA CAG CCC TCT GGM     146
Cys Phe Phe Pro Ala Phe Leu Val Xaa Val Xaa Ser Gln Pro Ser Gly
        -10                 -5                  1

TTT TCC ACC ACT GAG ACA CTT TGC GCT CAG GAC TTC AGT GAC GTC ATC     194
Phe Ser Thr Thr Glu Thr Leu Cys Ala Gln Asp Phe Ser Asp Val Ile
  5                  10                  15                  20

TTT CTG CGG CGC GCR GAC ACC CGC CGG TGG AAG AAG AAA CAG CTC CGC     242
Phe Leu Arg Arg Ala Asp Thr Arg Arg Trp Lys Lys Lys Gln Leu Arg
                25                  30                  35

CGC CGG                                                             248
Arg Arg
```

(2) INFORMATION FOR SEQ ID NO: 128:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 242 base pairs
(B) TYPE: NUCLEIC ACID
(C) STRANDEDNESS: DOUBLE
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Testis

(ix) FEATURE:
(A) NAME/KEY: sig_peptide
(B) LOCATION: 93..137
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 5
seq CSALFPLLSLLSC/KE

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 128:

```
ATGTGCTGAA ACTTAATCAG CAATGTGATG GTAATAGGTG GGGCCTTTAA AGGTGATTAA    60

GTCATGTGAG TGACCTTTAT AAAAAAGGCT TC ATG CGT TGT TCA GCT CTC TTT     113
                                    Met Arg Cys Ser Ala Leu Phe
                                    -15                 -10

CCC CTT CTA TCT CTT TTG TCA TGC AAA GAG AGG ATR TGG TGT TTG TCC     161
Pro Leu Leu Ser Leu Leu Ser Cys Lys Glu Arg Xaa Trp Cys Leu Ser
            -5                  1                   5

ACA TTG GAG GAT GCA GCG ACA DGG CGT CAC CTT GGA AGT AGA GAG CAG     209
Thr Leu Glu Asp Ala Ala Thr Xaa Arg His Leu Gly Ser Arg Glu Gln
     10                  15                  20

CCC TCA GGG GAT GCT GAG CCT GTG GAA GTA TGG                         242
Pro Ser Gly Asp Ala Glu Pro Val Glu Val Trp
```

25 30 35

(2) INFORMATION FOR SEQ ID NO: 129:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 145 base pairs
(B) TYPE: NUCLEIC ACID
(C) STRANDEDNESS: DOUBLE
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Ovary

(ix) FEATURE:
(A) NAME/KEY: sig_peptide
(B) LOCATION: 41..103
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 5
seq IISLLKLCSFCFI/KD

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 129:

```
AATTTAAGAT AATATCCAGT TCATGTAGAC ATGAATATAT ATG CTT TAT GAT CAA       55
                                           Met Leu Tyr Asp Gln
                                                -20

TAT TAC CTG ATA ATA TCA CTA CTA AAG CTA TGT TCT TTT TGC TTT ATT      103
Tyr Tyr Leu Ile Ile Ser Leu Leu Lys Leu Cys Ser Phe Cys Phe Ile
    -15                 -10                 -5

AAA GAT TTT AAA GCC AGC AAC ATC ACT TTG GTA GTG ATA TTG              145
Lys Asp Phe Lys Ala Ser Asn Ile Thr Leu Val Val Ile Leu
  1               5                  10
```

(2) INFORMATION FOR SEQ ID NO: 130:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 295 base pairs
(B) TYPE: NUCLEIC ACID
(C) STRANDEDNESS: DOUBLE
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Uterus

(ix) FEATURE:
(A) NAME/KEY: sig_peptide
(B) LOCATION: 71..265
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 5

seq LCSFLSLRFCTLS/FM

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 130:

```
AGGAGACCGT GCCCACCCCT AGATTGTTCT TAAGCTCTTT TTTGCATCTT TTACTTGCCT    60

AGACTCTGAA ATG GCT AAC TGT TTC CTA TCA CAT AAG AGC CAA ACT ATT      109
           Met Ala Asn Cys Phe Leu Ser His Lys Ser Gln Thr Ile
           -65                 -60                 -55

CTA ATT TCA AAG CCT GCT CTG ACT CAG TCC CAT TTT ACC TCT CCA GCC     157
Leu Ile Ser Lys Pro Ala Leu Thr Gln Ser His Phe Thr Ser Pro Ala
        -50                 -45                 -40

GGC TTG TTT CTA ACT GTT GAG AAA TCA CAC CTT TTG ACA AGG CTG TTT     205
Gly Leu Phe Leu Thr Val Glu Lys Ser His Leu Leu Thr Arg Leu Phe
    -35                 -30                 -25

TTT CAC TGG CTT TCG TTA GTG CTG TGC TCG TTT CTG TCT TTG AGA TTT     253
Phe His Trp Leu Ser Leu Val Leu Cys Ser Phe Leu Ser Leu Arg Phe
-20                 -15                 -10                     -5

TGC ACA TTA TCT TTT ATG TGC TCT TTT GCC CTT TTC CAC CTG             295
Cys Thr Leu Ser Phe Met Cys Ser Phe Ala Leu Phe His Leu
                 1               5                  10
```

(2) INFORMATION FOR SEQ ID NO: 131:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 298 base pairs
(B) TYPE: NUCLEIC ACID
(C) STRANDEDNESS: DOUBLE
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Testis

(ix) FEATURE:
(A) NAME/KEY: sig_peptide
(B) LOCATION: 20..73
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 5
seq LTYLLFLPDWAAV/FE

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 131:

```
AACGGACAGA TTTATTGGA ATG CAT GGA GCT GGT CTG ACC TAT TTA CTT TTC     52
                     Met His Gly Ala Gly Leu Thr Tyr Leu Leu Phe
                                 -15                 -10

CTT CCA GAC TGG GCT GCT GTA TTT GAA CTG TAC AAC TGT GAA GAT GAA     100
Leu Pro Asp Trp Ala Ala Val Phe Glu Leu Tyr Asn Cys Glu Asp Glu
        -5                  1                   5
```

```
CGC TGT TAC TTA GAC TTG GCC AGG CTG AGA GGC GTT CAC TAC ATC ACT     148
Arg Cys Tyr Leu Asp Leu Ala Arg Leu Arg Gly Val His Tyr Ile Thr
 10                 15                  20                  25

TGG CGA CGG CAG AAC AAA GTC TTT CCT CAG GAT AAG GGC CAC CAT CCA     196
Trp Arg Arg Gln Asn Lys Val Phe Pro Gln Asp Lys Gly His His Pro
                30                  35                  40

ACC CTG GGG GAG CAC CCG AAG TTC ACC AAC TAC TCT TTC GAT GTA GAA     244
Thr Leu Gly Glu His Pro Lys Phe Thr Asn Tyr Ser Phe Asp Val Glu
            45                  50                  55

GAA TTT ATG TAT CTT GTC CTT CAG GCT GCA GAC CAC GTA TTG CAA CAC     292
Glu Phe Met Tyr Leu Val Leu Gln Ala Ala Asp His Val Leu Gln His
        60                  65                  70

CCC GGG                                                             298
Pro Gly
    75
```

(2) INFORMATION FOR SEQ ID NO: 132:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 148 base pairs
(B) TYPE: NUCLEIC ACID
(C) STRANDEDNESS: DOUBLE
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Ovary

(ix) FEATURE:
(A) NAME/KEY: sig_peptide
(B) LOCATION: 26..70
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 4.9
seq CLSATLAFSGSFL/AP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 132:

```
ACGCCAAACT CCTCCAGCTG GCCCC ATG TGC TGC CTT TCT GCC ACG CTA GCC      52
                            Met Cys Cys Leu Ser Ala Thr Leu Ala
                            -15                 -10

TTT TCA GGC TCT TTT CTG GCT CCC CAC CTC ATC TTT TGC TGT TTC TCC     100
Phe Ser Gly Ser Phe Leu Ala Pro His Leu Ile Phe Cys Cys Phe Ser
    -5                  1               5                   10

CAC CTG AAT GTC ATC ATC CTC CTA TCC TCA TTA TCC CCT ATC CAC GGG     148
His Leu Asn Val Ile Ile Leu Leu Ser Ser Leu Ser Pro Ile His Gly
                15                  20                  25
```

(2) INFORMATION FOR SEQ ID NO: 133:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 172 base pairs
(B) TYPE: NUCLEIC ACID
(C) STRANDEDNESS: DOUBLE
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Ovary

(ix) FEATURE:
(A) NAME/KEY: sig_peptide
(B) LOCATION: 38..154
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 4.9
seq SGLRGLLLQEALG/AV

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 133:

```
AACAGAAGAA AGACAGCCTA GGAGCAGAGC CTCCCAG ATG GCT GAG TTG GAT CTA      55
                                         Met Ala Glu Leu Asp Leu
                                                         -35

ATG GCT CCA GGG CCA CTG CCC AGG GCC ACT GCT CAG CCC CCA GCC CCT      103
Met Ala Pro Gly Pro Leu Pro Arg Ala Thr Ala Gln Pro Pro Ala Pro
        -30                 -25                 -20

CTC AGC CCA GAC TCT GGG TTG AGG GGG CTG CTG TTG CAG GAG GCC CTG      151
Leu Ser Pro Asp Ser Gly Leu Arg Gly Leu Leu Leu Gln Glu Ala Leu
    -15                 -10                  -5

GGA GCA GTG CCG GAC CCC AGG                                          172
Gly Ala Val Pro Asp Pro Arg
     1               5
```

(2) INFORMATION FOR SEQ ID NO: 134:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 370 base pairs
(B) TYPE: NUCLEIC ACID
(C) STRANDEDNESS: DOUBLE
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Ovary

(ix) FEATURE:
(A) NAME/KEY: sig_peptide
(B) LOCATION: 203..286
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 4.9
seq FLVACPLFGVCLX/FF

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 134:

```
ACTTCAGTAA ATCTATTATT GATGTAATAC TTTTGTCTAA TTASCATTCA TATTCTAATT   60

TTGTCAGTTG TTCAATAATA TCCTTTTTGA CAATTTTTCC TCCAGTGAGG GATCAAGTCT  120

AGGGCTGGAT ATTGTGTTTC ATTGTCATGT ATCTTGAGTC CCCTTTAATC TGGGAGAGTT  180

CCTCAGCTTT GCTTTGTGTC TT ATG ACA TTA ACA CAT GGG AAT AAT ATC CTC   232
                         Met Thr Leu Thr His Gly Asn Asn Ile Leu
                                     -25                 -20

CAC CTC GCC AAC TTT TTT TTA GTA GCA TGT CCT TTA TTT GGG GTT TGC    280
His Leu Ala Asn Phe Phe Leu Val Ala Cys Pro Leu Phe Gly Val Cys
            -15                 -10                 -5

CTG AWR TTT TTC ATT CTT AGA TTC AGG TTA TAC ATT CAA GGC CCA AAT    328
Leu Xaa Phe Phe Ile Leu Arg Phe Arg Leu Tyr Ile Gln Gly Pro Asn
         1               5                  10

GTC ACA CAA GTG ATA TTG CAT CTG TCT CAG GGA ACC TTG AGC            370
Val Thr Gln Val Ile Leu His Leu Ser Gln Gly Thr Leu Ser
 15                 20                  25
```

(2) INFORMATION FOR SEQ ID NO: 135:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 228 base pairs
(B) TYPE: NUCLEIC ACID
(C) STRANDEDNESS: DOUBLE
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Ovary

(ix) FEATURE:
(A) NAME/KEY: sig_peptide
(B) LOCATION: 181..222
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 4.9
seq VLRWLPWPRGSHS/DS

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 135:

```
AAGTATCCAG CCTCAACATT CAGCAGAGGC CCCAGATCAG CGTCTGAGCC AGGCCAACAA   60

TGACCAAGGA GGATGGGATC CTGGGTGCAG CTCATCACAA GCGTCGGGTG AGTCCGAGGC  120

CCCAGCTCTC TGCCCTCCTG MTCCTCTGCT CTCTCCTGGT CCTCCCAGTT CTACTGGCTC  180

ATG GTG TTG AGA TGG TTG CCT TGG CCT AGG GGG TCA CAC AGC GAC TCG    228
Met Val Leu Arg Trp Leu Pro Trp Pro Arg Gly Ser His Ser Asp Ser
            -10                 -5                   1
```

(2) INFORMATION FOR SEQ ID NO: 136:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 166 base pairs
(B) TYPE: NUCLEIC ACID
(C) STRANDEDNESS: DOUBLE
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Uterus

(ix) FEATURE:
(A) NAME/KEY: sig_peptide
(B) LOCATION: 50..121
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 4.8
seq FSFLGTLFHKSNS/ED

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 136:

```
ATAGTATTGA TGCTGGGTCA AACTAGTTAG GAGGATTTTC AGTTCTCCC ATG AAA GCA    58
                                                      Met Lys Ala

AGG CTC TCT GGT AAT CTG ATT TGT TTT TCT TTT CTA GGA ACC CTC TTT     106
Arg Leu Ser Gly Asn Leu Ile Cys Phe Ser Phe Leu Gly Thr Leu Phe
    -20                 -15                 -10

CAT AAA TCA AAC TCA GAA GAC AGC TCT GTA GGA AAA GGA GAC TGG AAG     154
His Lys Ser Asn Ser Glu Asp Ser Ser Val Gly Lys Gly Asp Trp Lys
 -5                  1               5                  10

AAG AAA AAT AAG                                                     166
Lys Lys Asn Lys
         15
```

(2) INFORMATION FOR SEQ ID NO: 137:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 217 base pairs
(B) TYPE: NUCLEIC ACID
(C) STRANDEDNESS: DOUBLE
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Ovary

(ix) FEATURE:
(A) NAME/KEY: sig_peptide
(B) LOCATION: 107..154

(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 4.8
seq VCLVPQTPSLCLG/KG

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 137:

```
AATGAACGAA CGGGGAAAGT GCATGTTGTA GTTCTCAAAA CCCAAAAAAA TCTAAGAGAA    60

ACCCAGCAGC AAGAAACACA GAGGTTTGGG TGTCAGCATC GGAGGA ATG TCT CAC      115
                                                   Met Ser His
                                                       -15

GTC TGC CTT GTC CCC CAG ACC CCG TCC CTG TGT CTG GGC AAA GGC ACG     163
Val Cys Leu Val Pro Gln Thr Pro Ser Leu Cys Leu Gly Lys Gly Thr
        -10                     -5                   1

CCC CGC TCC AGG TCG GCC CCA TTT CAG AGC AGT GGC CCT CAT AGG CTT     211
Pro Arg Ser Arg Ser Ala Pro Phe Gln Ser Ser Gly Pro His Arg Leu
     5                  10                  15

TGT GCG                                                             217
Cys Ala
 20
```

(2) INFORMATION FOR SEQ ID NO: 138:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 296 base pairs
(B) TYPE: NUCLEIC ACID
(C) STRANDEDNESS: DOUBLE
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Spleen

(ix) FEATURE:
(A) NAME/KEY: sig_peptide
(B) LOCATION: 93..179
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 4.8
seq VLTSVNLFIGING/SV

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 138:

```
ACTGCTTCCA GCAKAAGTCC TATGTGTCCT CCACCAATCT GCCTGTGCTA GCCCTTCTAC    60

TTTTGCTGTA TGGGTGGTCA ATCACACCTC TC ATG TAC CCA GCC TCC TTT GTG     113
                                    Met Tyr Pro Ala Ser Phe Val
                                                        -25

TTC AAG ATC CCC AGC ACA GCC TAT GTG GTG CTC ACC AGC GTG AAC CTC     161
Phe Lys Ile Pro Ser Thr Ala Tyr Val Val Leu Thr Ser Val Asn Leu
        -20                 -15                     -10
```

```
TTC ATT GGC ATT AAT GGC AGC GTG GCC ACC TTT GTG CTG GAG CTG TTC     209
Phe Ile Gly Ile Asn Gly Ser Val Ala Thr Phe Val Leu Glu Leu Phe
     -5                  1                   5                  10

ACC GAC AAT AAG CTG AAT AAT ATC AAT GAT ATC CTG AAG TCC GTG TTC     257
Thr Asp Asn Lys Leu Asn Asn Ile Asn Asp Ile Leu Lys Ser Val Phe
                15                  20                  25

TTG ATC TTC CCA CAT TTT TGC CTG GGA CGA GGG CAG ACG                 296
Leu Ile Phe Pro His Phe Cys Leu Gly Arg Gly Gln Thr
            30                  35
```

(2) INFORMATION FOR SEQ ID NO: 139:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 290 base pairs
(B) TYPE: NUCLEIC ACID
(C) STRANDEDNESS: DOUBLE
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Testis

(ix) FEATURE:
(A) NAME/KEY: sig_peptide
(B) LOCATION: 165..254
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 4.8
seq RSSLWVTAPLVSA/CP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 139:

```
AAGAGCCTCT TGSATCCCCA CAGGGYAATG GGTGTBCCGA TCTCGCGGGG GACTCTGTGA    60

TCCGTGTTCC CCTGACCCTC CTAGTGCACA ACTTGGCCGG GCTCACTGGG CTCCTGCACC   120

ACTGCCTGTC AGGTCCGCTG CCAGCCCCAA GCCCCCCACC AGCC ATG AGC TCC TCC    176
                                                 Met Ser Ser Ser
                                                 -30

AGA AAG GAC CAC CTC GGC GCC ASA GCT CAG AGC CCC TCC CGG TCA TCA    224
Arg Lys Asp His Leu Gly Ala Xaa Ala Gln Ser Pro Ser Arg Ser Ser
    -25                 -20                 -15

TTG TGG GTA ACG GCC CCT CTG GTA TCT GCC TGT CCT ACC TGC TCT CCG    272
Leu Trp Val Thr Ala Pro Leu Val Ser Ala Cys Pro Thr Cys Ser Pro
-10                 -5                  1                   5

GCT ACA CAC CCT ACG GGG                                             290
Ala Thr His Pro Thr Gly
            10
```

(2) INFORMATION FOR SEQ ID NO: 140:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 397 base pairs
(B) TYPE: NUCLEIC ACID
(C) STRANDEDNESS: DOUBLE
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Spleen

(ix) FEATURE:
(A) NAME/KEY: sig_peptide
(B) LOCATION: 230..286
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 4.8
seq ATYLVQSSACCPA/IV

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 140:

```
ACCACGGGGA CAAGGACTGC KCCCACGATG GTGCTCCTGC CAVGCCCCAG CTGBACGGGG    60

AGTCCTGTGG GGCCCAGGCC TTGAACAGCC ACATGCCTGC TGAGACCGAG GAGCTGGGAC   120

GGTGGGGACC ACAGAGAGCA ACCTGATTAC CTCCCTGCTT GGGCTGTGCC AGAGCAAGAA   180

GAGTCGGGTG GCCTTGAAGG CCCAGGAGAA CCTGCTGCTC CTGGTGAGCC ATG GCC TCC  238
                                                      Met Ala Ser

CCA GCA GCT GCC ACC TAC CTG GTA CAG AGC AGC GCC TGC TGC CCT GCG     286
Pro Ala Ala Ala Thr Tyr Leu Val Gln Ser Ser Ala Cys Cys Pro Ala
    -15                 -10                 -5

ATC GTC CGG CAC CTT TGC CAG TBG TAC CGG TCC ATG CCT GTC TTC CTG     334
Ile Val Arg His Leu Cys Gln Xaa Tyr Arg Ser Met Pro Val Phe Leu
  1               5                  10                  15

GAC CCC GCA GAS ATT GCC ACC TTA GAG GGC ATC AGC TGG AGG TTA CCC     382
Asp Pro Ala Xaa Ile Ala Thr Leu Glu Gly Ile Ser Trp Arg Leu Pro
            20                  25                  30

AGT GCC CCG TCT GAT                                                 397
Ser Ala Pro Ser Asp
        35
```

(2) INFORMATION FOR SEQ ID NO: 141:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 378 base pairs
(B) TYPE: NUCLEIC ACID
(C) STRANDEDNESS: DOUBLE
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Testis

(ix) FEATURE:
(A) NAME/KEY: sig_peptide
(B) LOCATION: 172..354
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 4.7
seq LLPCNLHXSWLHS/SP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 141:

```
AGATTGGCTG GGCAGATGGG CTGACTGGCT GGGCAGATGG GTGGGTGAGT TCCCTCTCCC   60

CAGAGCCATC GGCCAGGTAC CAAAGCTCAG CTGTATGGAT TCCCAACAGG AGGACCTGCG  120

CTTCCCTGGG ACCCATTGTT GTACTGGATT AACAAGCGAC GGCGCTACGG C ATG AAT   177
                                                         Met Asn
                                                             -60

GCA GCC ATC AAC ACG GGC CCT GCC CCT GCT GTC ACC AAG ACT GAG ACT    225
Ala Ala Ile Asn Thr Gly Pro Ala Pro Ala Val Thr Lys Thr Glu Thr
                -55                 -50                 -45

GAG GTC CAG AAT CCA GAT GTT CTG TGG GAT TTG GAC ATC CCC GAA GCC    273
Glu Val Gln Asn Pro Asp Val Leu Trp Asp Leu Asp Ile Pro Glu Ala
            -40                 -35                 -30

AGG AGC CAT GCT GAC CAA GAC AGC AAC CCB NMG GCG GAA GCC CTG CTC    321
Arg Ser His Ala Asp Gln Asp Ser Asn Pro Xaa Ala Glu Ala Leu Leu
        -25                 -20                 -15

CCC TGC AAC CTG CAC TGM AGC TGG CTC CAC AGC AGC CCC AGG CCA GAT    369
Pro Cys Asn Leu His Xaa Ser Trp Leu His Ser Ser Pro Arg Pro Asp
    -10                 -5                   1                   5

CCC CAT TCC                                                        378
Pro His Ser
```

(2) INFORMATION FOR SEQ ID NO: 142:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 362 base pairs
(B) TYPE: NUCLEIC ACID
(C) STRANDEDNESS: DOUBLE
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Testis

(ix) FEATURE:
(A) NAME/KEY: sig_peptide
(B) LOCATION: 180..308
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 4.7

seq GIFLVIFCSESFS/LL

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 142:

```
AATGGAMTTC TGGGTTGACA RATGTTTTGT TGTGTTTTGT TTATWCCTCA TCTGTTCTCT   60

ATTGTTTCTA GTTTGTAGTC AGCATTCATA GGTGTACTTG ATTCCTCCTA TRWTATTAGN  120

NTCTAGCTGT TTTCAGGRAT TTCTCTTTKA TTTTTGAGTT CCAGTAGTTT GACTATAAT   179

ATG ATA AAC CTA CTT GTG GGT AAC TGC ATT TAT CTG CTT GGA GCT ATT    227
Met Ile Asn Leu Leu Val Gly Asn Cys Ile Tyr Leu Leu Gly Ala Ile
            -40                 -35                 -30

AGA GCT TCT TGC ATG TGT AGA TKB ATG TCT TTC GCC AAA TTT GGG ATT    275
Arg Ala Ser Cys Met Cys Arg Xaa Met Ser Phe Ala Lys Phe Gly Ile
        -25                 -20                 -15

TTT CTT GTA ATA TTT TGT TCT GAA TCA TTT TCT CTT CTC CTC TGG AAC    323
Phe Leu Val Ile Phe Cys Ser Glu Ser Phe Ser Leu Leu Leu Trp Asn
    -10                 -5                  1               5

TTC AGT TCA ATA TAT GTT AAG ACC TTT TGG CCA GTG GGG                362
Phe Ser Ser Ile Tyr Val Lys Thr Phe Trp Pro Val Gly
                10                  15
```

(2) INFORMATION FOR SEQ ID NO: 143:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 171 base pairs
(B) TYPE: NUCLEIC ACID
(C) STRANDEDNESS: DOUBLE
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Spleen

(ix) FEATURE:
(A) NAME/KEY: sig_peptide
(B) LOCATION: 16..72
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 4.7
seq LRFLLRDPGCLLA/QP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 143:

```
AAGACGGCGG TGCGC ATG CTC TGT TGC GGT CCG CTT CGG TTT CTG TTG CGG    51
                 Met Leu Cys Cys Gly Pro Leu Arg Phe Leu Leu Arg
                                 -15                 -10

GAC CCG GGG TGT CTC CTA GCG CAA CCG GAA CTA GCC TTC TGG GGG CCG     99
Asp Pro Gly Cys Leu Leu Ala Gln Pro Glu Leu Ala Phe Trp Gly Pro
        -5                  1               5
```

```
GCT TCC TTT ATC TCT GGC GGC CTT GTA GTC GTC TCC GAG ACT CCC CAC     147
Ala Ser Phe Ile Ser Gly Gly Leu Val Val Val Ser Glu Thr Pro His
 10                 15                  20                  25

CCC TCC TTC CCT CTT GAC CCC CCG                                     171
Pro Ser Phe Pro Leu Asp Pro Pro
                30
```

(2) INFORMATION FOR SEQ ID NO: 144:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 437 base pairs
(B) TYPE: NUCLEIC ACID
(C) STRANDEDNESS: DOUBLE
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Spleen

(ix) FEATURE:
(A) NAME/KEY: sig_peptide
(B) LOCATION: 360..416
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 4.7
seq ILLRMTVLPTLWT/RR

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 144:

```
AAGAGAGAAA CTTGGCGATC ACGTTTTCAC ATGATGCTCA CGCTCAGGGC GCTTCAATTA    60

TCCCTCCCCA CAAAGATAGG TGGCGCGTGT TTCAGGGTCT CTCGTCTCTC TCCTACAGAA   120

AAGAAAAAGA AAAAAATGTC ATTAGAAGAG GCGTAACACG TCAGTCCGTC CCCAGATCGA   180

GCCTGCGTGC TGCCGAAGCA GGGCGCCGAG TCCATGCGAA CTGCCACCTG ATCCGCTCTT   240

ATCAATGAAG CAGCCGATCA TGGCGGATGG CCCCCGGTGC AAGAGGCGCA AACAAGCCAA   300

TCCCAGGAGG AAAAACGTGG TGAACTATGA CAATGTAGTG GACACAGGTT CTGAAACAG    359

ATG AGG AAG ACA AGC TTC ATA TTG CTG AGG ATG ACG GTA TTG CCA ACC     407
Met Arg Lys Thr Ser Phe Ile Leu Leu Arg Met Thr Val Leu Pro Thr
            -15                 -10                     -5

CTC TGG ACC AGG AGA CGA GTC CAG CTA GTG                             437
Leu Trp Thr Arg Arg Arg Val Gln Leu Val
             1                   5
```

(2) INFORMATION FOR SEQ ID NO: 145:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 153 base pairs
(B) TYPE: NUCLEIC ACID

(C) STRANDEDNESS: DOUBLE
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Ovary

(ix) FEATURE:
(A) NAME/KEY: sig_peptide
(B) LOCATION: 31..99
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 4.6
seq VRVGLVLVXRALC/LX

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 145:

```
AGGGAAGGGA GGGCAGGCGG KGCTGGAGTB ATG TGG TGG AAA CCT GCT CCT GAG    54
                                 Met Trp Trp Lys Pro Ala Pro Glu
                                             -20

GAA GGG GTC CGG GTG GGG TTG GTG CTT GTG TSA AGG GCT CTG TGC CTC    102
Glu Gly Val Arg Val Gly Leu Val Leu Val Xaa Arg Ala Leu Cys Leu
-15                 -10                 -5                   1

TKT GTA CTC TCT CGG TTC ATG TTC ASA AAT CCT GGC CTT GGT GGC ATG    150
Xaa Val Leu Ser Arg Phe Met Phe Xaa Asn Pro Gly Leu Gly Gly Met
            5                  10                  15

GGG                                                                153
Gly
```

(2) INFORMATION FOR SEQ ID NO: 146:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 454 base pairs
(B) TYPE: NUCLEIC ACID
(C) STRANDEDNESS: DOUBLE
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Testis

(ix) FEATURE:
(A) NAME/KEY: sig_peptide
(B) LOCATION: 374..415
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 4.6
seq FNFLLGNSSCVYQ/RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 146:

```
AATTCTGGCC CAGCTTCTTC CCCAGCTCTA TCCTGCTTCC CTCCATCTCC TATAGGATTC    60
```

```
TCCTTAGAGT TCTCCCTCCA TTAGTAGTTG TCTTAGGGTC TGTTTCTGGG GAGCCCTGCC  120

TAAGACTCAT GCTACAAGAA GTTAAATAAG TTTCCCGAAG TCACACAGCT AGCCTCTCAT  180

CCCTTTTCTA CTGAGAGGAA GTGGAATGCA CTCCGACAAG GATAAGGTTT TATTGTGAGC  240

TGGCCTTGGA ATTAAACCAC CACCAACACA CTTTTGGATT ATCAGNNGGT GGAAGGAGTG  300

CAAATGCCAG TTACGGTGAT GCGTTCAACA TCCTTATTTC CAGTTCAGAA TTTCCCTGGA  360

GCTCCAAATT TTT ATG TTT AAT TTC TTA CTG GGC AAT TCC AGT TGT GTA     409
               Met Phe Asn Phe Leu Leu Gly Asn Ser Ser Cys Val
                               -10                  -5

TAT CAA AGG CCC ATC AGA TTA AAA CTC ATT ATC TTC CCA TCA GGG        454
Tyr Gln Arg Pro Ile Arg Leu Lys Leu Ile Ile Phe Pro Ser Gly
        1               5                  10
```

(2) INFORMATION FOR SEQ ID NO: 147:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 413 base pairs
(B) TYPE: NUCLEIC ACID
(C) STRANDEDNESS: DOUBLE
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Testis

(ix) FEATURE:
(A) NAME/KEY: sig_peptide
(B) LOCATION: 57..182
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 4.6
seq LDPAVSLSAPAFA/SA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 147:

```
DRAAACCGGA GCCACAGAGG ACAGGGTAGA GTCGCAGAAA GGAGAGACAC ACATAC ATG   59
                                                              Met

AAA AGA GGA GCT TTC TCC AAT CTT AAT GAT TCC CAG CTC TCA GCC TCG    107
Lys Arg Gly Ala Phe Ser Asn Leu Asn Asp Ser Gln Leu Ser Ala Ser
    -40                 -35                 -30

TTT CTG CAA CCC AGC CTG CAA GCA AAC TGT CCT GCT TTG GAC CCT GCT    155
Phe Leu Gln Pro Ser Leu Gln Ala Asn Cys Pro Ala Leu Asp Pro Ala
-25                 -20                 -15                 -10

GTG TCA CTC TCC GCA CCA GCC TTT GCC TCT GCT CTT CGC TCT ATG AAG    203
Val Ser Leu Ser Ala Pro Ala Phe Ala Ser Ala Leu Arg Ser Met Lys
                -5                  1               5

TCC TCC CAG GCT GCA CGG AAG GAC GAC TTT CTC AGG TCT CTT AGT GAT    251
```

```
Ser Ser Gln Ala Ala Arg Lys Asp Asp Phe Leu Arg Ser Leu Ser Asp
        10                  15                  20

GGA GAC TCA GGG ACA TCA GAA CAC ATC TCA GCG GTG GTG ACT AGC CCT     299
Gly Asp Ser Gly Thr Ser Glu His Ile Ser Ala Val Val Thr Ser Pro
    25                  30                  35

CGG ATT TCC TGC CAT GGT GCT GCC ATT CCC AMM GCM MGT GCC CWC TGM     347
Arg Ile Ser Cys His Gly Ala Ala Ile Pro Xaa Ala Xaa Ala Xaa Xaa
40                  45                  50                  55

MTA GGC TGT TCC TGC TGM ACC GAA CGM MTC CTC MTG MCA CCG CCC TCC     395
Xaa Gly Cys Ser Cys Xaa Thr Glu Arg Xaa Leu Xaa Xaa Pro Pro Ser
                60                  65                  70

CTC CTT TCT TTA GAA GCC                                             413
Leu Leu Ser Leu Glu Ala
            75
```

(2) INFORMATION FOR SEQ ID NO: 148:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 271 base pairs
(B) TYPE: NUCLEIC ACID
(C) STRANDEDNESS: DOUBLE
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Testis

(ix) FEATURE:
(A) NAME/KEY: sig_peptide
(B) LOCATION: 32..103
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 4.6
seq FFIFCSLNTLLLG/GV

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 148:

```
AACAACTATC CTGCCTGCTG CTTGCTGCAC C ATG AAG TCT GCC AAG CTG GGA       52
                                   Met Lys Ser Ala Lys Leu Gly
                                                   -20

TTT CTT CTA AGA TTC TTC ATC TTC TGC TCA TTG AAT ACC CTG TTA TTG     100
Phe Leu Leu Arg Phe Phe Ile Phe Cys Ser Leu Asn Thr Leu Leu Leu
        -15                 -10                 -5

GGT GGT GTT AAT AAA ATT GCG GAG AAG ATA TGT GGA GAC CTC AAA GAT     148
Gly Gly Val Asn Lys Ile Ala Glu Lys Ile Cys Gly Asp Leu Lys Asp
    1               5                   10                  15

CCC TGC AAA TTG GAC ATG AAT TTT GGA AGC TGC TAT GAA GTT CAC TTT     196
Pro Cys Lys Leu Asp Met Asn Phe Gly Ser Cys Tyr Glu Val His Phe
                20                  25                  30
```

```
AGA TAT TTC TAC AAC AGA ACC TCC AAA AGA TGT GAA ACT TTT GTC TTC     244
Arg Tyr Phe Tyr Asn Arg Thr Ser Lys Arg Cys Glu Thr Phe Val Phe
            35                  40                  45

TCC AGC TGT AAT GGC AAC CTT AAC GGG                                 271
Ser Ser Cys Asn Gly Asn Leu Asn Gly
        50                  55
```

(2) INFORMATION FOR SEQ ID NO: 149:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 150 base pairs
(B) TYPE: NUCLEIC ACID
(C) STRANDEDNESS: DOUBLE
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Testis

(ix) FEATURE:
(A) NAME/KEY: sig_peptide
(B) LOCATION: 31..75
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 4.6
seq ILFPLHSVIGSHP/QC

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 149:

```
AAGTTGCCTG AGGACAGCAG TSCAGTTGAC ATG GAT ATT CTC TTT CCT CTG CAC     54
                                 Met Asp Ile Leu Phe Pro Leu His
                                 -15                 -10

AGT GTT ATT GGG AGC CAT CCT CAG TGC CTC CCA GAG AGG WGG ACA GCG     102
Ser Val Ile Gly Ser His Pro Gln Cys Leu Pro Glu Arg Xaa Thr Ala
        -5                  1                   5

AGA ATG ATC AAG CTG AAG TGG GGG AAT GGC TCA GGA TCG GAT TTC GGG     150
Arg Met Ile Lys Leu Lys Trp Gly Asn Gly Ser Gly Ser Asp Phe Gly
10                  15                  20                  25
```

(2) INFORMATION FOR SEQ ID NO: 150:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 430 base pairs
(B) TYPE: NUCLEIC ACID
(C) STRANDEDNESS: DOUBLE
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Testis

(ix) FEATURE:
(A) NAME/KEY: sig_peptide
(B) LOCATION: 275..355
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 4.6
seq FGILILLSQRQWS/KN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 150:

```
GTTGGAAAAC AGTTTTGGCT CTGAGGACCC AGCAGTTGAC AAACAGGAGG CCTGGGACAA    60

GAGCAGTATG AGAAGTCAGA TCGCCTCTTT TAATGTCACT AGTCAGTACA GGCCTCGCCA   120

GACAAGTCTC TCCTCARMNT CACTTGGAAG AACAGGCCSD CTCTTCATGA TCCTGGGTTT   180

CCTAGACWTA TTTCCAGGAC TGTTATGGGG ATTAGGGCCA ACTGTAAAAG TGGCTGAGGA   240

GACTAGGTAA AGAGTGTTGT CTCACTTTAG AACA ATG CTG AAG GTG TTT AGA GCC   295
                                      Met Leu Lys Val Phe Arg Ala
                                                  -25

TGM CAT CCT AAA ATA TGC CAC TTT GGC ATA CTG ATT CTT CTG AGC CAG     343
Xaa His Pro Lys Ile Cys His Phe Gly Ile Leu Ile Leu Leu Ser Gln
-20                 -15                 -10                  -5

AGG CAA TGG AGC AAA AAC AGA TGC AGG GAA GGC TGT CTG ACC ACC CTC     391
Arg Gln Trp Ser Lys Asn Arg Cys Arg Glu Gly Cys Leu Thr Thr Leu
                  1               5                  10

TTT CTG TTT GAA GCG GAA CAT AAA AGT TCC CTT GTG AAA                 430
Phe Leu Phe Glu Ala Glu His Lys Ser Ser Leu Val Lys
        15                  20                  25
```

(2) INFORMATION FOR SEQ ID NO: 151:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 353 base pairs
(B) TYPE: NUCLEIC ACID
(C) STRANDEDNESS: DOUBLE
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Uterus

(ix) FEATURE:
(A) NAME/KEY: sig_peptide
(B) LOCATION: 219..320
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 4.6
seq LXWRKLAASWTLS/QE

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 151:

```
ACAATTAAAC CACACAGAAA ATGATGTGAC TCATCTTCAA AAGGAAATGA GCAATTGTAG   60

AGCAGGTGAA AACGCTGGCA TGGGTAGGTT CACTAAGGTG GGTGAGCAAG AAAGGACAGT  120

GGACACCCTG CCGTCCCCCC AGCACCCCGT GGCTCATTGC TGCAGTCAGC TGGAGGAGAG  180

GTGGCAGAGG TTGCAGAGCC AGGTCATCTC GGAGCTGG ATG CTT GTA AGG AAT GCA  236
                                          Met Leu Val Arg Asn Ala
                                                          -30

CGC AGG GGG TCC AGA GGG AGG TCT CCA TGG TGG AGG GCA GGG TGT CTM    284
Arg Arg Gly Ser Arg Gly Arg Ser Pro Trp Trp Arg Ala Gly Cys Leu
            -25                 -20                 -15

RTA TGG AGA AAA CTT GCA GCA AGC TGG ACT CTA TCT CAG GAA ATC TTC    332
Xaa Trp Arg Lys Leu Ala Ala Ser Trp Thr Leu Ser Gln Glu Ile Phe
        -10                 -5                  1

AGA GGA TCA AGG AAG GGC TCG                                        353
Arg Gly Ser Arg Lys Gly Ser
  5                 10
```

(2) INFORMATION FOR SEQ ID NO: 152:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 216 base pairs
(B) TYPE: NUCLEIC ACID
(C) STRANDEDNESS: DOUBLE
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Ovary

(ix) FEATURE:
(A) NAME/KEY: sig_peptide
(B) LOCATION: 61..147
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 4.5
seq FTLGLGYPIPTRL/QP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 152:

```
GATGGCGGCG ASGSGGACGG TSAAGGTTGC CTCCCGCCCG TCCGGGCTCT GATCCTCCCC   60

ATG ACT AAA GGG CAT CAC CAC CAG CAT CCC CTG CAT CCC CAC CCA CTC    108
Met Thr Lys Gly His His His Gln His Pro Leu His Pro His Pro Leu
            -25                 -20                 -15

TTC ACC CTG GGC TTG GGA TAC CCC ATA CCC ACT CGC CTG CAA CCA TGC    156
Phe Thr Leu Gly Leu Gly Tyr Pro Ile Pro Thr Arg Leu Gln Pro Cys
            -10                 -5                  1

ACA TTA AGC TCA GAC CCC CTT CTG GAC ATT ACC TGT TCC CTG AGA AGC    204
Thr Leu Ser Ser Asp Pro Leu Leu Asp Ile Thr Cys Ser Leu Arg Ser
    5                   10                  15
```

```
CCA AGC TCT GGG                                                  216
Pro Ser Ser Gly
 20
```

(2) INFORMATION FOR SEQ ID NO: 153:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 236 base pairs
(B) TYPE: NUCLEIC ACID
(C) STRANDEDNESS: DOUBLE
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Spleen

(ix) FEATURE:
(A) NAME/KEY: sig_peptide
(B) LOCATION: 162..230
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 4.5
seq RLHILFIVCLARG/KG

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 153:

```
AGCTGCTTAG TTTGCTAATT CTAGTGGTTC AAACCAGATT TCAAAATCTG GGCTAAATCT   60

CTGTCATGCT ATGACATGGC ATTTGACAGT AATTCCTGAA TATTTAATTG ATAGAAAAAC  120

AGAAAGCATG CATATTGTTT AGTACAATTG TGTGAACTGC T ATG ACA TAT CAT KRC  176
                                              Met Thr Tyr His Xaa
                                                          -20

ATA CAG TTT TCT GAA AGA CTG CAT ATT TTA TTC ATT GTA TGC CTA GCA    224
Ile Gln Phe Ser Glu Arg Leu His Ile Leu Phe Ile Val Cys Leu Ala
            -15                 -10                     -5

CGG GGA AAA GGG                                                    236
Arg Gly Lys Gly
          1
```

(2) INFORMATION FOR SEQ ID NO: 154:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 230 base pairs
(B) TYPE: NUCLEIC ACID
(C) STRANDEDNESS: DOUBLE
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Homo Sapiens

(F) TISSUE TYPE: Ovary

(ix) FEATURE:
(A) NAME/KEY: sig_peptide
(B) LOCATION: 9..146
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 4.5
seq LIYCGLSQPLTLG/VT

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 154:

```
ATTGTATC ATG TCT CAA TTT CCT CTC TGC AGC CCT CCG TGG AAA CCA CTT      50
         Met Ser Gln Phe Pro Leu Cys Ser Pro Pro Trp Lys Pro Leu
             -45                 -40                 -35

GTC AAG GTC TCC AGA AAC CTG AAA ATA AGG ATG TCC ATT CCA TGG CCA       98
Val Lys Val Ser Arg Asn Leu Lys Ile Arg Met Ser Ile Pro Trp Pro
        -30                 -25                 -20

CTC TCA GTC CTG ATT TAC TGT GGT CTC TCG CAG CCT TTG ACC CTG GGG      146
Leu Ser Val Leu Ile Tyr Cys Gly Leu Ser Gln Pro Leu Thr Leu Gly
    -15                 -10                  -5

GTC ACC TCT CCT TCC TTC CCC CAA AAC TCT TTC TTC CCT TGG CTT CCA      194
Val Thr Ser Pro Ser Phe Pro Gln Asn Ser Phe Phe Pro Trp Leu Pro
  1               5                  10                  15

GAA CAC CCC ACT CAC CTG GTC TCC TCT ACC CCA CAG                      230
Glu His Pro Thr His Leu Val Ser Ser Thr Pro Gln
            20                  25
```

(2) INFORMATION FOR SEQ ID NO: 155:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 445 base pairs
(B) TYPE: NUCLEIC ACID
(C) STRANDEDNESS: DOUBLE
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Testis

(ix) FEATURE:
(A) NAME/KEY: sig_peptide
(B) LOCATION: 26..100
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 4.4
seq AMGFLLMFDLTSQ/QS

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 155:

```
AAAAGGACAT CTGGCTGTGC AATCC ATG TTC CGG AGT CTC ACC ACT GCA TTT      52
                            Met Phe Arg Ser Leu Thr Thr Ala Phe
                            -25                 -20
```

```
TTC AGA GAC GCC ATG GGC TTC TTA TTA ATG TTT GAC CTC ACC AGT CAA     100
Phe Arg Asp Ala Met Gly Phe Leu Leu Met Phe Asp Leu Thr Ser Gln
    -15                 -10                 -5

CAG AGC TTC TTA AAT GTC AGA AAC TGG ATG AGC CAA CTG CAA GCA AAT     148
Gln Ser Phe Leu Asn Val Arg Asn Trp Met Ser Gln Leu Gln Ala Asn
  1               5                  10                  15

GCT TAT TGT GAA AAT CCA GAT ATA GTA TTA ATT GGC AAC AAG GCA GAC     196
Ala Tyr Cys Glu Asn Pro Asp Ile Val Leu Ile Gly Asn Lys Ala Asp
            20                  25                  30

CTA CCA GAT CAG AGG GAA GTC AAT GAA CGG CAA GCT CGG GAA CTG GCT     244
Leu Pro Asp Gln Arg Glu Val Asn Glu Arg Gln Ala Arg Glu Leu Ala
        35                  40                  45

GAC AAA TAT GGC ATA CCA TAT TTT GAA ACA AGT GCA GCA ACT GGA CAG     292
Asp Lys Tyr Gly Ile Pro Tyr Phe Glu Thr Ser Ala Ala Thr Gly Gln
    50                  55                  60

AAT GTG GAG AAA GCT GTA GAA ACC CTT TTG GAC TTA ATC ATG NRG CGA     340
Asn Val Glu Lys Ala Val Glu Thr Leu Leu Asp Leu Ile Met Xaa Arg
 65                  70                  75                  80

ATG GAA CAG TGT GTG GAG AAG ACA CAA ATC CCT GAT ACT GTC AAT GGT     388
Met Glu Gln Cys Val Glu Lys Thr Gln Ile Pro Asp Thr Val Asn Gly
                85                  90                  95

GGA AAT TCT GGA AAC TTG GAT GGG GAA AGC CAC CAG AGA AGA AAT GTA     436
Gly Asn Ser Gly Asn Leu Asp Gly Glu Ser His Gln Arg Arg Asn Val
            100                 105                 110

TCT GCT AGA                                                         445
Ser Ala Arg
        115
```

(2) INFORMATION FOR SEQ ID NO: 156:

(i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 319 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:
- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Testis

(ix) FEATURE:
- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 185..295
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.4
  seq LSYASSALSPCLX/AP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 156:

```
ATCACCTTCT TCTCCATCCT TSTCTGGGCC AGTCCCCARC CCAGTCCCTC TCCTGACCTG    60

CCCAGCCCAA GTCAGCCTTC AGCACGCGCT TTTCTGCACA CAGATATTCC AGGCCTACCT   120

GGCATTCCAG GACCTCCGMA ATGATGCTCC AGTCCCTTAC AAGCGCTTCC TGGATGAGGG   180

TGGC ATG GTG CTG ACC ACC CTC CCC TTG CCC TCT GCC AAC AGC CCT GTG    229
     Met Val Leu Thr Thr Leu Pro Leu Pro Ser Ala Asn Ser Pro Val
             -35                 -30                 -25

AAC ATG CCC ACC ACT GGC CCC AAC AGC CTG AGT TAT GCT AGC TCT GCC     277
Asn Met Pro Thr Thr Gly Pro Asn Ser Leu Ser Tyr Ala Ser Ser Ala
        -20                 -15                 -10

CTG TCC CCC TGT CTG AHC GCT CCA AAG TCC CCC CGA CTT GGG             319
Leu Ser Pro Cys Leu Xaa Ala Pro Lys Ser Pro Arg Leu Gly
    -5                  1                   5
```

(2) INFORMATION FOR SEQ ID NO: 157:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 270 base pairs
(B) TYPE: NUCLEIC ACID
(C) STRANDEDNESS: DOUBLE
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Testis

(ix) FEATURE:
(A) NAME/KEY: sig_peptide
(B) LOCATION: 106..195
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 4.3
seq LLPTLPWLPSTRL/LS

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 157:

```
AGCACAGCGC TGRRATGCCA GGTTCGGGTA GGAGGCCCCT TGGGGGRMNR ATTCTTTAGG    60

AAATTCCTTT AGAAGVAAAC AACTTGGGAC TGGATAGCGT GCGAT ATG CAG AGA AAT   117
                                                  Met Gln Arg Asn
                                                  -30

GCA ACT TTC ATT CAT TTG CAG TTA GCG ATC CGC CCT TCC CTG CTC CCC     165
Ala Thr Phe Ile His Leu Gln Leu Ala Ile Arg Pro Ser Leu Leu Pro
    -25                 -20                 -15

ACC CTT CCG TGG CTC CCC AGT ACC CGC CTG CTG TCG CCC ACA CCC TTA     213
Thr Leu Pro Trp Leu Pro Ser Thr Arg Leu Leu Ser Pro Thr Pro Leu
-10                 -5                  1                   5

GGA CAG CTT CGT GGC CCC CCG GGA DCG CAG AGG GCC ATG CCT ACC GCT     261
```

```
Gly Gln Leu Arg Gly Pro Pro Gly Xaa Gln Arg Ala Met Pro Thr Ala
            10                  15                  20

CAT TTA AGA                                                      270
His Leu Arg
        25
```

(2) INFORMATION FOR SEQ ID NO: 158:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 109 base pairs
(B) TYPE: NUCLEIC ACID
(C) STRANDEDNESS: DOUBLE
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Ovary

(ix) FEATURE:
(A) NAME/KEY: sig_peptide
(B) LOCATION: 50..94
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 4.3
seq ILFCFHSFHPLFQ/DT

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 158:

```
ACATATATCT ATCCTGACAA TATTTAGCAG TTCAAAAGGT AATAAGATT ATG AAT ATA    58
                                                      Met Asn Ile
                                                      -15

TTA TTT TGC TTT CAT TCT TTT CAC CCT CTA TTT CAA GAC ACT ATC GAA     106
Leu Phe Cys Phe His Ser Phe His Pro Leu Phe Gln Asp Thr Ile Glu
        -10                 -5                   1

TTT                                                                 109
Phe
  5
```

(2) INFORMATION FOR SEQ ID NO: 159:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 371 base pairs
(B) TYPE: NUCLEIC ACID
(C) STRANDEDNESS: DOUBLE
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Spleen

(ix) FEATURE:
(A) NAME/KEY: sig_peptide
(B) LOCATION: 198..257
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 4.3
seq FNFLFLVQLCILA/CD

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 159:

```
AAGATAAATT GGGGAATTCT AGGGAAACCC TTGAATACCA AGATAGAAAA CTAAAGTTTT   60

TACTTCATTT GGTCATGGGA AACTTGCACT GAGCATGGGA GTCAATAATT AGAAGCAAGT  120

KAAATTCAAA AAGTCGAACC CCATTCATAA AACCAGCTGA TAGTCTGAAA ATACGCTTTG  180

AGCTAAGCAA AGAATAC ATG TTG ACA AAT CGT AAC TAC TTT AAC TTC CTT      230
                   Met Leu Thr Asn Arg Asn Tyr Phe Asn Phe Leu
                   -20                 -15                 -10

TTT CTT GTA CAA TTG TGC ATC CTG GCT TGT GAC AAT GCA TAC CTT CAG     278
Phe Leu Val Gln Leu Cys Ile Leu Ala Cys Asp Asn Ala Tyr Leu Gln
                -5                   1               5

TCG TGT CCC CTC ACC TCA AAG ACT CCT CTG TTA CAA ACC CAC TCT GCT     326
Ser Cys Pro Leu Thr Ser Lys Thr Pro Leu Leu Gln Thr His Ser Ala
        10                  15                  20

CTT TTC TAT AAT AGT ACA TAT GGG ATT TTC CTA CTC CTA GGA GTG         371
Leu Phe Tyr Asn Ser Thr Tyr Gly Ile Phe Leu Leu Leu Gly Val
    25                  30                  35
```

(2) INFORMATION FOR SEQ ID NO: 160:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 363 base pairs
(B) TYPE: NUCLEIC ACID
(C) STRANDEDNESS: DOUBLE
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Testis

(ix) FEATURE:
(A) NAME/KEY: sig_peptide
(B) LOCATION: 190..267
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 4.3
seq ALCRFVGMQPCTA/QT

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 160:

```
AATTCTCAAC AGTTGCATTG GAATGTAAGG TCAGGGCACC ACTGAGTTCA GTACTTCAAA   60

ATTGCCGTGC TCTACCTCTC CCCAGTGCAC AAAAACACTC TCCACACCAA GCTGCTGCTG  120
```

```
CTGGGATGGA GGGATGGCGT CASGATTCAA GACTGTTTTT CCTACCTGTT CAGCACTTCT  180

TTCAGCGAT ATG AAG TTA AAT CCA GGC CAA GTT CCC ACC TGG TGG GAA GCA  231
          Met Lys Leu Asn Pro Gly Gln Val Pro Thr Trp Trp Glu Ala
              -25                 -20                 -15

CTG TGC AGG TTC GTG GGG ATG CAG CCC TGC ACA GCC CAG ACT GGA CTC    279
Leu Cys Arg Phe Val Gly Met Gln Pro Cys Thr Ala Gln Thr Gly Leu
        -10                 -5                  1

CTT CCC CAT GGA ACT CAC AAC ACA CGG GAG AGG CAG AGA GAT CCA AGC    327
Leu Pro His Gly Thr His Asn Thr Arg Glu Arg Gln Arg Asp Pro Ser
  5                 10                  15                  20

GCA CAG AAA AAC ACA AGA AGA TTC AGC CCT GTT GGG                    363
Ala Gln Lys Asn Thr Arg Arg Phe Ser Pro Val Gly
                25                  30
```

(2) INFORMATION FOR SEQ ID NO: 161:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 186 base pairs
(B) TYPE: NUCLEIC ACID
(C) STRANDEDNESS: DOUBLE
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Spleen

(ix) FEATURE:
(A) NAME/KEY: sig_peptide
(B) LOCATION: 97..177
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 4.3
seq LCLNLCPCSSSLL/SP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 161:

```
ACTCTTGTAG TGGMGCCGGC TTGCATCCCA GGTCGTGGCG GTTTTGGTGC CTGAAGCAGG   60

GAGCGCGGAG TCGTTCCCGA GAGAGGCGGC CAGGCT ATG CTC GCC GGT TTC CGG    114
                                        Met Leu Ala Gly Phe Arg
                                                    -25

CGT TCC GCT CCG GCC AGC CAG AGT CTC TGT CTC AAC CTG TGT CCG TGC    162
Arg Ser Ala Pro Ala Ser Gln Ser Leu Cys Leu Asn Leu Cys Pro Cys
    -20                 -15                 -10

TCC AGC AGT CTC CTC AGC CCG GCG                                    186
Ser Ser Ser Leu Leu Ser Pro Ala
 -5                 1
```

(2) INFORMATION FOR SEQ ID NO: 162:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 311 base pairs
(B) TYPE: NUCLEIC ACID
(C) STRANDEDNESS: DOUBLE
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Testis

(ix) FEATURE:
(A) NAME/KEY: sig_peptide
(B) LOCATION: 237..290
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 4.3
seq SFYLLFFLNDVPP/CP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 162:

```
ACAGRACAGG TTAAAGAGAT AATCATTTGG GACTCAAATG TCTCTCCCCC CGGGCACTTG   60

CATATGGGAC ATTGAGTCCT TTTGTTTTCC CTTGATCTAT AGCTCTTACC CCTCTGCCCA  120

GTAATTCCCT GAGGAAGAGG TAAAGATCAR AGTTGRTACT TTGTCCTTTC CTTCCKTCTT  180

CCCTTATTTT TAAAGCTGTC RSCCACACTG ATTCCTGCTC TAATAGCAGA GCAGAG ATG  239
                                                              Met

AAG GAA GGA GCT TCC TTC TAT CTG CTT TTC TTT CTC AAT GAT GTC CCA    287
Lys Glu Gly Ala Ser Phe Tyr Leu Leu Phe Phe Leu Asn Asp Val Pro
    -15                     -10                     -5

CCA TGT CCC CCT CAC ACC CCC GGG                                    311
Pro Cys Pro Pro His Thr Pro Gly
  1               5
```

(2) INFORMATION FOR SEQ ID NO: 163:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: NUCLEIC ACID
(C) STRANDEDNESS: DOUBLE
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Spleen

(ix) FEATURE:
(A) NAME/KEY: sig_peptide
(B) LOCATION: 305..391
(C) IDENTIFICATION METHOD: Von Heijne matrix

(D) OTHER INFORMATION: score 4.3
seq ETLLLKLSSQSRT/NR

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 163:

```
ATATTTCAGC TTCCACATTT TATTTCAACA ACATTAGTCA TCGTAGCTGC GTATTCCTGT   60

THTCAGTGTA GTAACGTTGA GCAHTTATGT TCCTAGCACT CTTCCAGGTA CCCTGTGCGT  120

TATGAGGCAG GCACATCTCT CCTGAAAGAA TTTATATTCT TGTCAGGGAA ATAAGGCTTC  180

AGATAAGAAA AAATTCGGGG GAAAGTGCCT AATTCCTTCT ACCCTAACCT GCCTCCATTT  240

CCTCCCTCCT CCGAGTTGAG ATGATTGGGT CAGAGCCAGC TCTTCCTGGG CTTGGGAAGA  300

GGAG ATG GGG CTT GAG TGC TGC TGC CCC CCT CAT AAC CTC AGA GTC TAT  349
     Met Gly Leu Glu Cys Cys Cys Pro Pro His Asn Leu Arg Val Tyr
                     -25                 -20                 -15

ATT GAG ACT CTC TTG CTC AAA CTC TCC TCG CAG AGT AGA ACG AAC AGG    397
Ile Glu Thr Leu Leu Leu Lys Leu Ser Ser Gln Ser Arg Thr Asn Arg
            -10                  -5                   1

CTG                                                                400
Leu
```

(2) INFORMATION FOR SEQ ID NO: 164:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 376 base pairs
(B) TYPE: NUCLEIC ACID
(C) STRANDEDNESS: DOUBLE
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Testis

(ix) FEATURE:
(A) NAME/KEY: sig_peptide
(B) LOCATION: 275..337
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 4.2
seq VLSIAASLLQCRL/AV

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 164:

```
AATCTGAAAC AGTTCTAGTC TCAAGCATTT TGGATGAGGG ATACCCATCC TCTATTTTAT   60

CACCATTTTC ATGCTGTATT AAAATGAAAT TGCCAACTCA GTTCAAAGGA ATTTTTCTTC  120

TTAGCTTTAC ATTGTTGATT CATGGTGGAG GCGAACAAAC TATCGACTGG TGGGTTGGAT  180

ACCTTGGTCC AGAGAGGTCC TTGTGACATA TCTCATGGCC CATTACCTAG GTGATGTGAG  240
```

```
TCTTGCCTTC TGCCTGCAAT AAAGTTTTGT TGGA ATG CAG CTA TGC CCA TTT ACT  295
                                      Met Gln Leu Cys Pro Phe Thr
                                          -20                 -15

AGT GTA TTG TCC ATA GCT GCT TCT CTG CTA CAA TGT AGA TTA GCA GTT    343
Ser Val Leu Ser Ile Ala Ala Ser Leu Leu Gln Cys Arg Leu Ala Val
                -10                 -5                  1

GTA ACA GAG ACT ATA TGG CCC CCC CAG VNT TGG                        376
Val Thr Glu Thr Ile Trp Pro Pro Gln Xaa Trp
        5                   10
```

(2) INFORMATION FOR SEQ ID NO: 165:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 354 base pairs
(B) TYPE: NUCLEIC ACID
(C) STRANDEDNESS: DOUBLE
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Testis

(ix) FEATURE:
(A) NAME/KEY: sig_peptide
(B) LOCATION: 139..270
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 4.2
seq QLLFKLNSTWCRA/LQ

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 165:

```
ACCCCYAGAA GTTATAAGGA AASGCCTTCC AACTTGATAC AGTTGCTTTT CTTTCCTGAA   60

TCCCCTGTTT ACTGGAAATT TCATTGGATT TTGGGAGGAG AGAGGTCTGA AGGAAGGAAA  120

GGCCTGTTTT CTGCTGTA ATG GAT GTA ACA TGC TGC TTT GAT GCA GTT GAA    171
                    Met Asp Val Thr Cys Cys Phe Asp Ala Val Glu
                                    -40                 -35

GGA AGT GAC TTC AGG GTT TGC TGT CAT GGA TGC GTG TCT TGG CTG TGT    219
Gly Ser Asp Phe Arg Val Cys Cys His Gly Cys Val Ser Trp Leu Cys
        -30                 -25                 -20

CTC CAG ATG CTG CAG CTT TTA TTC AAG CTT AAT AGC ACT TGG TGC AGA    267
Leu Gln Met Leu Gln Leu Leu Phe Lys Leu Asn Ser Thr Trp Cys Arg
    -15                 -10                 -5

GCA CTC CAG AGT GAA ACC TCA TTG GCT TCC CGG CGC CTG TGG ATG TGG    315
Ala Leu Gln Ser Glu Thr Ser Leu Ala Ser Arg Arg Leu Trp Met Trp
    1               5                   10                  15

GTC TCT CAT CTG AYG GAG TTC TTT ACT GTG ACC CCC TGG                354
Val Ser His Leu Xaa Glu Phe Phe Thr Val Thr Pro Trp
                20                  25
```

(2) INFORMATION FOR SEQ ID NO: 166:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 84 base pairs
(B) TYPE: NUCLEIC ACID
(C) STRANDEDNESS: DOUBLE
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Ovary

(ix) FEATURE:
(A) NAME/KEY: sig_peptide
(B) LOCATION: 7..72
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 4.2
seq HCFCFTLFSYSSS/FF

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 166:

```
AAGGAC ATG AGA CAA GGA CCT GGG GCC CCA CTC CAT TGC TTC TGT TTC        48
       Met Arg Gln Gly Pro Gly Ala Pro Leu His Cys Phe Cys Phe
               -20                 -15                 -10

ACC CTT TTT TCC TAC TCC TCC TCC TTT TTT TTT TTT                        84
Thr Leu Phe Ser Tyr Ser Ser Ser Phe Phe Phe Phe
            -5                  1
```

(2) INFORMATION FOR SEQ ID NO: 167:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 140 base pairs
(B) TYPE: NUCLEIC ACID
(C) STRANDEDNESS: DOUBLE
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Testis

(ix) FEATURE:
(A) NAME/KEY: sig_peptide
(B) LOCATION: 72..116
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 4.2
seq ITLLGIWLTXRLQ/FP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 167:

```
ACAAGCCCCC GGCTTGCTCA TTTCATCCAG GTGAGGAGTC TGGAGTAGAG CAGGGCTTCT   60

GAAATGGTGA C ATG CAC ATC ACT CTC CTG GGC ATC TGG TTA ACA KGC AGG   110
             Met His Ile Thr Leu Leu Gly Ile Trp Leu Thr Xaa Arg
             -15                 -10                 -5

CTC CAG TTC CCC AGG TCT GGG CGG GCT GGG                            140
Leu Gln Phe Pro Arg Ser Gly Arg Ala Gly
        1               5
```

(2) INFORMATION FOR SEQ ID NO: 168:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 316 base pairs
(B) TYPE: NUCLEIC ACID
(C) STRANDEDNESS: DOUBLE
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Spleen

(ix) FEATURE:
(A) NAME/KEY: sig_peptide
(B) LOCATION: 245..295
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 4.2
seq SWVCLLSAGTAFE/DY

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 168:

```
ATTTAGGATT TTAGACTTTA GGGATTTTGA TCTTTGGGGA TTTCAATATT TGGGATTATG   60

GTATTTGAGA TGGTCTCTTT TAGGATTATG ATCCAAACCC ATCTCAGGAA TGTGTGAAAT  120

TTACAGTAGT CCATCCCCAT CCCGGGCTGT AGAAATGTAG GACCCACAAG CCTTCGTTAC  180

AGAGCCACTT ACTGCCCCAT GGAGTTCCCA GGTAGATGAC AGTAGCGGGG AGGATACATG  240

GCAC ATG TTA TAT GGC TCT TGG GTG TGC CTT CTC TCA GCA GGC ACT GCC   289
     Met Leu Tyr Gly Ser Trp Val Cys Leu Leu Ser Ala Gly Thr Ala
             -15                 -10                 -5

TTT GAA GAT TAT CAT TTG GGG GGT ACG                                316
Phe Glu Asp Tyr His Leu Gly Gly Thr
        1               5
```

(2) INFORMATION FOR SEQ ID NO: 169:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 208 base pairs
(B) TYPE: NUCLEIC ACID
(C) STRANDEDNESS: DOUBLE
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Uterus

(ix) FEATURE:
(A) NAME/KEY: sig_peptide
(B) LOCATION: 59..154
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 4.2
seq XXXXFLLGRRVVG/ES

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 169:

```
ACTATTTTTC CCTTCATTGT CTTTACTTTG CTTCAGAAGA ATAGTCTGTG ATGACGCC       58

ATG TTA TTT TTT CCC CTT CTT TCT TTC CGA TTT CTA CCC TCA GAG AGT      106
Met Leu Phe Phe Pro Leu Leu Ser Phe Arg Phe Leu Pro Ser Glu Ser
        -30                 -25                 -20

TTG TTG AAA GKC BTA WTG SYT TTT TTG CTG GGG AGG AGG GTA GTA GGA      154
Leu Leu Lys Xaa Xaa Xaa Xaa Phe Leu Leu Gly Arg Arg Val Val Gly
    -15                 -10                 -5

GAA TCA CNT TTT ATT TTC ACA TGT GGA AAT TTG CTT TTA ATT TGG CCT      202
Glu Ser Xaa Phe Ile Phe Thr Cys Gly Asn Leu Leu Leu Ile Trp Pro
  1               5                  10                  15

TAC GGG                                                              208
Tyr Gly
```

(2) INFORMATION FOR SEQ ID NO: 170:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 187 base pairs
(B) TYPE: NUCLEIC ACID
(C) STRANDEDNESS: DOUBLE
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Testis

(ix) FEATURE:
(A) NAME/KEY: sig_peptide
(B) LOCATION: 113..160
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 4.2
seq WAILGCWGTLSRG/HL

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 170:

```
ATGAAAATTT TCCATGCTGT YTGAGGAAAC ATATTTTGTG GGAGCAGATC ATTATCATGA     60
```

```
GAGTTGAAAC AAAAAAACTA CATGGAGGTG GAACCTGCCA GCCCAGTGGT GG ATG CCA  118
                                                          Met Pro
                                                              -15

GTC TGG GCC ATA CTG GGC TGC TGG GGC ACA CTC AGC AGG GGA CAT CTG    166
Val Trp Ala Ile Leu Gly Cys Trp Gly Thr Leu Ser Arg Gly His Leu
            -10                 -5                   1

CCT GTG TCC TTG GAC CCA AAG                                        187
Pro Val Ser Leu Asp Pro Lys
        5
```

(2) INFORMATION FOR SEQ ID NO: 171:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 253 base pairs
(B) TYPE: NUCLEIC ACID
(C) STRANDEDNESS: DOUBLE
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Ovary

(ix) FEATURE:
(A) NAME/KEY: sig_peptide
(B) LOCATION: 134..247
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 4.1
seq GILCGSLPGPSLC/PP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 171:

```
ACAAGTTCAC CTGGCCTCCT CTTCTCCAGC CTCAGTCACC TTCTGCTGAA CAGCTCCACC   60

TTGGCCTTGC TTACTCACAG ACTAAGCCAG ATGACCTGCC TGCAGAGCCT CAGGTGAGTG  120

ACCGAGCGGC CCC ATG GGA ATG AGT GGG AAG AAA CAC TTC CCA CTC AGT     169
               Met Gly Met Ser Gly Lys Lys His Phe Pro Leu Ser
                           -35                 -30

TGG GAC CAC ATC CAG GGA AGC ACT GAG GCC ACC TCC CAG GGG ATC CTT    217
Trp Asp His Ile Gln Gly Ser Thr Glu Ala Thr Ser Gln Gly Ile Leu
    -25                 -20                 -15

TGC GGA TCC CTC CCA GGC CCA TCC CTG TGC CCT CCG                    253
Cys Gly Ser Leu Pro Gly Pro Ser Leu Cys Pro Pro
-10                 -5                   1
```

(2) INFORMATION FOR SEQ ID NO: 172:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 362 base pairs

(B) TYPE: NUCLEIC ACID
(C) STRANDEDNESS: DOUBLE
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Testis

(ix) FEATURE:
(A) NAME/KEY: sig_peptide
(B) LOCATION: 141..251
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 4
seq PLSLDCGHSLCRA/CI

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 172:

```
AACACCCACC CTGGCTTTTC TTCACCTCTT CAACCAGGAG CCGAGATTTC TGTTGCTCTG   60

AAGCCATCCA GGGGTCTTTA ACCAGAAGAG AGAGGAGAGC CTCAGGAGTT AGGACCAGAA  120

GAAGCCAGGG AAKCAGTGCA ATG GCT TCA AAA ATC TTG CTT AAC GTA CAA GAG  173
                      Met Ala Ser Lys Ile Leu Leu Asn Val Gln Glu
                              -35                     -30

GAG GTG ACC TGT CCC ATC TGC CTG GAG CTG TTG ACA GAA CCC TTG AGT     221
Glu Val Thr Cys Pro Ile Cys Leu Glu Leu Leu Thr Glu Pro Leu Ser
    -25                 -20                 -15

CTA GAC TGT GGC CAC AGC CTC TGC CGA GCC TGC ATC ACT GTG AGC AAC     269
Leu Asp Cys Gly His Ser Leu Cys Arg Ala Cys Ile Thr Val Ser Asn
-10                 -5                   1                   5

AAG GAG GCA GTG ACC AGC ATG GGA GGA AAA AGC AGC TGT CCT GTG TGT     317
Lys Glu Ala Val Thr Ser Met Gly Gly Lys Ser Ser Cys Pro Val Cys
            10                  15                  20

GGT ATC AGT KAC TCA KTT GAA CAT CTA CAG GCT AAT CAG CAT CGG         362
Gly Ile Ser Xaa Ser Xaa Glu His Leu Gln Ala Asn Gln His Arg
        25                  30                  35
```

(2) INFORMATION FOR SEQ ID NO: 173:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 140 base pairs
(B) TYPE: NUCLEIC ACID
(C) STRANDEDNESS: DOUBLE
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Testis

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
(B) LOCATION: 48..89
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 4
seq YYMVCLFFRLIFS/EH

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 173:

```
AGGAGATAGC CTCGTAGAAA TGACAACCAC AATGTTAATA CTAACAT ATG TAT TAC      56
                                                    Met Tyr Tyr

ATG GTT TGT TTG TTC TTT CGC TTA ATA TTT TCA GAG CAC CTA CCT ATT     104
Met Val Cys Leu Phe Phe Arg Leu Ile Phe Ser Glu His Leu Pro Ile
    -10                 -5                      1               5

ATA GGC ACT GTC ACT TCT CAC AAA ACT GGG ACA GGG                     140
Ile Gly Thr Val Thr Ser His Lys Thr Gly Thr Gly
                10                  15
```

(2) INFORMATION FOR SEQ ID NO: 174:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 158 base pairs
(B) TYPE: NUCLEIC ACID
(C) STRANDEDNESS: DOUBLE
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Ovary

(ix) FEATURE:
(A) NAME/KEY: sig_peptide
(B) LOCATION: 15..122
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 4
seq KLAGLWSPGLVPA/AP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 174:

```
AAGTGTCGCG ATAA ATG GGC GCC GGC GGA SGG AGG GAG ATC CGA GCG GCG      50
                Met Gly Ala Gly Gly Xaa Arg Glu Ile Arg Ala Ala
                    -35                 -30                 -25

GCG GCA AGC TGG CTG CGA GCG GCT GAG CAC TCC AAG CTC GCC GGC CTT      98
Ala Ala Ser Trp Leu Arg Ala Ala Glu His Ser Lys Leu Ala Gly Leu
                -20                 -15                 -10

TGG TCT CCA GGA CTT GTC CCA GCA GCC CCT CGA ACT GAG AAT TAC ACC     146
Trp Ser Pro Gly Leu Val Pro Ala Ala Pro Arg Thr Glu Asn Tyr Thr
            -5                      1               5

ATC GGA CCC CTG                                                     158
Ile Gly Pro Leu
    10
```

(2) INFORMATION FOR SEQ ID NO: 175:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 291 base pairs
(B) TYPE: NUCLEIC ACID
(C) STRANDEDNESS: DOUBLE
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Testis

(ix) FEATURE:
(A) NAME/KEY: sig_peptide
(B) LOCATION: 52..231
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 4
seq LVRRTLLVAALRA/WM

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 175:

```
AAGGAAACAG CAACCAGAGG GAGATGATCA CCTGAACCAC TGCTCCAAAC C ATG GGC     57
                                                         Met Gly
                                                         -60

AGT AAA TGC TGT AAA GGT GGT CCA GAT GAA GAT GCA GTA GAA AGA CAG     105
Ser Lys Cys Cys Lys Gly Gly Pro Asp Glu Asp Ala Val Glu Arg Gln
            -55                 -50                 -45

AGG CGG CAG AAG TTG CTT CTT GCA CAA CTG CAT CAC AGA AAA AGG GTG     153
Arg Arg Gln Lys Leu Leu Leu Ala Gln Leu His His Arg Lys Arg Val
        -40                 -35                 -30

AAR GCA GCT GGG CAG ATC CAG GCC TGG TGG CGT GGG GTC CTG GTG CGC     201
Lys Ala Ala Gly Gln Ile Gln Ala Trp Trp Arg Gly Val Leu Val Arg
    -25                 -20                 -15

AGG ACC CTG CTG GTT GCT GCC CTC AGG GCC TGG ATG ATT CAG TGC TGG     249
Arg Thr Leu Leu Val Ala Ala Leu Arg Ala Trp Met Ile Gln Cys Trp
-10                 -5                  1               5

TGG AGG ACG TTG GTG CAG AGA CGG ATC CGT CAG CGG CGG CAG             291
Trp Arg Thr Leu Val Gln Arg Arg Ile Arg Gln Arg Arg Gln
            10                  15                  20
```

(2) INFORMATION FOR SEQ ID NO: 176:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 192 base pairs
(B) TYPE: NUCLEIC ACID
(C) STRANDEDNESS: DOUBLE
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Ovary

(ix) FEATURE:
(A) NAME/KEY: sig_peptide
(B) LOCATION: 103..180
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 4
seq SIHSWQLLTSAQP/QQ

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 176:

```
CGGCAACGCG CGGCGGCTCA ACGGCCTGGC AGAGGTTTCA GCGCTGAGCA GGCCTGAGTT   60

CCGTCATGGC CCTCTATTAT GACCACCAGA TAGAAGCCCC GG ATG CAG CAG GGT    114
                                               Met Gln Gln Gly
                                                   -25

CAC CCT CAT TTA TCA GCT GGC ACC CTG TCC ATC CAT TCT TGG CAG TTG   162
His Pro His Leu Ser Ala Gly Thr Leu Ser Ile His Ser Trp Gln Leu
        -20                 -15                 -10

CTT ACA TCA GCA CAA CCT CAA CAG GCA GGG                           192
Leu Thr Ser Ala Gln Pro Gln Gln Ala Gly
    -5                  1
```

(2) INFORMATION FOR SEQ ID NO: 177:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 174 base pairs
(B) TYPE: NUCLEIC ACID
(C) STRANDEDNESS: DOUBLE
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Ovary

(ix) FEATURE:
(A) NAME/KEY: sig_peptide
(B) LOCATION: 1..147
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 4
seq ATCCLSLFQWCAV/LR

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 177:

```
ATG TCT AGA TAT GAG TMA GGA TCC TCC TTA TTG CCA TTT CCA GAC CAT    48
Met Ser Arg Tyr Glu Xaa Gly Ser Ser Leu Leu Pro Phe Pro Asp His
                -45                 -40                 -35

TTC TCT GTT TAC TCC TTT AAA ASA RAT AGT TTT TTT GAA GCG TAC AGC    96
```

```
Phe Ser Val Tyr Ser Phe Lys Xaa Xaa Ser Phe Phe Glu Ala Tyr Ser
            -30                 -25                 -20

ATT TCA GAT TAT GCC ACC TGC TGT CTC TCC TTA TTT CAG TGG TGT GCA     144
Ile Ser Asp Tyr Ala Thr Cys Cys Leu Ser Leu Phe Gln Trp Cys Ala
        -15                 -10                 -5

GTT CTG AGA TTC CTG TCT CTG CCC CTT CCG                             174
Val Leu Arg Phe Leu Ser Leu Pro Leu Pro
      1               5
```

(2) INFORMATION FOR SEQ ID NO: 178:

(i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 226 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:
- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Ovary

(ix) FEATURE:
- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 140..211
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 3.9
  seq LLLHHYLLLFITT/SR

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 178:

```
ACAGTTGTGG CTCTCAACTC TCCTTTTTGT GTACTGCTAT ACTTGAGTAG CACACAGCCA    60

TACCAATTTC CAGGGTGCTC AGATTCATTC TACCCTTTCC TACTGGAAGA GGTAAAAAAG   120

CAACACCCTA GAATCTGAT ATG ATT TAT TTT ATC AAA ATA AAC AAT AAG CTA    172
                     Met Ile Tyr Phe Ile Lys Ile Asn Asn Lys Leu
                                     -20                 -15

CTG CTT TTG CAC CAT TAC TTG CTT CTA TTT ATA ACA ACC TCT CGC CCC    220
Leu Leu Leu His His Tyr Leu Leu Leu Phe Ile Thr Thr Ser Arg Pro
            -10                 -5                  1

ACA GGG                                                             226
Thr Gly
      5
```

(2) INFORMATION FOR SEQ ID NO: 179:

(i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 129 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE

(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Ovary

(ix) FEATURE:
(A) NAME/KEY: sig_peptide
(B) LOCATION: 28..108
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 3.9
seq LSWALCLSQSGYY/HP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 179:

```
AGGGTATATT TCNTGTCCCC TAGGAGC ATG GAG CTT TTG TAC CTT AAA GTT AAG    54
                              Met Glu Leu Leu Tyr Leu Lys Val Lys
                                      -25                 -20

AGA GGA CAA AAG GAT CTG AGC TGG GCT TTG TGC CTT TCC CAG AGT GGT     102
Arg Gly Gln Lys Asp Leu Ser Trp Ala Leu Cys Leu Ser Gln Ser Gly
            -15                 -10                 -5

TAT TAC CAC CCT TCC CAC CCC CAT TGG                                 129
Tyr Tyr His Pro Ser His Pro His Trp
         1               5
```

(2) INFORMATION FOR SEQ ID NO: 180:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 158 base pairs
(B) TYPE: NUCLEIC ACID
(C) STRANDEDNESS: DOUBLE
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Ovary

(ix) FEATURE:
(A) NAME/KEY: sig_peptide
(B) LOCATION: 36..77
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 3.9
seq TLAVTLSALGATG/LF

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 180:

```
AGAGGCCAGA TTMTGCAGGC CTGTGGGCTG ACACA ATG ACT TTG GCT GTT ACT      53
                                       Met Thr Leu Ala Val Thr
                                                       -10

CTG AGT GCA TTG GGG GCC ACC GGA TTG TTT AAG GAG GCT TGT GAT CTA     101
```

```
Leu Ser Ala Leu Gly Ala Thr Gly Leu Phe Lys Glu Ala Cys Asp Leu
            -5                  1              5

ACC TTT TTA AAC ATA GGT CAG ATC ACA AGC YTC CTT AAA CAA TCC GGT     149
Thr Phe Leu Asn Ile Gly Gln Ile Thr Ser Xaa Leu Lys Gln Ser Gly
    10                  15                  20

GGC CCC CAG                                                         158
Gly Pro Gln
 25
```

(2) INFORMATION FOR SEQ ID NO: 181:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 330 base pairs
(B) TYPE: NUCLEIC ACID
(C) STRANDEDNESS: DOUBLE
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Uterus

(ix) FEATURE:
(A) NAME/KEY: sig_peptide
(B) LOCATION: 115..237
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 3.9
seq CRCLITLPRSCRP/ST

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 181:

```
ATTTGACGTG TCTGTTTCAT GTYTCCTTTG AGTAAAACCT AATCTTTCTC AATAGAGAAG    60

TTTATTCTTG AAGTATGTGK KCTCAGTTCA TTCSCCTGAG TGACACAAGC TCCC ATG     117
                                                            Met

CTT GGG CCA CCC TTG CAG CCC GGA AGC CAT GGG AAG GTC CTC GCC CCT     165
Leu Gly Pro Pro Leu Gln Pro Gly Ser His Gly Lys Val Leu Ala Pro
-40                 -35                 -30                 -25

CAG GGC AGT AGT GGC CTG ACA CCC CCC TTC CCG TGC AGG TGT CTG ATA     213
Gln Gly Ser Ser Gly Leu Thr Pro Pro Phe Pro Cys Arg Cys Leu Ile
                -20                 -15                 -10

ACT CTG CCG CGG TCG TGC CGG CCC AGT ACA TCT GTG CCC CGG RCA GCA     261
Thr Leu Pro Arg Ser Cys Arg Pro Ser Thr Ser Val Pro Arg Xaa Ala
            -5                  1               5

AGC ACA CGT TCC TCG CAG CGC CCG SSC AGC TCC TGC TGG MGA AGT TCC     309
Ser Thr Arg Ser Ser Gln Arg Pro Xaa Ser Ser Cys Trp Arg Ser Ser
    10                  15                  20

TGC AGC ACC ACA GCC ACC ATG                                         330
Cys Ser Thr Thr Ala Thr Met
 25                 30
```

(2) INFORMATION FOR SEQ ID NO: 182:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 207 base pairs
(B) TYPE: NUCLEIC ACID
(C) STRANDEDNESS: DOUBLE
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Testis

(ix) FEATURE:
(A) NAME/KEY: sig_peptide
(B) LOCATION: 64..144
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 3.8
seq QLXLILVHFPAYS/VE

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 182:

```
AAACTGCCAT CYGCAACTGA ACTTTGGCAG TAAACACAGC TTAGTTGTCT CAGAGGATTC   60

ACA ATG GGA AAT GTT TGT AGT TGC TGC CTC AGA GCA AGA TAT CAR CAG    108
    Met Gly Asn Val Cys Ser Cys Cys Leu Arg Ala Arg Tyr Gln Gln
            -25                 -20                 -15

TTG DCT TTA ATT TTA GTT CAT TTC CCA GCA TAT TCT GTT GAA GAT CAA    156
Leu Xaa Leu Ile Leu Val His Phe Pro Ala Tyr Ser Val Glu Asp Gln
        -10                 -5                  1

AGA GTG GAT CCT GGG GTG CCA GGG GAA TCC ACC GTC TGC CAC CAC AAT    204
Arg Val Asp Pro Gly Val Pro Gly Glu Ser Thr Val Cys His His Asn
  5                 10                  15                  20

CGG                                                                207
Arg
```

(2) INFORMATION FOR SEQ ID NO: 183:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 130 base pairs
(B) TYPE: NUCLEIC ACID
(C) STRANDEDNESS: DOUBLE
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Spleen

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
(B) LOCATION: 8..70
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 3.8
seq PRCVISCIHGVWC/EE

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 183:

```
ACTCTGC ATG CTT TAT GGC CTT GGC TCT GGG CCA AGG TGT GTG ATC TCC      49
        Met Leu Tyr Gly Leu Gly Ser Gly Pro Arg Cys Val Ile Ser
            -20                 -15                 -10

TGC ATT CAT GGT GTG TGG TGT GAG GAG GGG GAT GGG TCC CTG CCC CGT      97
Cys Ile His Gly Val Trp Cys Glu Glu Gly Asp Gly Ser Leu Pro Arg
        -5                  1               5

CTG CAC GTG GCC CTC ATG ATT CCC GCG CTA GGG                         130
Leu His Val Ala Leu Met Ile Pro Ala Leu Gly
 10                  15                  20
```

(2) INFORMATION FOR SEQ ID NO: 184:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 298 base pairs
(B) TYPE: NUCLEIC ACID
(C) STRANDEDNESS: DOUBLE
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Testis

(ix) FEATURE:
(A) NAME/KEY: sig_peptide
(B) LOCATION: 62..187
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 3.8
seq VTPLDSCPPSAHS/AP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 184:

```
ACAGCTTCCA CTCTTGTCTC CCTAAACCCT GTTTTCCTCA CAGTAACTAG AATTGTCCTT    60

A ATG CAT AGA ATC ATG ACT CTC CTT CAT CTC AAA GCT CTC CAA CAG CTT   109
  Met His Arg Ile Met Thr Leu Leu His Leu Lys Ala Leu Gln Gln Leu
          -40                 -35                 -30

CAG AAT AAA ATC CAT GTC CCC AGG ATG CTC CCA GGG CCT GTG ACC CCT     157
Gln Asn Lys Ile His Val Pro Arg Met Leu Pro Gly Pro Val Thr Pro
    -25                 -20                 -15

CTG GAC TCA TGC CCT CCT TCT GCT CAT TCT GCT CCA TCA CTG CTC ACT     205
Leu Asp Ser Cys Pro Pro Ser Ala His Ser Ala Pro Ser Leu Leu Thr
-10                 -5                  1               5
```

```
TCC CAG CTA CCC CTC CAA CAC ACC AAT GCG CCC CCA CCT CAC GGC CTC     253
Ser Gln Leu Pro Leu Gln His Thr Asn Ala Pro Pro Pro His Gly Leu
            10                  15                  20

TCC CTG CGC CGT GCC CTC CAC TGG ATT GCC CTT CCC TTG ATG GGG         298
Ser Leu Arg Arg Ala Leu His Trp Ile Ala Leu Pro Leu Met Gly
        25                  30                  35
```

(2) INFORMATION FOR SEQ ID NO: 185:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 149 base pairs
(B) TYPE: NUCLEIC ACID
(C) STRANDEDNESS: DOUBLE
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Ovary

(ix) FEATURE:
(A) NAME/KEY: sig_peptide
(B) LOCATION: 93..131
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 3.8
seq MLFLVLFYSAIFL/FT

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 185:

```
AAACAACAAA AAAAAGTTTA AAAATTGGAA ACCACCAAAA GGTAGTATTA AAAGGGAAAT    60

AAAAATTACT CATAATCCCA GAACGCAGTC AT ATG CTA TTT TTA GTC TTA TTT     113
                                    Met Leu Phe Leu Val Leu Phe
                                                -10

TAT TCA GCC ATT TTT CTC TTT ACA CTA ACT TTT TTT                     149
Tyr Ser Ala Ile Phe Leu Phe Thr Leu Thr Phe Phe
     -5                  1               5
```

(2) INFORMATION FOR SEQ ID NO: 186:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 180 base pairs
(B) TYPE: NUCLEIC ACID
(C) STRANDEDNESS: DOUBLE
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Ovary

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
(B) LOCATION: 133..174
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 3.8
seq VSLCVAALFPLQA/YG

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 186:

```
AAAGAGTACC TGAAAACCTT AGAGAACCCT GGGGAAATAT TTATAGCCAG GCTTCTTGGA   60

GACTCTGGGA ACAGGAAAGT CAGGAACCCT GCCTTTCAGG AACTGCTGTA TCTCAGTCGM  120

MTTCTTCATT TC ATG GTT TCT CTC TGT GTA GCT GCT TTA TTT CCT CTT CAG  171
              Met Val Ser Leu Cys Val Ala Ala Leu Phe Pro Leu Gln
                              -10                 -5

GCT TAC GGG                                                        180
Ala Tyr Gly
     1
```

(2) INFORMATION FOR SEQ ID NO: 187:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 283 base pairs
(B) TYPE: NUCLEIC ACID
(C) STRANDEDNESS: DOUBLE
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Testis

(ix) FEATURE:
(A) NAME/KEY: sig_peptide
(B) LOCATION: 218..268
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 3.7
seq LFYIPSILTLLLA/CR

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 187:

```
AAAATTCTTC CASAATGCTA ATGTAAATCT AATCAGCCTT TAGAATTTAA AGGCTTAAAA   60

AAGACTAAAG AAAAGTAACA ACCAAATGCA ATATGTAGAA CTTATATGGA GCCTGATTCG  120

AACATCAAGT ATAAAGAGAT ATTTTTGAGA AAATTGAGAA ATTTTAAAAC ATGAMATBAG  180

TATTATATGA TATTGAMGAC TGCTGCTTTT TCAMGAC ATG TCC TCA AAT TTA TTT   235
                                         Met Ser Ser Asn Leu Phe
                                                     -15

TAC ATT CCT TCC ATA CTA ACT CTT CTC CTT GCA TGT MGA CAG ACA GGG    283
Tyr Ile Pro Ser Ile Leu Thr Leu Leu Leu Ala Cys Arg Gln Thr Gly
    -10                 -5                      1              5
```

(2) INFORMATION FOR SEQ ID NO: 188:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 121 base pairs
(B) TYPE: NUCLEIC ACID
(C) STRANDEDNESS: DOUBLE
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Ovary

(ix) FEATURE:
(A) NAME/KEY: sig_peptide
(B) LOCATION: 2..106
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 3.7
seq IKQFILCLGTCRG/EM

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 188:

```
T ATG GGG CTT TTG AGA AAG TGT TTT CCC GTG ATG CTG GGG GGA AAC ACA     49
  Met Gly Leu Leu Arg Lys Cys Phe Pro Val Met Leu Gly Gly Asn Thr
  -35                 -30                 -25                 -20

CAT ATT CAA ATT ACT TGT ATA AAA CAG TTT ATT CTG TGT TTA GGA ACT       97
His Ile Gln Ile Thr Cys Ile Lys Gln Phe Ile Leu Cys Leu Gly Thr
                -15                 -10                 -5

TGT AGG GGT GAA ATG CTG ACC AGG                                      121
Cys Arg Gly Glu Met Leu Thr Arg
              1               5
```

(2) INFORMATION FOR SEQ ID NO: 189:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 148 base pairs
(B) TYPE: NUCLEIC ACID
(C) STRANDEDNESS: DOUBLE
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Ovary

(ix) FEATURE:
(A) NAME/KEY: sig_peptide
(B) LOCATION: 56..97
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 3.7
seq MLPLFCSPWESGG/RT

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 189:

```
TAAGCCGAGA AACTTCCGTA CTGTGTTAAA AACTGTTTGA GGAACACTGG ATTAA ATG     58
                                                             Met

ATG CTT CCA CTG TTC TGC TCT CCC TGG GAA AGC GGA GGC AGA ACG GTG     106
Met Leu Pro Leu Phe Cys Ser Pro Trp Glu Ser Gly Gly Arg Thr Val
            -10                 -5                  1

AAG CAG AGT GAA GGN YCT TGT TWA TTC CAG GCC CCC CAT GGG             148
Lys Gln Ser Glu Gly Xaa Cys Xaa Phe Gln Ala Pro His Gly
     5                   10                  15
```

(2) INFORMATION FOR SEQ ID NO: 190:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 140 base pairs
(B) TYPE: NUCLEIC ACID
(C) STRANDEDNESS: DOUBLE
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Uterus

(ix) FEATURE:
(A) NAME/KEY: sig_peptide
(B) LOCATION: 27..71
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 3.7
seq KLLSDLSVDSARC/KP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 190:

```
ATCTTAACAG AACTTTACAG ACTAGC ATG GCA AAG CTT CTC TCC GAT CTT AGT     53
                             Met Ala Lys Leu Leu Ser Asp Leu Ser
                             -15                 -10

GTG GAC AGT GCT CGC TGC AAG CCT GGG AAT AAC CTT ACC AAA TCA CTC     101
Val Asp Ser Ala Arg Cys Lys Pro Gly Asn Asn Leu Thr Lys Ser Leu
     -5                  1                   5                  10

TTG AAC ATT CAT GAT AAA CAA CTT CAA CAT GAC CCA CGG                 140
Leu Asn Ile His Asp Lys Gln Leu Gln His Asp Pro Arg
                15                  20
```

(2) INFORMATION FOR SEQ ID NO: 191:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 417 base pairs
(B) TYPE: NUCLEIC ACID
(C) STRANDEDNESS: DOUBLE
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Testis

(ix) FEATURE:
(A) NAME/KEY: sig_peptide
(B) LOCATION: 199..252
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 3.7
seq VCWGHLLPARVST/RS

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 191:

```
AGAGAYCAAC TCTATTTGAG CAASAGTKAG GAAGATTTCC CTGTCTCCCA GCTGAGTAAC   60

CACTCAGGTT TATTTAAATC CAGTTTAAAT ATGGTTTCAG TAATGATTTT CCAATGGTCT  120

ACAGCAAAGA ATGGTGCTCC AAGCCTGAAC ATTGAGCACG ACCCAGGTCA TATGCACAAC  180

ACGACAGGTT GAGCGTCC ATG TGT GGC TAC TGG GTT TGC TGG GGA CAC CTC     231
                    Met Cys Gly Tyr Trp Val Cys Trp Gly His Leu
                                -15                 -10

TTG CCT GCC AGG GTG AGC ACA CGC AGC AGT GAG CAG CCC CGT GTG ACC     279
Leu Pro Ala Arg Val Ser Thr Arg Ser Ser Glu Gln Pro Arg Val Thr
        -5                  1               5

CCA CGG GAT GAG GAT GCC ATG ATG TCA GCA TCC CTT CTG ACT TGG AGG     327
Pro Arg Asp Glu Asp Ala Met Met Ser Ala Ser Leu Leu Thr Trp Arg
 10                  15                  20                  25

TAT GTG ACA TTC ATG GTG CCA ATG CCA CTG TCA CCT TGC AGA TCA GTC     375
Tyr Val Thr Phe Met Val Pro Met Pro Leu Ser Pro Cys Arg Ser Val
                30                  35                  40

TGG GTT TGC TTC AGA CAG AAG ATC CTG GAA TAT GTT CAN GCA             417
Trp Val Cys Phe Arg Gln Lys Ile Leu Glu Tyr Val Xaa Ala
            45                  50                  55
```

(2) INFORMATION FOR SEQ ID NO: 192:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 167 base pairs
(B) TYPE: NUCLEIC ACID
(C) STRANDEDNESS: DOUBLE
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Uterus

(ix) FEATURE:
(A) NAME/KEY: sig_peptide

(B) LOCATION: 66..137
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 3.7
seq AILGLSTFLNLLS/IN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 192:

```
AGCTGCGCAC AGATSATTGA ATTGCGGGGT TGCTGTAGGA ACCGCTGCTA TTGCCGCAGG   60

AGGAG ATG AAG TTA TCT TGT GCA GGC TGT GCA GAC ACA GCC ATT TTG GGA  110
      Met Lys Leu Ser Cys Ala Gly Cys Ala Asp Thr Ala Ile Leu Gly
                      -20                 -15                 -10

CTC AGC ACT TTC CTT AAT TTA CTT TCC ATC AAC CTG CTC GGA ATG ATT     158
Leu Ser Thr Phe Leu Asn Leu Leu Ser Ile Asn Leu Leu Gly Met Ile
                -5                  1               5

TCT TTC TCT                                                         167
Ser Phe Ser
        10
```

(2) INFORMATION FOR SEQ ID NO: 193:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 248 base pairs
(B) TYPE: NUCLEIC ACID
(C) STRANDEDNESS: DOUBLE
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Spleen

(ix) FEATURE:
(A) NAME/KEY: sig_peptide
(B) LOCATION: 75..137
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 3.7
seq FSLGSCPAGPLSA/CV

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 193:

```
ATGTCACATT TAASNAGAGG CCAGAGCTTG TCCAAAATGG CTGTCCRWAM ACGACCCCAC   60

ACTTGCGTTA GAAG ATG ATA CCT TTT TCA GGG ACA GTT TTC TCT CTT GGC     110
                Met Ile Pro Phe Ser Gly Thr Val Phe Ser Leu Gly
                    -20                 -15                 -10

TCC TGT CCC GCT GGC CCT CTG TCT GCC TGT GTC CCT GAC CAT GGC TCC     158
Ser Cys Pro Ala Gly Pro Leu Ser Ala Cys Val Pro Asp His Gly Ser
                -5                  1               5

CTG CAG TAC CCT TTA ACG ATT TAT CAG CAA GAC TGT KGA ACG CAT ARS     206
Leu Gln Tyr Pro Leu Thr Ile Tyr Gln Gln Asp Cys Xaa Thr His Xaa
        10                  15                  20
```

```
TGC CCA AGA TGC CTG TCC CTC CCC CTC CAG CAC CCC CGA CAG            248
Cys Pro Arg Cys Leu Ser Leu Pro Leu Gln His Pro Arg Gln
     25                  30                  35
```

(2) INFORMATION FOR SEQ ID NO: 194:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 360 base pairs
(B) TYPE: NUCLEIC ACID
(C) STRANDEDNESS: DOUBLE
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Testis

(ix) FEATURE:
(A) NAME/KEY: sig_peptide
(B) LOCATION: 70..174
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 3.7
seq PAVSLSAPAFASA/LR

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 194:

```
AGAGGACAGG GTAGAGTCGC AGAAAGGAGA GACACACATA CATGGAAAGA GGAGCYTTCT   60

CCAATCTTA ATG ATT CCC AGC TCT CAG CCT CGT TTC TGM AAC CCA GCC TGC  111
          Met Ile Pro Ser Ser Gln Pro Arg Phe Xaa Asn Pro Ala Cys
          -35                 -30                 -25

AAG CAA ACT GTC CTG CTT WGG GAC CCT GCT GTG TCA CTC TCC GCA CCA    159
Lys Gln Thr Val Leu Leu Xaa Asp Pro Ala Val Ser Leu Ser Ala Pro
    -20                 -15                 -10

GCC TTT GCC TCT GCT CTT CGC TCT ATG AMG TCC TCC CAG GCT GCA CGG    207
Ala Phe Ala Ser Ala Leu Arg Ser Met Xaa Ser Ser Gln Ala Ala Arg
 -5                   1               5                  10

AAG GAC GAC TTT CTC AGG TCT CTT AGT GAT GGA GAC TCA GGG ACA TCA    255
Lys Asp Asp Phe Leu Arg Ser Leu Ser Asp Gly Asp Ser Gly Thr Ser
            15                  20                  25

GAA CAC ATC TCA GCG GTG GTG ACT AGC CCT CGG ATT TCC TGC CAT GGT    303
Glu His Ile Ser Ala Val Val Thr Ser Pro Arg Ile Ser Cys His Gly
        30                  35                  40

GCT GCC ATT CCC ACC GCC CGT GCC CTC TGC CTA YGC TGT TCC TGC TGC    351
Ala Ala Ile Pro Thr Ala Arg Ala Leu Cys Leu Xaa Cys Ser Cys Cys
     45                  50                  55

ACC GAA CGC                                                        360
Thr Glu Arg
 60
```

(2) INFORMATION FOR SEQ ID NO: 195:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 226 base pairs
(B) TYPE: NUCLEIC ACID
(C) STRANDEDNESS: DOUBLE
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Ovary

(ix) FEATURE:
(A) NAME/KEY: sig_peptide
(B) LOCATION: 161..205
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 3.6
seq PTFLLISDSFLTS/QP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 195:

```
ATTGGCCTGC TCTTCCTGAT ACCTACTTGG TCACTACTTA ATTACATTTT GTTTGTGTAT   60

CTTTTTTCTT CAGGCTGTAA ATTCTCTAAA GGCATTTTGC TTATTTTGGT GTCACAATTG  120

TTTAGGCCAT GCGCCTAGGT CTTCTTAAAA CACCTCTCTC ATG GCT CCT ACT TTT    175
                                            Met Ala Pro Thr Phe
                                            -15

CTA CTT ATT TCT GAT TCT TTT CTG ACT TCT CAG CCT TCT TTT TTT TTT    223
Leu Leu Ile Ser Asp Ser Phe Leu Thr Ser Gln Pro Ser Phe Phe Phe
-10                 -5                   1                  5

TTT                                                                226
Phe
```

(2) INFORMATION FOR SEQ ID NO: 196:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 362 base pairs
(B) TYPE: NUCLEIC ACID
(C) STRANDEDNESS: DOUBLE
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Testis

(ix) FEATURE:
(A) NAME/KEY: sig_peptide
(B) LOCATION: 219..275
(C) IDENTIFICATION METHOD: Von Heijne matrix

(D) OTHER INFORMATION: score 3.6
seq LSLLGIKIQWCLS/EN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 196:

```
AAAAAATACA CKGAGATTAT GTACGATTTA GTGATTTGGT GGGATAATTA TAAATCGTGG   60

AATAATTTAT ATATGTGGAG TAAGAAGAGA GGGGTCAAAC CTTTTGGTAC AAGCAACATC  120

TTGTTGCCAC CACCTTGATT TTCTCATAGG TGCTATTGTG TCCTAAGAGT RGRACAGRSR  180

RGRAAACAAA GATAATTAAA CACAAGTCAG GTTACAAC ATG ATA TCT TTA ATT GTA  236
                                         Met Ile Ser Leu Ile Val
                                                             -15

CTT TCT CTG CTT GGT ATC AAG ATT CAG TGG TGC TTG TCA GAA AAT ACC    284
Leu Ser Leu Leu Gly Ile Lys Ile Gln Trp Cys Leu Ser Glu Asn Thr
            -10                 -5                   1

TTG TTC TGT GAC TCT GAC TAT CTC TTG AGT CCC AAG GCT CCA ATT GAG    332
Leu Phe Cys Asp Ser Asp Tyr Leu Leu Ser Pro Lys Ala Pro Ile Glu
     5                  10                  15

CCT TTA TCT TTC AAC CTT ACC ACC CAG GGG                            362
Pro Leu Ser Phe Asn Leu Thr Thr Gln Gly
 20                 25
```

(2) INFORMATION FOR SEQ ID NO: 197:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 263 base pairs
(B) TYPE: NUCLEIC ACID
(C) STRANDEDNESS: DOUBLE
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Ovary

(ix) FEATURE:
(A) NAME/KEY: sig_peptide
(B) LOCATION: 129..257
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 3.6
seq LLYFNTFLPRKVA/RV

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 197:

```
ATTAAGTCCT GCATTTTGTA AGAGGCAAAT GGAGAGTAAC AGAAGAGTGT CTTTTCTCCT   60

GGTTTTGGAG TCTTGCACTG GCCATGAGTG TTGKGACTGA TGGTCRACCC AGGCGGGCAT  120

TTTAATAA ATG GCC TGT GAT TCT TTT TTG AAA GAT GCT CTT CCA CAA GAG   170
         Met Ala Cys Asp Ser Phe Leu Lys Asp Ala Leu Pro Gln Glu
                     -40                 -35                 -30
```

```
TTA AGC CAG TTA GRR TTC CTG TTT CCT CTT GTT GAT ATG AGA GAA GAT      218
Leu Ser Gln Leu Xaa Phe Leu Phe Pro Leu Val Asp Met Arg Glu Asp
                -25                 -20                 -15

CTC CTG TAT TTT AAC ACG TTT TTA CCA AGA AAG GTG GCA CGG GTG          263
Leu Leu Tyr Phe Asn Thr Phe Leu Pro Arg Lys Val Ala Arg Val
            -10                 -5                  1
```

(2) INFORMATION FOR SEQ ID NO: 198:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 216 base pairs
(B) TYPE: NUCLEIC ACID
(C) STRANDEDNESS: DOUBLE
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Uterus

(ix) FEATURE:
(A) NAME/KEY: sig_peptide
(B) LOCATION: 13..171
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 3.6
seq FLILHFFPQQIRK/KI

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 198:

```
ATTCTCAATC AA ATG TTG CTA TTG AAT GAA AAC CTC AAA GCA GAA ATT CAA    51
              Met Leu Leu Leu Asn Glu Asn Leu Lys Ala Glu Ile Gln
                          -50                 -45

AAG AAT GAA GCT CAA GGC AGC TGT ATC TTG TTT CTG TTT TGC TTT GAG      99
Lys Asn Glu Ala Gln Gly Ser Cys Ile Leu Phe Leu Phe Cys Phe Glu
-40                 -35                 -30                 -25

AGT CAG AAT ATG CGA TCA AAA TCT ATC TTC CCC TTC CTT ATC CTT CAT     147
Ser Gln Asn Met Arg Ser Lys Ser Ile Phe Pro Phe Leu Ile Leu His
                -20                 -15                 -10

TTT TTT CCC CAG CAG ATA AGA AAA AAA ATA GTG GTG CTT CTT TTA GGA     195
Phe Phe Pro Gln Gln Ile Arg Lys Lys Ile Val Val Leu Leu Leu Gly
            -5                  1               5

CTT AAT TCT CAG AAG GCA GGG                                         216
Leu Asn Ser Gln Lys Ala Gly
     10                 15
```

(2) INFORMATION FOR SEQ ID NO: 199:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 125 base pairs

(B) TYPE: NUCLEIC ACID
(C) STRANDEDNESS: DOUBLE
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Spleen

(ix) FEATURE:
(A) NAME/KEY: sig_peptide
(B) LOCATION: 6..83
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 3.5
seq LLPFTFLSLKAFL/QX

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 199:

```
AGCTG ATG ATA AGT AAG TAT GTG CAT TAT AGC TTG ACT GAC TTA CTA TTA    50
      Met Ile Ser Lys Tyr Val His Tyr Ser Leu Thr Asp Leu Leu Leu
          -25                 -20                 -15

CCT TTT ACA TTC TTA AGC CTT AAA GCC TTT CTG CAG YYA AGA GTT TTA      98
Pro Phe Thr Phe Leu Ser Leu Lys Ala Phe Leu Gln Xaa Arg Val Leu
    -10                 -5                  1               5

ATG TCT CTT CCT CAA CAC AAG CCC TGG                                 125
Met Ser Leu Pro Gln His Lys Pro Trp
                10
```

(2) INFORMATION FOR SEQ ID NO: 200:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 194 base pairs
(B) TYPE: NUCLEIC ACID
(C) STRANDEDNESS: DOUBLE
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Testis

(ix) FEATURE:
(A) NAME/KEY: sig_peptide
(B) LOCATION: 42..122
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 3.5
seq CSLLSSFCALHFG/LK

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 200:

```
AATATGTGAT CAAACGCCCA GGAGCCAGCT GGTGASAAAG A ATG GCG AGG ACA ATG    56
                                              Met Ala Arg Thr Met
                                                          -25
```

```
GGA GTT CCC AGA GCA TGC AAG GCC TTC TGT AGC CTC CTC TCC AGC TTC     104
Gly Val Pro Arg Ala Cys Lys Ala Phe Cys Ser Leu Leu Ser Ser Phe
        -20                 -15                 -10

TGT GCA TTA CAC TTT GGG CTC AAG AAA CAG TAT GGT ACT TCT TAC CTC     152
Cys Ala Leu His Phe Gly Leu Lys Lys Gln Tyr Gly Thr Ser Tyr Leu
     -5                   1               5                  10

CAT GCC TGT GCT TAT GCT AGC CCC TTG ACC TGG GGT CCC TGG             194
His Ala Cys Ala Tyr Ala Ser Pro Leu Thr Trp Gly Pro Trp
                 15                  20
```

(2) INFORMATION FOR SEQ ID NO: 201:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 348 base pairs
(B) TYPE: NUCLEIC ACID
(C) STRANDEDNESS: DOUBLE
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Testis

(ix) FEATURE:
(A) NAME/KEY: sig_peptide
(B) LOCATION: 262..306
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 3.5
seq LCFLLPHHRLQEA/RX

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 201:

```
ATTTCGCGGC GCTCGCBGMA CYHSGWTGTT CAGCACCTTC GGTCCGGTTG AGGTTGTCAA    60

GTCGGMCCAA ACAGGTTGTT TCTCTGCAGT TTCCAACATG GCAGGGMSGT TTAATAGACA   120

TGGATAAGAA GTCCACTCAC AGAAATCCTG AAGATGCCAG GGCTGGCAAA TATGAAGGTA   180

AACACAAACG AAAGAAAAGA AGAAAGCAAA ACCAAAACCA GCACCGATCC CGACATAGAT   240

CAGTGACGTC TTTTTCTTCA G ATG ATC CTA TGT TTC CTT CTT CCT CAT CAT     291
                        Met Ile Leu Cys Phe Leu Leu Pro His His
                        -15                 -10

CGT CTT CAG GAA GCC AGA YAG ATT CAA GTA TTG AAG ATK CTT CCA AGG     339
Arg Leu Gln Glu Ala Arg Xaa Ile Gln Val Leu Lys Xaa Leu Pro Arg
 -5                   1               5                  10

GAA AAA TTA                                                         348
Glu Lys Leu
```

(2) INFORMATION FOR SEQ ID NO: 202:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 255 base pairs
(B) TYPE: NUCLEIC ACID
(C) STRANDEDNESS: DOUBLE
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Spleen

(ix) FEATURE:
(A) NAME/KEY: sig_peptide
(B) LOCATION: 7..84
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 3.5
seq QCFFVCFSPKIYG/VI

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 202:

```
AATAAC ATG CAA GAC TAC GTT TCA CAT GCA GTA CGG CGC CAC TGT CAG        48
       Met Gln Asp Tyr Val Ser His Ala Val Arg Arg His Cys Gln
           -25                 -20                 -15

TGT TTT TTT GTT TGT TTT TCC CCC AAG ATT TAT GGC GTA ATA ACA TGG       96
Cys Phe Phe Val Cys Phe Ser Pro Lys Ile Tyr Gly Val Ile Thr Trp
        -10                 -5                  1

ACC GTC CTG ATA ACT GGA GCC CGG GTT CTG TCA GAG CCC CAG AGG TTG      144
Thr Val Leu Ile Thr Gly Ala Arg Val Leu Ser Glu Pro Gln Arg Leu
  5                  10                  15                  20

TGG GTT AGA CTT GAT GAC ATA ACA GCA AAT GCA GCG TGT GGT TAC AGA      192
Trp Val Arg Leu Asp Asp Ile Thr Ala Asn Ala Ala Cys Gly Tyr Arg
                 25                  30                  35

AAG CAA GAG CCG CGG AAG ACG TTT GAA AAC AAT TGG GAA AAT TTG TAT      240
Lys Gln Glu Pro Arg Lys Thr Phe Glu Asn Asn Trp Glu Asn Leu Tyr
             40                  45                  50

ACG GAC TGG AAC TGG                                                  255
Thr Asp Trp Asn Trp
         55
```

(2) INFORMATION FOR SEQ ID NO: 203:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 224 base pairs
(B) TYPE: NUCLEIC ACID
(C) STRANDEDNESS: DOUBLE
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Homo Sapiens

(F) TISSUE TYPE: Testis

(ix) FEATURE:
(A) NAME/KEY: sig_peptide
(B) LOCATION: 120..212
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 3.5
seq VLLNLALSHFNNC/GL

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 203:

```
AGATYTTATA ATCTTGCTAC AAAGAAAGTA GGACAGTCTC AGCCTTTAAG AATGTCACTA    60

TAACAGTTTT TTTTTCCTT AAGGATATTT TAAACAGGAA AGTAGACAAC CGGGTAAGC     119

ATG GAG TTT GCT CAT GCT GCC GAA TGT GTG TCT TTT GCC CTA AAT GAA     167
Met Glu Phe Ala His Ala Ala Glu Cys Val Ser Phe Ala Leu Asn Glu
    -30                 -25                 -20

ACG CAC GTT CTT CTA AAT TTA GCC CTA TCA CAT TTT AAC AAT TGT GGC     215
Thr His Val Leu Leu Asn Leu Ala Leu Ser His Phe Asn Asn Cys Gly
-15                 -10                 -5                    1

CTC GCA GTG                                                          224
Leu Ala Val
```

(2) INFORMATION FOR SEQ ID NO: 204:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 276 base pairs
(B) TYPE: NUCLEIC ACID
(C) STRANDEDNESS: DOUBLE
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Ovary

(ix) FEATURE:
(A) NAME/KEY: sig_peptide
(B) LOCATION: 133..222
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 3.5
seq LLAASWLPRDAPC/EA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 204:

```
ACAGATTGCT TTCCAAGCTG AACATATGCA ACTGTATTGC TAAACTTACC AATTTCAGGG    60

AATCTGGGCG TCAAAAGCAT CCACATCCCT GCAGCAGGCC CCTGGGGAGG TAGGCAGGGT   120

GACAGCTGGG AA ATG GGR AAC CAG GGC TTT CCA TAC CTG TCT CCT TCT CTC   171
              Met Gly Asn Gln Gly Phe Pro Tyr Leu Ser Pro Ser Leu
              -30                 -25                 -20
```

```
AGT GTC CAG GAT CTT CTT GCT GCT TCA TGG CTG CCC CGA GAT GCT CCC     219
Ser Val Gln Asp Leu Leu Ala Ala Ser Trp Leu Pro Arg Asp Ala Pro
        -15                 -10                 -5

TGT GAG GCC CCC CCG GGC CTG CCT TCA CAG ACA ATG CTC TGT GCC CCT     267
Cys Glu Ala Pro Pro Gly Leu Pro Ser Gln Thr Met Leu Cys Ala Pro
      1             5                  10                  15

GGA CCA AGG                                                         276
Gly Pro Arg
```

(2) INFORMATION FOR SEQ ID NO: 205:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 196 base pairs
(B) TYPE: NUCLEIC ACID
(C) STRANDEDNESS: DOUBLE
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Ovary

(ix) FEATURE:
(A) NAME/KEY: sig_peptide
(B) LOCATION: 68..133
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 3.5
seq AQLASPLLPGATP/VA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 205:

```
AACAAATTGA TCTTGTGTGA TGAGTGTAAT AAAGCCTTCC ACCTGTTTTG TCTGAGGCCG     60

GCCCTCT ATG AAG TAC CAG ATG GTG AGT GGC AGT GCC CAG CTT GCC AGC     109
        Met Lys Tyr Gln Met Val Ser Gly Ser Ala Gln Leu Ala Ser
                -20                 -15                 -10

CCG CTA CTG CCA GGC GCA ACT CCC GTG GCA GGA ACT ATA CTG AAG AGT     157
Pro Leu Leu Pro Gly Ala Thr Pro Val Ala Gly Thr Ile Leu Lys Ser
            -5                  1               5

CTG CTT CTG AGG ACA GTG AAG ATG ATG AGA GTG TAT GGG                 196
Leu Leu Leu Arg Thr Val Lys Met Met Arg Val Tyr Gly
    10                  15                  20
```

(2) INFORMATION FOR SEQ ID NO: 206:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 145 base pairs
(B) TYPE: NUCLEIC ACID
(C) STRANDEDNESS: DOUBLE
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Testis

(ix) FEATURE:
(A) NAME/KEY: other
(B) LOCATION: 55..94
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 100
region 1..40
id AA134726
est

(ix) FEATURE:
(A) NAME/KEY: other
(B) LOCATION: 89..121
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 93
region 34..66
id AA134726
est

(ix) FEATURE:
(A) NAME/KEY: other
(B) LOCATION: 72..140
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 95
region 1..69
id R17226
est

(ix) FEATURE:
(A) NAME/KEY: sig_peptide
(B) LOCATION: 41..103
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 12.7
seq ILFLLSWSGPLQG/QQ

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 206:

```
AGTACGTTCC TTCTACTCTG GCACCACTCT CCAGGCTGCC ATG GGG CCC AGC ACC       55
                                            Met Gly Pro Ser Thr
                                                -20

CCT CTC CTC ATC TTG TTC CTT TTG TCA TGG TCG GGA CCC CTC CAA GGA      103
Pro Leu Leu Ile Leu Phe Leu Leu Ser Trp Ser Gly Pro Leu Gln Gly
    -15                 -10                 -5

CAG CAG CAC CAC CTT GTG GAG TAC ATG GAA CGC CGA CAC GGG              145
Gln Gln His His Leu Val Glu Tyr Met Glu Arg Arg His Gly
  1               5                  10
```

(2) INFORMATION FOR SEQ ID NO: 207:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 172 base pairs

```
        (B) TYPE: NUCLEIC ACID
        (C) STRANDEDNESS: DOUBLE
        (D) TOPOLOGY: LINEAR

  (ii) MOLECULE TYPE: CDNA

  (vi) ORIGINAL SOURCE:
        (A) ORGANISM: Homo Sapiens
        (F) TISSUE TYPE: Ovary

  (ix) FEATURE:
        (A) NAME/KEY: other
        (B) LOCATION: 73..169
        (C) IDENTIFICATION METHOD: blastn
        (D) OTHER INFORMATION:  identity 100
                                region 73..169
                                id W25639
                                est

  (ix) FEATURE:
        (A) NAME/KEY: other
        (B) LOCATION: 37..81
        (C) IDENTIFICATION METHOD: blastn
        (D) OTHER INFORMATION:  identity 91
                                region 38..82
                                id W25639
                                est

  (ix) FEATURE:
        (A) NAME/KEY: other
        (B) LOCATION: 42..169
        (C) IDENTIFICATION METHOD: blastn
        (D) OTHER INFORMATION:  identity 100
                                region 1..128
                                id AA040016
                                est

  (ix) FEATURE:
        (A) NAME/KEY: other
        (B) LOCATION: 34..169
        (C) IDENTIFICATION METHOD: blastn
        (D) OTHER INFORMATION:  identity 96
                                region 23..158
                                id R72515
                                est

  (ix) FEATURE:
        (A) NAME/KEY: other
        (B) LOCATION: 47..169
        (C) IDENTIFICATION METHOD: blastn
        (D) OTHER INFORMATION:  identity 99
                                region 1..123
                                id T84313
                                est

  (ix) FEATURE:
        (A) NAME/KEY: sig_peptide
        (B) LOCATION: 86..145
        (C) IDENTIFICATION METHOD: Von Heijne matrix
        (D) OTHER INFORMATION:  score 7.4
                                seq LVFCVGLLTMAKA/ES
```

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 207:

```
AAGGGGGTCC AAAGTGCTCA GCCCCCGGGG CACAGCAGGA CGTTTGGGGG CCTTCTTTCA   60

GCAGGGGACA GCCCGATTGG GGACA ATG GCG TCT CTT GGC CAC ATC TTG GTT    112
                            Met Ala Ser Leu Gly His Ile Leu Val
                            -20                 -15

TTC TGT GTG GGT CTC CTC ACC ATG GCC AAG GCA GAA AGT CCA AAG GAA    160
Phe Cys Val Gly Leu Leu Thr Met Ala Lys Ala Glu Ser Pro Lys Glu
    -10                 -5                  1               5

CAC GAC CCG AGG                                                    172
His Asp Pro Arg
```

(2) INFORMATION FOR SEQ ID NO: 208:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 193 base pairs
(B) TYPE: NUCLEIC ACID
(C) STRANDEDNESS: DOUBLE
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Testis

(ix) FEATURE:
(A) NAME/KEY: other
(B) LOCATION: 46..192
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 98
region 5..151
id R14826
est

(ix) FEATURE:
(A) NAME/KEY: other
(B) LOCATION: 46..192
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 91
region 129..275
id W55137
est

(ix) FEATURE:
(A) NAME/KEY: other
(B) LOCATION: 57..192
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 91
region 1..136
id W64115
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 57..192
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 91
region 1..136
id W75505
est

(ix) FEATURE:
(A) NAME/KEY: other
(B) LOCATION: 78..192
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 97
region 1..115
id W20303
est

(ix) FEATURE:
(A) NAME/KEY: sig_peptide
(B) LOCATION: 53..121
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 7.3
seq ALSLLLVSGSLLP/GP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 208:

```
ACTCAATAAA TGTTTTCCGC ATTAAGACGC TTCTTAGGAG TCTTCATGGA GG ATG TCG    58
                                                          Met Ser

GGT TCG TCG CTG CCC AGC GCC CTG GCC CTC TCG CTG TTG CTG GTC TCT     106
Gly Ser Ser Leu Pro Ser Ala Leu Ala Leu Ser Leu Leu Leu Val Ser
    -20                 -15                 -10

GGC TCC CTC CTC CCA GGG CCA GGC GCC GCT CAG AAC GAG CCA AGG ATT     154
Gly Ser Leu Leu Pro Gly Pro Gly Ala Ala Gln Asn Glu Pro Arg Ile
 -5                   1               5                  10

GTC ACC AGT GAA GAG GTC ATT ATT CGA GAC AGC CCC GTG                 193
Val Thr Ser Glu Glu Val Ile Ile Arg Asp Ser Pro Val
            15                  20
```

(2) INFORMATION FOR SEQ ID NO: 209:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 247 base pairs
(B) TYPE: NUCLEIC ACID
(C) STRANDEDNESS: DOUBLE
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Ovary

(ix) FEATURE:
(A) NAME/KEY: other
(B) LOCATION: 71..207

(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 100
region 1..137
id R73005
est

(ix) FEATURE:
(A) NAME/KEY: other
(B) LOCATION: 80..207
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 100
region 1..128
id N26942
est

(ix) FEATURE:
(A) NAME/KEY: other
(B) LOCATION: 86..207
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 100
region 1..122
id W02954
est

(ix) FEATURE:
(A) NAME/KEY: other
(B) LOCATION: 112..207
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 100
region 1..96
id T24907
est

(ix) FEATURE:
(A) NAME/KEY: other
(B) LOCATION: 137..207
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 100
region 1..71
id AA130938
est

(ix) FEATURE:
(A) NAME/KEY: sig_peptide
(B) LOCATION: 53..223
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 7.1
seq VGLAVVSLGGSRG/SG

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 209:

```
AACTGACAAG ACGTGGGCCA AGAGGGGTCA CCGCCCCCGG AGCGGCGCGN AS ATG ATG    58
                                                          Met Met

GAA GTC GTA GTA GGA AAT GGC GTC GTG GCA TTG AGG GGC ATC CCT CCT     106
Glu Val Val Val Gly Asn Gly Val Val Ala Leu Arg Gly Ile Pro Pro
-55                 -50                 -45                 -40

AGA ACC TCC AGG AAA AGC TCG CGG AAG ACG AGG TTC TGC GGA GAG AGA     154
Arg Thr Ser Arg Lys Ser Ser Arg Lys Thr Arg Phe Cys Gly Glu Arg
```

```
           -35                    -30                    -25

GGC TCC AAG CAG TCT GGG AAG TGT AGT CCA GTT GGC TTA GCA GTA GTT    202
Gly Ser Lys Gln Ser Gly Lys Cys Ser Pro Val Gly Leu Ala Val Val
            -20                 -15                 -10

TCG TTG GGG GGG AGC CGA GGT TCC GGG AAG GGG CTA GGC CGA CTG        247
Ser Leu Gly Gly Ser Arg Gly Ser Gly Lys Gly Leu Gly Arg Leu
        -5                  1               5
```

(2) INFORMATION FOR SEQ ID NO: 210:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 373 base pairs
(B) TYPE: NUCLEIC ACID
(C) STRANDEDNESS: DOUBLE
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Testis

(ix) FEATURE:
(A) NAME/KEY: other
(B) LOCATION: 252..375
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 98
region 1..124
id AA081350
est

(ix) FEATURE:
(A) NAME/KEY: other
(B) LOCATION: 318..375
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 98
region 1..58
id AA046671
est

(ix) FEATURE:
(A) NAME/KEY: sig_peptide
(B) LOCATION: 200..247
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 6.7
seq CFSLVLLLTSIWT/TR

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 210:

```
AATTTTTCCC CCAGTGACCT TGACAAGTCA GAAGCTTGAA AGCAGGGAAA TCCGGATGTC    60

TCGGTTATGA AGTGGAGCAG TGAGTGTGAG CCTCAACATA GTTCCAGAAC TCTCCATCCG   120

GACTAGTTAT TGAGCATCTG CCTCTCATAT CACCAGTGGC CATCTGAGGT GTTTCCCTGG   180

CTCTGAAGGG GTAGGCACG ATG GCC AGG TGC TTC AGC CTG GTG TTG CTT CTC    232
```

```
                        Met Ala Arg Cys Phe Ser Leu Val Leu Leu Leu
                            -15                     -10

ACT TCC ATC TGG ACC ACG AGG CTC CTG GTC CAA GGC TCT TTG CGT GCA     280
Thr Ser Ile Trp Thr Thr Arg Leu Leu Val Gln Gly Ser Leu Arg Ala
 -5                 1               5                   10

GAA GAG CTT TCC ATC CAG GTG TCA TGC AGA ATK ATG GGG ATC ACC CTT     328
Glu Glu Leu Ser Ile Gln Val Ser Cys Arg Xaa Met Gly Ile Thr Leu
            15                  20                  25

GTB AGC AAA AAG GCG AAC CAG CAG CTG AAT TTC ACA GAA GCT AAG         373
Val Ser Lys Lys Ala Asn Gln Gln Leu Asn Phe Thr Glu Ala Lys
        30                  35                  40
```

(2) INFORMATION FOR SEQ ID NO: 211:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 438 base pairs
(B) TYPE: NUCLEIC ACID
(C) STRANDEDNESS: DOUBLE
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Spleen

(ix) FEATURE:
(A) NAME/KEY: other
(B) LOCATION: 149..355
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 100
region 1..207
id R16604
est

(ix) FEATURE:
(A) NAME/KEY: other
(B) LOCATION: 354..407
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 100
region 207..260
id R16604
est

(ix) FEATURE:
(A) NAME/KEY: other
(B) LOCATION: 149..362
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 98
region 1..214
id N99558
est

(ix) FEATURE:
(A) NAME/KEY: other
(B) LOCATION: 380..428

(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 93
region 237..285
id N99558
est

(ix) FEATURE:
(A) NAME/KEY: sig_peptide
(B) LOCATION: 31..93
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 5.6
seq CLSCLLIPLALWS/II

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 211:

```
GAAATCTCCC GCAGTTCTAA GCAGGGCAAA ATG GGG TCT CGG AAG TGT GGA GGC      54
                                 Met Gly Ser Arg Lys Cys Gly Gly
                                     -20                 -15

TGC CTA AGT TGT TTG CTG ATT CCG CTT GCA CTT TGG AGT ATA ATC GTG     102
Cys Leu Ser Cys Leu Leu Ile Pro Leu Ala Leu Trp Ser Ile Ile Val
            -10                 -5                   1

AAC ATA TTA TTG TAT TTC CCG AAT GGG CAA ACT TCC TAT GCA TCC AGC     150
Asn Ile Leu Leu Tyr Phe Pro Asn Gly Gln Thr Ser Tyr Ala Ser Ser
    5                   10                  15

AAT AAA CTC ACC AAC TAC GTG TGG TAT TTT GAA GGA ATC TGT TTC TCA     198
Asn Lys Leu Thr Asn Tyr Val Trp Tyr Phe Glu Gly Ile Cys Phe Ser
 20                  25                  30                  35

GGC ATC ATG ATG CTT ATA GTA ACA ACA GTT CTT CTG GTA CTG GAG AAT     246
Gly Ile Met Met Leu Ile Val Thr Thr Val Leu Leu Val Leu Glu Asn
                40                  45                  50

AAT AAC AAC TAT AAA TGT TGC CAG AGT GAA AAC TGC AGC AAA AAA TAT     294
Asn Asn Asn Tyr Lys Cys Cys Gln Ser Glu Asn Cys Ser Lys Lys Tyr
            55                  60                  65

GTG ACA CTG CTG TCA ATT ATC TTT TCT TCC CTC GGA ATT GCT TTT TCT     342
Val Thr Leu Leu Ser Ile Ile Phe Ser Ser Leu Gly Ile Ala Phe Ser
        70                  75                  80

GGA TAC TGC CTG GTC ATC TCT GCC TTG GGT CTT GTC CAA GGG CCA TAT     390
Gly Tyr Cys Leu Val Ile Ser Ala Leu Gly Leu Val Gln Gly Pro Tyr
    85                  90                  95

TGC CGC ACC CTT GAT GGC TGG GAG TAT GCT TTT GAA GGC ACT GCT GGA     438
Cys Arg Thr Leu Asp Gly Trp Glu Tyr Ala Phe Glu Gly Thr Ala Gly
100                 105                 110                 115
```

(2) INFORMATION FOR SEQ ID NO: 212:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 378 base pairs
(B) TYPE: NUCLEIC ACID
(C) STRANDEDNESS: DOUBLE
(D) TOPOLOGY: LINEAR

```
(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:
      (A) ORGANISM: Homo Sapiens
      (F) TISSUE TYPE: Uterus

(ix) FEATURE:
      (A) NAME/KEY: other
      (B) LOCATION: 251..376
      (C) IDENTIFICATION METHOD: blastn
      (D) OTHER INFORMATION:  identity 100
                              region 1..126
                              id R16604
                              est

(ix) FEATURE:
      (A) NAME/KEY: other
      (B) LOCATION: 251..376
      (C) IDENTIFICATION METHOD: blastn
      (D) OTHER INFORMATION:  identity 96
                              region 1..126
                              id N99558
                              est

(ix) FEATURE:
      (A) NAME/KEY: sig_peptide
      (B) LOCATION: 133..195
      (C) IDENTIFICATION METHOD: Von Heijne matrix
      (D) OTHER INFORMATION:  score 5.6
                              seq CLSCLLIPLALWS/II

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 212:


ATTTGTTCTC CAAACAGTAA ACCAGTATTT CACACTGAGA TTGTCGGCTG CGGGTATATT    60

CCAATTCCCC GTCTCCTCAT GAATATGAAG TGAAGGGCTC TGAMCCTKGG AAGTGGTTCT   120

AAGCAGGGCA AA ATG GGG TCT CGG AAG TGT GGA GGC TGC CTA AGT TGT TTG   171
              Met Gly Ser Arg Lys Cys Gly Gly Cys Leu Ser Cys Leu
                  -20                 -15                 -10

CTG ATT CCG CTT GCA CTT TGG AGT ATA ATC GTG AAC ATA TTA TTG TAT      219
Leu Ile Pro Leu Ala Leu Trp Ser Ile Ile Val Asn Ile Leu Leu Tyr
             -5                   1               5

TTC CCG AAT GGG CAA ACT TCC TAT GCA TCC AGC AAT AAA CTC ACC AAC      267
Phe Pro Asn Gly Gln Thr Ser Tyr Ala Ser Ser Asn Lys Leu Thr Asn
     10                  15                  20

TAC GTG TGG TAT TTT GAA GGA ATC TGT TTC TCA GGC ATC ATG ATG CTT      315
Tyr Val Trp Tyr Phe Glu Gly Ile Cys Phe Ser Gly Ile Met Met Leu
 25                  30                  35                  40

ATA GTA ACA ACA GTT CTT CTG GTA CTG GAG AAT AAT AAC AAC TAT AAA      363
Ile Val Thr Thr Val Leu Leu Val Leu Glu Asn Asn Asn Asn Tyr Lys
                 45                  50                  55

TGT TGC CAG AGT GGG                                                  378
Cys Cys Gln Ser Gly
```

60

(2) INFORMATION FOR SEQ ID NO: 213:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 230 base pairs
(B) TYPE: NUCLEIC ACID
(C) STRANDEDNESS: DOUBLE
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Testis

(ix) FEATURE:
(A) NAME/KEY: other
(B) LOCATION: 53..227
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 99
region 190..364
id AA043641
est

(ix) FEATURE:
(A) NAME/KEY: other
(B) LOCATION: 92..227
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 99
region 1..136
id N98697
est

(ix) FEATURE:
(A) NAME/KEY: other
(B) LOCATION: 69..102
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 94
region 393..426
id AA147010
est

(ix) FEATURE:
(A) NAME/KEY: other
(B) LOCATION: 53..119
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 97
region 435..501
id AA142584
est

(ix) FEATURE:
(A) NAME/KEY: sig_peptide
(B) LOCATION: 159..209
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 5.3
seq ILFGVSFVFLTHC/TI

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 213:

```
AAACTTTAGC ACATCATTTT GGCATTCTAG AATATTTCAT CTACCATACT ATAATTACCT   60

GAAGACATCA GGAGAATACA AACTTGCAGG TGTTTTTCTT GGAGGTCGTT CAATGGGCTC  120

AAGAGCAGCT GCTTCTGTAA TGTGTCACAT TGAGCCAG ATG ATG GTG ATG ATT TTG  176
                                         Met Met Val Met Ile Leu
                                                 -15

TTC GGG GTC TCA TTT GTA TTT CTT ACC CAC TGC ACC ATC CAA AGC AGC    224
Phe Gly Val Ser Phe Val Phe Leu Thr His Cys Thr Ile Gln Ser Ser
    -10                 -5                   1               5

TGC GGG                                                            230
Cys Gly
```

(2) INFORMATION FOR SEQ ID NO: 214:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 394 base pairs
(B) TYPE: NUCLEIC ACID
(C) STRANDEDNESS: DOUBLE
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Testis

(ix) FEATURE:
(A) NAME/KEY: other
(B) LOCATION: 310..393
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 98
region 1..84
id HUM426A07B
est

(ix) FEATURE:
(A) NAME/KEY: sig_peptide
(B) LOCATION: 293..349
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 4.4
seq VLVSLPHPHPALT/CC

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 214:

```
AAACCTTGTT GCTAGGGACC GGGCGGTTTG CGGCAACCGT GGGCACTGCT GAATTTGAAT   60

TGAGGGGCGA GGGAAAAGTT TTCCTCAGGT GTGGTGGGGA GAGGGAGGCG GATGCCGGNG  120

AAACCGTAGG KACGCGGTCA GAAAGGCGAC GGGCTGTCGG AGTTGGAAAG GGACGCCTGG  180

TTTCCCCCCA AGCGAACCGG GATGGGAAGT GACTTCAATG AGATTGAACT TCAGCTGGAT  240
```

```
TGAAAGAGAG GCTAGAAGTT CCGCTTGCCA GCAGCCTCCT TAGTAGAGCG GA ATG AGT  298
                                                          Met Ser

AAT ACC CAC ACG GTG CTT GTC TCA CTT CCC CAT CCG CAC CCG GCC CTC   346
Asn Thr His Thr Val Leu Val Ser Leu Pro His Pro His Pro Ala Leu
        -15                 -10                 -5

ACC TGC TGT CAC CTC GGC CWC CCA CAC CCG GTC CGC GCT CCC CGC CCG   394
Thr Cys Cys His Leu Gly Xaa Pro His Pro Val Arg Ala Pro Arg Pro
    1               5                   10                  15
```

(2) INFORMATION FOR SEQ ID NO: 215:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 473 base pairs
(B) TYPE: NUCLEIC ACID
(C) STRANDEDNESS: DOUBLE
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Testis

(ix) FEATURE:
(A) NAME/KEY: other
(B) LOCATION: 111..321
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 90
region 1..211
id N41784
est

(ix) FEATURE:
(A) NAME/KEY: other
(B) LOCATION: 143..237
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 97
region 5..99
id T70115
est

(ix) FEATURE:
(A) NAME/KEY: sig_peptide
(B) LOCATION: 99..416
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 4.1
seq IITLACVPMTSFT/RN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 215:

```
ACAGCATCCT TTTCAAGGAT ADCTGAACAG AACCTTCTAA GTCTCAGACA CGTAAACCCA   60

AGTGTGGCAA AGGAACTCAT TGCTCTCGAA ATGCATAT ATG TKG GTT TAT AGA CTG  116
                                          Met Xaa Val Tyr Arg Leu
                                              -105
```

```
CAA ACT CAA GAR AAG CCC AAC ACT ACT GTK CAA GTT CCA GCC TTT CTT    164
Gln Thr Gln Glu Lys Pro Asn Thr Thr Val Gln Val Pro Ala Phe Leu
-100                -95                 -90                 -85

CAA GAG CTG GTA GAT CGG GAT AAT TCC AAA TTT GAG GAG TGG TGT ATT    212
Gln Glu Leu Val Asp Arg Asp Asn Ser Lys Phe Glu Glu Trp Cys Ile
                -80                 -75                 -70

GAA ATG GCT GAG ATG CGT AAS AAA GTG TGG ATA AAG GAA AAG CAA AAC    260
Glu Met Ala Glu Met Arg Xaa Lys Val Trp Ile Lys Glu Lys Gln Asn
            -65                 -60                 -55

ACG AAG AGG TTA AGG AGC TGT ACC AAA GGT TAC CTG CTG GAG CTG AGC    308
Thr Lys Arg Leu Arg Ser Cys Thr Lys Gly Tyr Leu Leu Glu Leu Ser
        -50                 -45                 -40

CCT ATG AGT TTG TCT CTC TGG AAT GGC TGC AAA AGT GGT TGG ATG AAT    356
Pro Met Ser Leu Ser Leu Trp Asn Gly Cys Lys Ser Gly Trp Met Asn
    -35                 -30                 -25

CAG CAA NTA CCA AAC CTA TTG ATA ATC ACG CTT GCC TGT GTT CCC ATG    404
Gln Gln Xaa Pro Asn Leu Leu Ile Ile Thr Leu Ala Cys Val Pro Met
-20                 -15                 -10                  -5

ACA AGC TTC ACC CGG AAT AAA ATA TCA ATT ATG AAG AGG ATA TCT GAA    452
Thr Ser Phe Thr Arg Asn Lys Ile Ser Ile Met Lys Arg Ile Ser Glu
                  1               5                  10

TAT GCA GCK GAC ATT TTC TAT                                        473
Tyr Ala Ala Asp Ile Phe Tyr
        15
```

(2) INFORMATION FOR SEQ ID NO: 216:

(i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 134 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:
- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Testis

(ix) FEATURE:
- (A) NAME/KEY: other
- (B) LOCATION: 63..133
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97
  region 152..222
  id AA043974
  est

(ix) FEATURE:
- (A) NAME/KEY: other
- (B) LOCATION: 98..133
- (C) IDENTIFICATION METHOD: blastn

(D) OTHER INFORMATION: identity 100
region 1..36
id W05501
est

(ix) FEATURE:
(A) NAME/KEY: sig_peptide
(B) LOCATION: 54..116
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 3.9
seq LIAVVIIILLIFT/SV

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 216:

```
AGACTTTGCT GATTTAGCTT ATGGAAGAGG AACCAGAAAT TTGTCCTTGA ATA ATG       56
                                                           Met

TTT CCC GTG TTG GGC TGG ATC TTG ATA GCA GTW GTY ATC ATC ATT CTT     104
Phe Pro Val Leu Gly Trp Ile Leu Ile Ala Val Val Ile Ile Ile Leu
-20                 -15                 -10                 -5

CTG ATT TTT ACA TCT GTC ACC CGA TGC CTG                             134
Leu Ile Phe Thr Ser Val Thr Arg Cys Leu
                1               5
```

(2) INFORMATION FOR SEQ ID NO: 217:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 202 base pairs
(B) TYPE: NUCLEIC ACID
(C) STRANDEDNESS: DOUBLE
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Testis

(ix) FEATURE:
(A) NAME/KEY: other
(B) LOCATION: 153..199
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 97
region 1..47
id R14297
est

(ix) FEATURE:
(A) NAME/KEY: sig_peptide
(B) LOCATION: 8..64
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 3.9
seq SVCLCPCLNKGQS/EN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 217:

```
AAGCAAG ATG TTC TCC TGC TGT ATC TCA GTT TGT CTA TGT CCT TGT CTC      49
        Met Phe Ser Cys Cys Ile Ser Val Cys Leu Cys Pro Cys Leu
                        -15                 -10

AAC AAA GGC CAA AGT GAG AAT CTT TCC AGA GAC TGC GGW CAT TGG CTG      97
Asn Lys Gly Gln Ser Glu Asn Leu Ser Arg Asp Cys Gly His Trp Leu
 -5                 1               5                   10

AAC CCT CAC CAT CGA CGC CTC TGG CCA TTT GGC AGA AGG CAC CCA CAG     145
Asn Pro His His Arg Arg Leu Trp Pro Phe Gly Arg Arg His Pro Gln
            15                  20                  25

GAT TGT GGA CTC TTC CAA GAT TCA CAA TGR TAT GGT GAA TCC AAA GAC     193
Asp Cys Gly Leu Phe Gln Asp Ser Gln Xaa Tyr Gly Glu Ser Lys Asp
        30                  35                  40

TGG AAC GGG                                                         202
Trp Asn Gly
    45
```

(2) INFORMATION FOR SEQ ID NO: 218:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 406 base pairs
(B) TYPE: NUCLEIC ACID
(C) STRANDEDNESS: DOUBLE
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Uterus

(ix) FEATURE:
(A) NAME/KEY: other
(B) LOCATION: 338..403
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 98
region 38..103
id W78795
est

(ix) FEATURE:
(A) NAME/KEY: other
(B) LOCATION: 338..403
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 98
region 405..470
id AA151030
est

(ix) FEATURE:
(A) NAME/KEY: other
(B) LOCATION: 338..403
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 98
region 6..71
id H48640

est

(ix) FEATURE:
(A) NAME/KEY: other
(B) LOCATION: 338..403
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 98
region 73..138
id R99176
est

(ix) FEATURE:
(A) NAME/KEY: other
(B) LOCATION: 338..403
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 93
region 48..113
id W79571
est

(ix) FEATURE:
(A) NAME/KEY: sig_peptide
(B) LOCATION: 143..229
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 3.5
seq LTYLLLLSPIKYP/LD

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 218:

```
ATCGTATTGG CACAGTTCTC TATGTAAGCA ATTTGAGAGG GAAGCAAAGG GGAAAAGTTT   60

GAGTTAGCTG TTCTCTGTCC TAGAATTTCC CTGCATTAAT CTTGTCCTTG AAAATATATA  120

TAATACTGGT CCCTTAAACT CC ATG AGG CTT TGT CTC ATT ATG TAT TGT TCT   172
                         Met Arg Leu Cys Leu Ile Met Tyr Cys Ser
                                         -25                 -20

TTT GGT ACC CTT TCC CAC TTA ACT TAC CTT TTG CTC CTA AGT CCT ATA    220
Phe Gly Thr Leu Ser His Leu Thr Tyr Leu Leu Leu Leu Ser Pro Ile
            -15                 -10                  -5

AAA TAC CCC TTG GAT CTG GAT TTT TTA TAC CCG ATT TTC TCC ACT GTG    268
Lys Tyr Pro Leu Asp Leu Asp Phe Leu Tyr Pro Ile Phe Ser Thr Val
             1               5                  10

TAT AAA AGG TAT ATT GTG ACT GTA AAT TTT TGT ATA TCA TGT TCT GAG    316
Tyr Lys Arg Tyr Ile Val Thr Val Asn Phe Cys Ile Ser Cys Ser Glu
     15                  20                  25

AGC TTC TTA CTT TCT GAT CTC ATA GCA CTA TTC CTG ATC AGA GAA CTC    364
Ser Phe Leu Leu Ser Asp Leu Ile Ala Leu Phe Leu Ile Arg Glu Leu
 30                  35                  40                  45

CAG TTG CTT CAA CAC ACA GTA TCA GTA GTG CAG CCA CCC ACG            406
Gln Leu Leu Gln His Thr Val Ser Val Val Gln Pro Pro Thr
                 50                  55
```

(2) INFORMATION FOR SEQ ID NO: 219:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 210 base pairs
(B) TYPE: NUCLEIC ACID
(C) STRANDEDNESS: DOUBLE
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Testis

(ix) FEATURE:
(A) NAME/KEY: other
(B) LOCATION: complement(118..206)
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 97
region 144..232
id T77881
est

(ix) FEATURE:
(A) NAME/KEY: other
(B) LOCATION: complement(64..118)
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 98
region 231..285
id T77881
est

(ix) FEATURE:
(A) NAME/KEY: other
(B) LOCATION: complement(126..206)
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 100
region 139..219
id R01713
est

(ix) FEATURE:
(A) NAME/KEY: sig_peptide
(B) LOCATION: 70..147
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 10.5
seq LLLALLLPVQVSS/FV

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 219:

```
AACCAGCCAG GAGCCACCCA TCCTCCAGCA CACTGAGCAG CAAGCTGGAC ACACGGCACA   60

CTGATCCAA ATG GGT AAG GGG ATG GTG GCG ATG CTC ATT CTG GGT CTG CTA  111
          Met Gly Lys Gly Met Val Ala Met Leu Ile Leu Gly Leu Leu
              -25                 -20                 -15

CTT CTG GCG CTG CTC CTA CCC GTG CAG GTT TCT TCA TTT GTT CCT TTA    159
Leu Leu Ala Leu Leu Leu Pro Val Gln Val Ser Ser Phe Val Pro Leu
        -10                 -5                   1

ACC AGT ATG CCG GAA GCT ACT GCA GCC GAA ACC ACA AAG CCC TCC AAT    207
```

```
Thr Ser Met Pro Glu Ala Thr Ala Ala Glu Thr Thr Lys Pro Ser Asn
  5                 10                  15                  20

GGG                                                                  210
Gly
```

(2) INFORMATION FOR SEQ ID NO: 220:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 189 base pairs
(B) TYPE: NUCLEIC ACID
(C) STRANDEDNESS: DOUBLE
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Testis

(ix) FEATURE:
(A) NAME/KEY: other
(B) LOCATION: 2..170
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 98
region 4..172
id H56777
est

(ix) FEATURE:
(A) NAME/KEY: sig_peptide
(B) LOCATION: 25..87
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 9.5
seq LLVLFVLLANVQG/PG

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 220:

```
AAGAAAGGCT GGCCTCTCTT CAAC ATG GGA TCT TCT GGA CTT TTG AGC CTC       51
                           Met Gly Ser Ser Gly Leu Leu Ser Leu
                               -20                 -15

CTG GTG CTA TTC GTC CTC TTA GCG AAT GTC CAG GGA CCT GGT CTG ACT      99
Leu Val Leu Phe Val Leu Leu Ala Asn Val Gln Gly Pro Gly Leu Thr
        -10                  -5                   1

GAT TGG TTA TTT CCC AGG AGA TGT CCC AAA ATC AGA GAA GAA TGT GAA     147
Asp Trp Leu Phe Pro Arg Arg Cys Pro Lys Ile Arg Glu Glu Cys Glu
  5                 10                  15                  20

TTC CAA GAA AGG GAT GTG TGT ACA AAG GAC AGA CAA TGC CGA             189
Phe Gln Glu Arg Asp Val Cys Thr Lys Asp Arg Gln Cys Arg
                 25                  30
```

(2) INFORMATION FOR SEQ ID NO: 221:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 323 base pairs
(B) TYPE: NUCLEIC ACID
(C) STRANDEDNESS: DOUBLE
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Ovary

(ix) FEATURE:
(A) NAME/KEY: other
(B) LOCATION: 52..258
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 95
region 10..216
id R60167
est

(ix) FEATURE:
(A) NAME/KEY: other
(B) LOCATION: 235..319
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 98
region 194..278
id R60167
est

(ix) FEATURE:
(A) NAME/KEY: other
(B) LOCATION: 143..258
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 92
region 90..205
id R17888
est

(ix) FEATURE:
(A) NAME/KEY: other
(B) LOCATION: 55..145
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 98
region 1..91
id R17888
est

(ix) FEATURE:
(A) NAME/KEY: other
(B) LOCATION: 235..316
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 98
region 183..264
id R17888
est

(ix) FEATURE:
(A) NAME/KEY: other
(B) LOCATION: 141..258
(C) IDENTIFICATION METHOD: blastn

(D) OTHER INFORMATION: identity 91
region 85..202
id N40052
est

(ix) FEATURE:
(A) NAME/KEY: other
(B) LOCATION: 56..144
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 97
region 1..89
id N40052
est

(ix) FEATURE:
(A) NAME/KEY: other
(B) LOCATION: 235..319
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 97
region 180..264
id N40052
est

(ix) FEATURE:
(A) NAME/KEY: other
(B) LOCATION: 58..257
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 98
region 1..200
id AA039912
est

(ix) FEATURE:
(A) NAME/KEY: other
(B) LOCATION: 248..319
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 98
region 190..261
id AA039912
est

(ix) FEATURE:
(A) NAME/KEY: other
(B) LOCATION: 50..319
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 97
region 1..270
id R54127
est

(ix) FEATURE:
(A) NAME/KEY: sig_peptide
(B) LOCATION: 90..194
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 8.3
seq NLLLLHCVSRSHS/QN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 221:

AGGAAAGGCC TGACCACGCA GTTCTTGGGT CTGTGCTGCT GGCCTGGGGT TGTGGTTGAG 60

```
GCCGTGTCTC CGCTCCTGTG CCCGGGAAG ATG GTG CTA GGT GGT TGC CCG GTT     113
                                Met Val Leu Gly Gly Cys Pro Val
                                -35                 -30

AGT TAC TTA CTT CTG TGC GGC CAG GCG GCT TTG CTG CTG GGG AAT TTA     161
Ser Tyr Leu Leu Leu Cys Gly Gln Ala Ala Leu Leu Leu Gly Asn Leu
        -25                 -20                 -15

CTT CTG CTG CAT TGT GTG TCT CGG AGC CAC TCG CAA AAT GCG ACC GCT     209
Leu Leu Leu His Cys Val Ser Arg Ser His Ser Gln Asn Ala Thr Ala
    -10                 -5                   1               5

GAG CCT GAG CTC ACA TCC GCT GGC GCC CCC AGC CGG AGG GCC CCG GGG     257
Glu Pro Glu Leu Thr Ser Ala Gly Ala Pro Ser Arg Arg Ala Pro Gly
                 10                  15                  20

GTG CTG CGA GCT GGG AAT ATG GCG ACC CCC ACT CTC CGG TCA TCC TCT     305
Val Leu Arg Ala Gly Asn Met Ala Thr Pro Thr Leu Arg Ser Ser Ser
            25                  30                  35

GCT CTT ACC TAC CTT GGG                                             323
Ala Leu Thr Tyr Leu Gly
        40
```

(2) INFORMATION FOR SEQ ID NO: 222:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 165 base pairs
(B) TYPE: NUCLEIC ACID
(C) STRANDEDNESS: DOUBLE
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Testis

(ix) FEATURE:
(A) NAME/KEY: other
(B) LOCATION: 31..143
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 99
region 271..383
id W16767
est

(ix) FEATURE:
(A) NAME/KEY: sig_peptide
(B) LOCATION: 34..87
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 8.3
seq LLSLSSLPLVLLG/WE

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 222:

```
AACCAGACTT CTGACCCCTT GGGCAACAGC CAG ATG GAG ACT GGT CGC CTT TTG     54
```

```
                                      Met Glu Thr Gly Arg Leu Leu
                                                  -15

AGC CTC AGC TCT CTT CCT CTT GTT CTC CTA GGG TGG GAG TAC AGC AGC     102
Ser Leu Ser Ser Leu Pro Leu Val Leu Leu Gly Trp Glu Tyr Ser Ser
    -10                 -5                   1                5

CAA ACG CTG AAC TTA GTC CCA TCC ACT TCC ATC TTA TCC TTT GTG CCC     150
Gln Thr Leu Asn Leu Val Pro Ser Thr Ser Ile Leu Ser Phe Val Pro
                10                  15                   20

TTC ATC CCC CGA GTG                                                 165
Phe Ile Pro Arg Val
             25
```

(2) INFORMATION FOR SEQ ID NO: 223:

```
     (i) SEQUENCE CHARACTERISTICS:
           (A) LENGTH: 201 base pairs
           (B) TYPE: NUCLEIC ACID
           (C) STRANDEDNESS: DOUBLE
           (D) TOPOLOGY: LINEAR

    (ii) MOLECULE TYPE: CDNA

    (vi) ORIGINAL SOURCE:
           (A) ORGANISM: Homo Sapiens
           (F) TISSUE TYPE: Ovary

    (ix) FEATURE:
           (A) NAME/KEY: other
           (B) LOCATION: 24..203
           (C) IDENTIFICATION METHOD: blastn
           (D) OTHER INFORMATION:  identity 97
                                   region 1..180
                                   id HSC1PF091
                                   est

    (ix) FEATURE:
           (A) NAME/KEY: other
           (B) LOCATION: 114..203
           (C) IDENTIFICATION METHOD: blastn
           (D) OTHER INFORMATION:  identity 98
                                   region 78..167
                                   id H03709
                                   est

    (ix) FEATURE:
           (A) NAME/KEY: other
           (B) LOCATION: 35..107
           (C) IDENTIFICATION METHOD: blastn
           (D) OTHER INFORMATION:  identity 98
                                   region 1..73
                                   id H03709
                                   est

    (ix) FEATURE:
           (A) NAME/KEY: sig_peptide
           (B) LOCATION: 25..81
```

```
        (C) IDENTIFICATION METHOD: Von Heijne matrix
        (D) OTHER INFORMATION:  score 8.2
                                seq QVLALVLVAALWG/GT

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 223:


AAAGTAGAAG ACAGCGGCGT TGCC ATG GCG GCG TCT CTG GGG CAG GTG TTG        51
                           Met Ala Ala Ser Leu Gly Gln Val Leu
                                           -15

GCT CTG GTG CTG GTG GCC GCT CTG TGG GGT GGC ACG CAG CCG CTG CTG       99
Ala Leu Val Leu Val Ala Ala Leu Trp Gly Gly Thr Gln Pro Leu Leu
-10                 -5                   1                   5

AAG CGG GCC TCC GCC GGC CTG CAG CGG GTT CAT GAG CCG ACC TGG GCC      147
Lys Arg Ala Ser Ala Gly Leu Gln Arg Val His Glu Pro Thr Trp Ala
            10                  15                  20

CAG CAG TTG CTA CAG GAG ATG AAG ACC CTC TTC TTG AAT ACT GAG TAC      195
Gln Gln Leu Leu Gln Glu Met Lys Thr Leu Phe Leu Asn Thr Glu Tyr
        25                  30                  35

CTG ATG                                                              201
Leu Met
     40


(2) INFORMATION FOR SEQ ID NO: 224:

     (i) SEQUENCE CHARACTERISTICS:
          (A) LENGTH: 462 base pairs
          (B) TYPE: NUCLEIC ACID
          (C) STRANDEDNESS: DOUBLE
          (D) TOPOLOGY: LINEAR

    (ii) MOLECULE TYPE: CDNA

    (vi) ORIGINAL SOURCE:
          (A) ORGANISM: Homo Sapiens
          (F) TISSUE TYPE: Spleen

    (ix) FEATURE:
          (A) NAME/KEY: other
          (B) LOCATION: 6..119
          (C) IDENTIFICATION METHOD: blastn
          (D) OTHER INFORMATION:  identity 92
                                  region 1..114
                                  id N83684
                                  est

    (ix) FEATURE:
          (A) NAME/KEY: other
          (B) LOCATION: 147..241
          (C) IDENTIFICATION METHOD: blastn
          (D) OTHER INFORMATION:  identity 97
                                  region 112..206
                                  id N83684
                                  est
```

```
(ix) FEATURE:
     (A) NAME/KEY: other
     (B) LOCATION: 283..323
     (C) IDENTIFICATION METHOD: blastn
     (D) OTHER INFORMATION:  identity 100
                             region 245..285
                             id N83684
                             est

(ix) FEATURE:
     (A) NAME/KEY: other
     (B) LOCATION: 327..361
     (C) IDENTIFICATION METHOD: blastn
     (D) OTHER INFORMATION:  identity 97
                             region 287..321
                             id N83684
                             est

(ix) FEATURE:
     (A) NAME/KEY: other
     (B) LOCATION: 150..299
     (C) IDENTIFICATION METHOD: blastn
     (D) OTHER INFORMATION:  identity 98
                             region 177..326
                             id H94179
                             est

(ix) FEATURE:
     (A) NAME/KEY: other
     (B) LOCATION: 23..109
     (C) IDENTIFICATION METHOD: blastn
     (D) OTHER INFORMATION:  identity 90
                             region 41..127
                             id H94179
                             est

(ix) FEATURE:
     (A) NAME/KEY: other
     (B) LOCATION: 17..90
     (C) IDENTIFICATION METHOD: blastn
     (D) OTHER INFORMATION:  identity 100
                             region 1..74
                             id AA093069
                             est

(ix) FEATURE:
     (A) NAME/KEY: other
     (B) LOCATION: 144..194
     (C) IDENTIFICATION METHOD: blastn
     (D) OTHER INFORMATION:  identity 90
                             region 123..173
                             id AA093069
                             est

(ix) FEATURE:
     (A) NAME/KEY: other
     (B) LOCATION: 150..249
     (C) IDENTIFICATION METHOD: blastn
     (D) OTHER INFORMATION:  identity 97
                             region 198..297
                             id T67190
```

est

(ix) FEATURE:
(A) NAME/KEY: sig_peptide
(B) LOCATION: 211..387
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 8.1
seq FLLGISNLSQVRA/SN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 224:

```
AGCGGGTGTT GAGAGCGGTG TGGTAGGTGT TGTAGCCGCT ATGGTGAAGT TCGCTTTGTA   60

GCGGCCCCGG CTAGAGAGTT GGCCTGTTCC CTGCCTTTGT GACCCGGAGG AGCTTTTGGG  120

GTGCGTCAAG CCCCTGGCCT GAGGCAGCGA DCTGGTTTGT GGCCTGTTTG ATTCCTGTCA  180

GAGGTTTGCT GACCCAAGAC AGTATCGAAA ATG CAT ATT AAG TCA ATT ATT CTA   234
                                 Met His Ile Lys Ser Ile Ile Leu
                                                 -55

GAG GGA TTC AAG TCC TAT GCT CAG AGG ACC GAA GTC AAT GGT TTT GAC   282
Glu Gly Phe Lys Ser Tyr Ala Gln Arg Thr Glu Val Asn Gly Phe Asp
    -50                 -45                 -40

CCC CTC TTC AAT GCT ATC ACT GGC TTA AAT GGT AGT GGG AAA TCC AAC   330
Pro Leu Phe Asn Ala Ile Thr Gly Leu Asn Gly Ser Gly Lys Ser Asn
-35                 -30                 -25                 -20

ATA TTG GAC TCC ATC TGC TTT TTG CTG GGC ATC TCC AAC CTG TCT CAG   378
Ile Leu Asp Ser Ile Cys Phe Leu Leu Gly Ile Ser Asn Leu Ser Gln
                -15                 -10                 -5

GTT CGG GCT TCT AAT TTA CAA GAT TTA GTT TAC AAA AAT GGG CAG GCT   426
Val Arg Ala Ser Asn Leu Gln Asp Leu Val Tyr Lys Asn Gly Gln Ala
             1               5                  10

GGT ATT ACC AAA GCC TCT GTG TCA ATC AMT TTT GAT                   462
Gly Ile Thr Lys Ala Ser Val Ser Ile Xaa Phe Asp
    15                  20                  25
```

(2) INFORMATION FOR SEQ ID NO: 225:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 473 base pairs
(B) TYPE: NUCLEIC ACID
(C) STRANDEDNESS: DOUBLE
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Testis

(ix) FEATURE:
(A) NAME/KEY: other
(B) LOCATION: 280..404

```
        (C) IDENTIFICATION METHOD: blastn
        (D) OTHER INFORMATION:  identity 97
                                region 165..289
                                id N46466
                                est

  (ix) FEATURE:
        (A) NAME/KEY: other
        (B) LOCATION: 76..168
        (C) IDENTIFICATION METHOD: blastn
        (D) OTHER INFORMATION:  identity 98
                                region 52..144
                                id N46466
                                est

  (ix) FEATURE:
        (A) NAME/KEY: other
        (B) LOCATION: 405..469
        (C) IDENTIFICATION METHOD: blastn
        (D) OTHER INFORMATION:  identity 96
                                region 289..353
                                id N46466
                                est

  (ix) FEATURE:
        (A) NAME/KEY: other
        (B) LOCATION: complement(405..469)
        (C) IDENTIFICATION METHOD: blastn
        (D) OTHER INFORMATION:  identity 96
                                region 180..244
                                id W86648
                                est

  (ix) FEATURE:
        (A) NAME/KEY: other
        (B) LOCATION: complement(343..404)
        (C) IDENTIFICATION METHOD: blastn
        (D) OTHER INFORMATION:  identity 95
                                region 244..305
                                id W86648
                                est

  (ix) FEATURE:
        (A) NAME/KEY: other
        (B) LOCATION: complement(297..347)
        (C) IDENTIFICATION METHOD: blastn
        (D) OTHER INFORMATION:  identity 100
                                region 302..352
                                id W86648
                                est

  (ix) FEATURE:
        (A) NAME/KEY: other
        (B) LOCATION: 273..358
        (C) IDENTIFICATION METHOD: blastn
        (D) OTHER INFORMATION:  identity 96
                                region 38..123
                                id W86523
                                est

  (ix) FEATURE:
```

(A) NAME/KEY: other
(B) LOCATION: 357..404
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 91
region 123..170
id W86523
est

(ix) FEATURE:
(A) NAME/KEY: other
(B) LOCATION: 405..436
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 96
region 170..201
id W86523
est

(ix) FEATURE:
(A) NAME/KEY: sig_peptide
(B) LOCATION: 285..341
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 8
seq WGFLCVLFTAVHP/AP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 225:

```
AAGMSAGGGG AAGCGCCCAA GGTCACACAG CTGGGATGTG GCAGAGCTGG GGTTCCAGCT    60

CCTGTTCCCA TTGCTGGACA GCTGCCACAT CTGGCACCCA ATTTAGGACC CCGCGGGGAG   120

GCCCAAGCCC CGGGGGTGGC GGGGGATCCT AGAGGAAAGT GGCAAGGCCA GGACCCTGGA   180

GCAGAGCCAG AGTAGAAAAC TGAGGCTCTG AGAGATGAAG CTACTTGCCA AGGTCACGCA   240

GCACAGTCAC ATCCTACTGA ACATCATCCT GTTCTCTGGG TGGA ATG TCA CCA TCG    296
                                                 Met Ser Pro Ser

CCC AGG TGG GGA TTT TTG TGT GTT TTG TTC ACT GCT GTA CAC CCA GCC     344
Pro Arg Trp Gly Phe Leu Cys Val Leu Phe Thr Ala Val His Pro Ala
-15                 -10                  -5                   1

CCC AGC ACA GCG CCT GTC CAG GAC AAG TGC CCA GTA AAC ACT TGG GAA     392
Pro Ser Thr Ala Pro Val Gln Asp Lys Cys Pro Val Asn Thr Trp Glu
              5                  10                  15

GCA ATG CAB VMG GTC CTC CCA GCA GCT CCT GCA AAC AGA CCC CCG ACC     440
Ala Met Xaa Xaa Val Leu Pro Ala Ala Pro Ala Asn Arg Pro Pro Thr
         20                  25                  30

CAA GCC TTT CCT TCT GCM TCC ACT GCC ACA GGG                         473
Gln Ala Phe Pro Ser Ala Ser Thr Ala Thr Gly
     35                  40
```

(2) INFORMATION FOR SEQ ID NO: 226:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 250 base pairs
(B) TYPE: NUCLEIC ACID

(C) STRANDEDNESS: DOUBLE
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Testis

(ix) FEATURE:
(A) NAME/KEY: other
(B) LOCATION: complement(1..189)
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 99
region 1..189
id R47502
est

(ix) FEATURE:
(A) NAME/KEY: sig_peptide
(B) LOCATION: 56..127
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 7.8
seq FLLCLCIAYWAST/AV

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 226:

```
AATTCTCATC GCGATTGCAC TCATCAAAGA AGCCAGCAGG GCTGTGGGAT ACGTC ATG     58
                                                             Met

TGC TCC TTG CTC TAC CCA CTG GTC ACC TTC TTC TTG CTG TGC CTC TGC     106
Cys Ser Leu Leu Tyr Pro Leu Val Thr Phe Phe Leu Leu Cys Leu Cys
        -20                 -15                 -10

ATC GCC TAC TGG GCC AGC ACT GCT GTC TTC CTG TCC ACT TCC AAC GAA     154
Ile Ala Tyr Trp Ala Ser Thr Ala Val Phe Leu Ser Thr Ser Asn Glu
     -5                   1               5

GCG GTC TAT AAG ATC TTT GAT GAC AGC CCC TGC CCA TTT ACT GCG AAA     202
Ala Val Tyr Lys Ile Phe Asp Asp Ser Pro Cys Pro Phe Thr Ala Lys
 10                  15                  20                  25

ACC TGC AAC CCA GAG ACC TTC CCC TCC TCC AAT GAG CCC CGC CAT GGG     250
Thr Cys Asn Pro Glu Thr Phe Pro Ser Ser Asn Glu Pro Arg His Gly
                30                  35                  40
```

(2) INFORMATION FOR SEQ ID NO: 227:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 176 base pairs
(B) TYPE: NUCLEIC ACID
(C) STRANDEDNESS: DOUBLE
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Homo Sapiens

(F) TISSUE TYPE: Spleen

(ix) FEATURE:
(A) NAME/KEY: other
(B) LOCATION: complement(51..119)
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 100
region 404..472
id AA099571
est

(ix) FEATURE:
(A) NAME/KEY: other
(B) LOCATION: complement(118..174)
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 100
region 348..404
id AA099571
est

(ix) FEATURE:
(A) NAME/KEY: sig_peptide
(B) LOCATION: 24..71
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 7.6
seq FLFFSTLFSSIFT/EA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 227:

```
AAAAGCTTTG GAGATATTGA ATC ATG TTA CCA TTT CTG TTT TTT TCC ACC CTG    53
                          Met Leu Pro Phe Leu Phe Phe Ser Thr Leu
                              -15                 -10

TTT TCT TCC ATA TTT ACT GAA GCT CAG AAG CAG TAT TGG GTC TGC AAC     101
Phe Ser Ser Ile Phe Thr Glu Ala Gln Lys Gln Tyr Trp Val Cys Asn
     -5                  1               5                  10

TCA TCC GAT GCA AGT ATT CAT ACA CCT ACT GTG ATA AAA TGC AAT ACC     149
Ser Ser Asp Ala Ser Ile His Thr Pro Thr Val Ile Lys Cys Asn Thr
                 15                  20                  25

CAA TTT CAA TTA ATG TTA ACC CCT GGG                                 176
Gln Phe Gln Leu Met Leu Thr Pro Gly
             30                  35
```

(2) INFORMATION FOR SEQ ID NO: 228:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 383 base pairs
(B) TYPE: NUCLEIC ACID
(C) STRANDEDNESS: DOUBLE
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Testis

(ix) FEATURE:
(A) NAME/KEY: other
(B) LOCATION: 103..248
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 97
region 12..157
id W56658
est

(ix) FEATURE:
(A) NAME/KEY: other
(B) LOCATION: 255..385
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 99
region 164..294
id W56658
est

(ix) FEATURE:
(A) NAME/KEY: other
(B) LOCATION: 18..248
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 96
region 1..231
id AA127477
est

(ix) FEATURE:
(A) NAME/KEY: other
(B) LOCATION: 123..385
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 98
region 1..263
id N40410
est

(ix) FEATURE:
(A) NAME/KEY: other
(B) LOCATION: complement(340..371)
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 93
region 354..385
id R93185
est

(ix) FEATURE:
(A) NAME/KEY: sig_peptide
(B) LOCATION: 126..167
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 7.5
seq VALNLILVPCCAA/WC

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 228:

AATTGTATGT TACGATGTTG TATTGATTTT TAAGAAAGTA ATTKRATTTG TAAAACTTCT 60

GCTCGTTTAC ACTGCACATT GAATACAGGT AACTAATTGG WWGGAGAGGG GAGGTCACTC 120

TTTTG ATG GTG GCC CTG AAC CTC ATT CTG GTT CCC TGC TGC GCT GCT TGG 170

```
        Met Val Ala Leu Asn Leu Ile Leu Val Pro Cys Cys Ala Ala Trp
                        -10                     -5                    1

TGT GAC CCA CGG AGG ATC CAC TCC CAG GAT GAC GTG CTC CGT AGC TCT    218
Cys Asp Pro Arg Arg Ile His Ser Gln Asp Asp Val Leu Arg Ser Ser
            5                   10                  15

GCT GCT GAT ACT GGG TCT GCG ATG CAG CGG CGT GAG GCC TGG GCT GGT    266
Ala Ala Asp Thr Gly Ser Ala Met Gln Arg Arg Glu Ala Trp Ala Gly
        20                  25                  30

TGG AGA AGG TCA CAA CCC TTC TCT GTT GGT CTG CCT TCT GCT GAA AGA    314
Trp Arg Arg Ser Gln Pro Phe Ser Val Gly Leu Pro Ser Ala Glu Arg
    35                  40                  45

CTC GAG AAC CAA CCA GGG AAG CTG TCC TGG AGG TCC CTG GTC GGA GAG    362
Leu Glu Asn Gln Pro Gly Lys Leu Ser Trp Arg Ser Leu Val Gly Glu
 50                  55                  60                  65

GGA CAT AGA ATC TGT GAC CTC                                        383
Gly His Arg Ile Cys Asp Leu
                70
```

(2) INFORMATION FOR SEQ ID NO: 229:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 372 base pairs
(B) TYPE: NUCLEIC ACID
(C) STRANDEDNESS: DOUBLE
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Testis

(ix) FEATURE:
(A) NAME/KEY: other
(B) LOCATION: 83..291
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 97
region 69..277
id AA149265
est

(ix) FEATURE:
(A) NAME/KEY: other
(B) LOCATION: 12..57
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 95
region 1..46
id AA149265
est

(ix) FEATURE:
(A) NAME/KEY: other
(B) LOCATION: 321..351
(C) IDENTIFICATION METHOD: blastn

```
        (D) OTHER INFORMATION:  identity 93
                                region 310..340
                                id AA149265
                                est

    (ix) FEATURE:
        (A) NAME/KEY: other
        (B) LOCATION: 81..372
        (C) IDENTIFICATION METHOD: blastn
        (D) OTHER INFORMATION:  identity 98
                                region 53..344
                                id W39570
                                est

    (ix) FEATURE:
        (A) NAME/KEY: other
        (B) LOCATION: 27..57
        (C) IDENTIFICATION METHOD: blastn
        (D) OTHER INFORMATION:  identity 93
                                region 2..32
                                id W39570
                                est

    (ix) FEATURE:
        (A) NAME/KEY: other
        (B) LOCATION: 81..372
        (C) IDENTIFICATION METHOD: blastn
        (D) OTHER INFORMATION:  identity 98
                                region 55..346
                                id N41332
                                est

    (ix) FEATURE:
        (A) NAME/KEY: other
        (B) LOCATION: 24..57
        (C) IDENTIFICATION METHOD: blastn
        (D) OTHER INFORMATION:  identity 94
                                region 1..34
                                id N41332
                                est

    (ix) FEATURE:
        (A) NAME/KEY: sig_peptide
        (B) LOCATION: 10..168
        (C) IDENTIFICATION METHOD: Von Heijne matrix
        (D) OTHER INFORMATION:  score 7.1
                                seq IAVGLGVAALAFA/GR

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 229:

AGCCTTGCC ATG GCT GCC CGT GGT GTC ATC GCT CCA GTT GGC GAG AGT YTG    51
          Met Ala Ala Arg Gly Val Ile Ala Pro Val Gly Glu Ser Leu
                      -50                 -45                 -40

CGC TAC GCT GAG TAC TTG CAG CCC TCG GCC AAA CGG CCA GAC GCC GAC      99
Arg Tyr Ala Glu Tyr Leu Gln Pro Ser Ala Lys Arg Pro Asp Ala Asp
            -35                 -30                 -25

GTC GAC CAG CAG AGA CTG GTA AGA AGT TTG ATA GCT GTA GGA CTG GGT     147
Val Asp Gln Gln Arg Leu Val Arg Ser Leu Ile Ala Val Gly Leu Gly
```

```
            -20                 -15                 -10

GTT GCA GCT CTT GCA TTT GCA GGT CGC TAC GCA TTT CGG ATC TGG AAA     195
Val Ala Ala Leu Ala Phe Ala Gly Arg Tyr Ala Phe Arg Ile Trp Lys
         -5                   1               5

CCT CTA GAA CAA GTT ATC ACA GAA ACT GCA AAG AAG ATT TCA ACT CCT     243
Pro Leu Glu Gln Val Ile Thr Glu Thr Ala Lys Lys Ile Ser Thr Pro
 10                  15                  20                  25

AGC TTT TCA TCC TAC TAT AAA GGA GGA TTT GAA CAG AAA ATG AGT AGG     291
Ser Phe Ser Ser Tyr Tyr Lys Gly Gly Phe Glu Gln Lys Met Ser Arg
                 30                  35                  40

CGA GAA GCT GGT CTT ATT TTA GGT GTA AGC CCA TCT GCT GGC AAG GCT     339
Arg Glu Ala Gly Leu Ile Leu Gly Val Ser Pro Ser Ala Gly Lys Ala
             45                  50                  55

AAG ATT AGA ACA GCT CAT AGG AGA GTC ATG ATT                         372
Lys Ile Arg Thr Ala His Arg Arg Val Met Ile
         60                  65
```

(2) INFORMATION FOR SEQ ID NO: 230:

(i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 254 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:
- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Testis

(ix) FEATURE:
- (A) NAME/KEY: other
- (B) LOCATION: 3..249
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100
  region 1..247
  id HUM225B05B
  est

(ix) FEATURE:
- (A) NAME/KEY: other
- (B) LOCATION: 3..135
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 96
  region 1..133
  id HUM224A06B
  est

(ix) FEATURE:
- (A) NAME/KEY: other
- (B) LOCATION: 131..183
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 92

region 128..180
id HUM224A06B
est

(ix) FEATURE:
(A) NAME/KEY: other
(B) LOCATION: 182..223
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 95
region 178..219
id HUM224A06B
est

(ix) FEATURE:
(A) NAME/KEY: other
(B) LOCATION: complement(2..165)
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 100
region 1..164
id R81598
est

(ix) FEATURE:
(A) NAME/KEY: sig_peptide
(B) LOCATION: 126..170
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 7.1
seq KLKLLSLLRPSLC/IP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 230:

```
AACACAAGCA AAACTTTTAA ATATTTGAAT TGACAGTTAC ATGTTTCATA ACTTTGTATG    60

TCTATTGGTT GTGCAGGTGT AATTTTTTCC CTTTTTGATT AGGGTTACAA AATTTAGAGA   120

CCAGT ATG ATT AAG TTG AAG CTC CTT AGC CTC CTT CGA CCT AGT CTC TGC  170
      Met Ile Lys Leu Lys Leu Leu Ser Leu Leu Arg Pro Ser Leu Cys
      -15                 -10                     -5

ATA CCT CAA CTT TTA CGT ACC AAT GCT ACT CTG CTG TTC ACA ATT GCC      218
Ile Pro Gln Leu Leu Arg Thr Asn Ala Thr Leu Leu Phe Thr Ile Ala
  1               5                  10                  15

TCA TGT AAT CTG CAG ATT CCT GCC TCC CCA CGA CGG                      254
Ser Cys Asn Leu Gln Ile Pro Ala Ser Pro Arg Arg
             20                  25
```

(2) INFORMATION FOR SEQ ID NO: 231:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 143 base pairs
(B) TYPE: NUCLEIC ACID
(C) STRANDEDNESS: DOUBLE
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Spleen

(ix) FEATURE:
(A) NAME/KEY: other
(B) LOCATION: 100..144
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 97
region 95..139
id T95183
est

(ix) FEATURE:
(A) NAME/KEY: other
(B) LOCATION: 56..105
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 90
region 52..101
id T95183
est

(ix) FEATURE:
(A) NAME/KEY: other
(B) LOCATION: 100..144
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 97
region 101..145
id R48890
est

(ix) FEATURE:
(A) NAME/KEY: other
(B) LOCATION: 73..105
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 90
region 75..107
id R48890
est

(ix) FEATURE:
(A) NAME/KEY: sig_peptide
(B) LOCATION: 18..77
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 6.5
seq GLCVLQLTTAVTS/AF

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 231:

```
AACCTTCACA GTGTGAG ATG CCT AGT GTG AAC AGT GCT GGA TTA TGT GTC        50
                   Met Pro Ser Val Asn Ser Ala Gly Leu Cys Val
                   -20                 -15                 -10

TTG CAG TTG ACA ACG GCA GTR ACC AGT GCC TTT TTA CTA GCA AAA GTG       98
Leu Gln Leu Thr Thr Ala Val Thr Ser Ala Phe Leu Leu Ala Lys Val
                -5                   1               5

AAT CCT TTC GAA RCT TTT CTC TCA AGG GGC TTT TGG CTA TGT GCT          143
Asn Pro Phe Glu Xaa Phe Leu Ser Arg Gly Phe Trp Leu Cys Ala
        10                  15                  20
```

(2) INFORMATION FOR SEQ ID NO: 232:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 178 base pairs
(B) TYPE: NUCLEIC ACID
(C) STRANDEDNESS: DOUBLE
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Ovary

(ix) FEATURE:
(A) NAME/KEY: other
(B) LOCATION: complement(118..179)
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 90
region 296..357
id T92237
est

(ix) FEATURE:
(A) NAME/KEY: sig_peptide
(B) LOCATION: 86..145
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 6.4
seq ALFLLVSXYMIRS/GT

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 232:

```
ACAGAGAMTA ACGATGTTTC TTATTTGAAT CCAGTGAAAG TACTCATGCT TTGTGTTCTT    60

GGGAATTACT GAGTTCAAAT TCCTA ATG ATG CTT GGG TTA CAC TTT GCT TTG     112
                            Met Met Leu Gly Leu His Phe Ala Leu
                            -20                 -15

TTT CTC CTA GTT TCT KTW TAT ATG ATC CGG AGT GGC ACT GGT AAT AAG     160
Phe Leu Leu Val Ser Xaa Tyr Met Ile Arg Ser Gly Thr Gly Asn Lys
    -10                 -5                  1               5

ATT GAA GAA GGT GGG CGG                                             178
Ile Glu Glu Gly Gly Arg
                10
```

(2) INFORMATION FOR SEQ ID NO: 233:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 181 base pairs
(B) TYPE: NUCLEIC ACID
(C) STRANDEDNESS: DOUBLE
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

```
(vi) ORIGINAL SOURCE:
      (A) ORGANISM: Homo Sapiens
      (F) TISSUE TYPE: Testis

(ix) FEATURE:
      (A) NAME/KEY: other
      (B) LOCATION: 32..178
      (C) IDENTIFICATION METHOD: blastn
      (D) OTHER INFORMATION:  identity 97
                              region 2..148
                              id H42383
                              est

(ix) FEATURE:
      (A) NAME/KEY: other
      (B) LOCATION: 35..178
      (C) IDENTIFICATION METHOD: blastn
      (D) OTHER INFORMATION:  identity 93
                              region 5..148
                              id R67703
                              est

(ix) FEATURE:
      (A) NAME/KEY: other
      (B) LOCATION: 145..178
      (C) IDENTIFICATION METHOD: blastn
      (D) OTHER INFORMATION:  identity 91
                              region 29..62
                              id W90193
                              est

(ix) FEATURE:
      (A) NAME/KEY: sig_peptide
      (B) LOCATION: 38..76
      (C) IDENTIFICATION METHOD: Von Heijne matrix
      (D) OTHER INFORMATION:  score 6.4
                              seq MALLLSVLRVLLG/GF

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 233:

ATCGGCGGGG CCAACCCACG GTGGGGGGAG CGCGGCC ATG GCG CTC CTG CTT TCG     55
                                        Met Ala Leu Leu Leu Ser
                                                        -10

GTG CTG CGT GTA CTG CTG GGC GGC TTC TTC GCG CTC GTG GGG TTG GCC     103
Val Leu Arg Val Leu Leu Gly Gly Phe Phe Ala Leu Val Gly Leu Ala
        -5                  1               5

AAG CTC TCG GAG GAG ATC TCG GCT CCA GTD TCG GAG CGG ATG AAT GCC     151
Lys Leu Ser Glu Glu Ile Ser Ala Pro Val Ser Glu Arg Met Asn Ala
 10                 15                  20                  25

CTG TTC GTR MAG TTT GCT GAG GTG CTC GGG                             181
Leu Phe Val Xaa Phe Ala Glu Val Leu Gly
                30                  35


(2) INFORMATION FOR SEQ ID NO: 234:
```

```
      (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 156 base pairs
            (B) TYPE: NUCLEIC ACID
            (C) STRANDEDNESS: DOUBLE
            (D) TOPOLOGY: LINEAR

      (ii) MOLECULE TYPE: CDNA

      (vi) ORIGINAL SOURCE:
            (A) ORGANISM: Homo Sapiens
            (F) TISSUE TYPE: Ovary

      (ix) FEATURE:
            (A) NAME/KEY: other
            (B) LOCATION: 100..154
            (C) IDENTIFICATION METHOD: blastn
            (D) OTHER INFORMATION:  identity 94
                                    region 111..165
                                    id HSC2EB021
                                    est

      (ix) FEATURE:
            (A) NAME/KEY: other
            (B) LOCATION: 100..154
            (C) IDENTIFICATION METHOD: blastn
            (D) OTHER INFORMATION:  identity 94
                                    region 37..91
                                    id T31104
                                    est

      (ix) FEATURE:
            (A) NAME/KEY: sig_peptide
            (B) LOCATION: 34..84
            (C) IDENTIFICATION METHOD: Von Heijne matrix
            (D) OTHER INFORMATION:  score 6.2
                                    seq LWLSLVAWHWGEA/VL

      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 234:


ACTTTTTTCA CGCTACTCCC CCGGAGTGCT TGG ATG TTG AAG AGT CTC TGG TTG     54
                                     Met Leu Lys Ser Leu Trp Leu
                                                 -15

AGC CTT GTG GCC TGG CAC TGG GGT GAG GCT GTC CTC CTC TCC CCT CAT     102
Ser Leu Val Ala Trp His Trp Gly Glu Ala Val Leu Leu Ser Pro His
-10                 -5                   1                   5

CTC CCT GCA GCG GCA GAA TGG CCC CGG GCA GCG TGT GAT TCG GGA GGT     150
Leu Pro Ala Ala Ala Glu Trp Pro Arg Ala Ala Cys Asp Ser Gly Gly
            10                  15                  20

GAA CCG                                                             156
Glu Pro


(2) INFORMATION FOR SEQ ID NO: 235:

      (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 254 base pairs
```

(B) TYPE: NUCLEIC ACID
(C) STRANDEDNESS: DOUBLE
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Ovary

(ix) FEATURE:
(A) NAME/KEY: other
(B) LOCATION: 75..152
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 96
region 109..186
id R38459
est

(ix) FEATURE:
(A) NAME/KEY: other
(B) LOCATION: 148..200
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 100
region 183..235
id R38459
est

(ix) FEATURE:
(A) NAME/KEY: sig_peptide
(B) LOCATION: 183..227
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 6.1
seq IVTWLLXSFMSSA/EE

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 235:

```
AATACTTTGG CAGCTTCTTC ACGTCGGTCC TCTCCGCGCG CGGGTAGGAA CCGTCCACGG   60

CCTTAAAGAA GCCTCCTCAC CAGCCATACT TCCCATTGCC TCCAGCTGTT GCACGGAGGT  120

TTCACATCAT ATTTCCAGAA GGCTCCTGGA AAGAGTGAAT ATGTGTCGCA TCCAGAGAGC  180

TG ATG GGG ATT GTG ACT TGG CTG CTG TMA TCC TTC ATG TCA AGC GCA     227
   Met Gly Ile Val Thr Trp Leu Leu Xaa Ser Phe Met Ser Ser Ala
   -15                 -10                 -5

GAA GAA TCT GTG TCA GCC CGC ACA CGG                                254
Glu Glu Ser Val Ser Ala Arg Thr Arg
  1               5
```

(2) INFORMATION FOR SEQ ID NO: 236:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 190 base pairs
(B) TYPE: NUCLEIC ACID
(C) STRANDEDNESS: DOUBLE
(D) TOPOLOGY: LINEAR

```
(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:
      (A) ORGANISM: Homo Sapiens
      (F) TISSUE TYPE: Uterus

(ix) FEATURE:
      (A) NAME/KEY: other
      (B) LOCATION: 83..175
      (C) IDENTIFICATION METHOD: blastn
      (D) OTHER INFORMATION:  identity 98
                              region 80..172
                              id T62095
                              est

(ix) FEATURE:
      (A) NAME/KEY: other
      (B) LOCATION: 37..82
      (C) IDENTIFICATION METHOD: blastn
      (D) OTHER INFORMATION:  identity 93
                              region 35..80
                              id T62095
                              est

(ix) FEATURE:
      (A) NAME/KEY: other
      (B) LOCATION: 2..36
      (C) IDENTIFICATION METHOD: blastn
      (D) OTHER INFORMATION:  identity 100
                              region 1..35
                              id T62095
                              est

(ix) FEATURE:
      (A) NAME/KEY: other
      (B) LOCATION: 71..187
      (C) IDENTIFICATION METHOD: blastn
      (D) OTHER INFORMATION:  identity 99
                              region 85..201
                              id N43024
                              est

(ix) FEATURE:
      (A) NAME/KEY: other
      (B) LOCATION: 4..71
      (C) IDENTIFICATION METHOD: blastn
      (D) OTHER INFORMATION:  identity 92
                              region 17..84
                              id N43024
                              est

(ix) FEATURE:
      (A) NAME/KEY: other
      (B) LOCATION: 37..187
      (C) IDENTIFICATION METHOD: blastn
      (D) OTHER INFORMATION:  identity 98
                              region 26..176
                              id W42796
                              est
```

(ix) FEATURE:
(A) NAME/KEY: other
(B) LOCATION: 86..187
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 92
region 114..215
id AA030227
est

(ix) FEATURE:
(A) NAME/KEY: other
(B) LOCATION: 86..187
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 92
region 51..152
id AA118270
est

(ix) FEATURE:
(A) NAME/KEY: sig_peptide
(B) LOCATION: 80..163
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 6
seq IGLMFLMLGCALP/IY

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 236:

```
GTAGCGCGTC TTGGGTCTCC CGGCTGCCGC TGCTGCCGCC GCCGCCTCGG GTCGTGGAGC    60

CAGGAGCGAC GTCACCGCC ATG GCA GGC ATC AAA GCT TTG ATT AGT TTG TCC   112
                     Met Ala Gly Ile Lys Ala Leu Ile Ser Leu Ser
                                 -25                 -20

TTT GGA GGA GCA ATC GGA CTG ATG TTT TTG ATG CTT GGA TGT GCC CTT    160
Phe Gly Gly Ala Ile Gly Leu Met Phe Leu Met Leu Gly Cys Ala Leu
        -15                 -10                 -5

CCA ATA TAC AAC AAA TAC TGG CCC CCC GGG                            190
Pro Ile Tyr Asn Lys Tyr Trp Pro Pro Gly
     1              5
```

(2) INFORMATION FOR SEQ ID NO: 237:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 222 base pairs
(B) TYPE: NUCLEIC ACID
(C) STRANDEDNESS: DOUBLE
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Ovary

(ix) FEATURE:
(A) NAME/KEY: other
(B) LOCATION: complement(139..168)

(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 93
region 270..299
id W73179
est

(ix) FEATURE:
(A) NAME/KEY: other
(B) LOCATION: complement(139..168)
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 93
region 295..324
id R59325
est

(ix) FEATURE:
(A) NAME/KEY: other
(B) LOCATION: complement(113..144)
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 93
region 218..249
id R06388
est

(ix) FEATURE:
(A) NAME/KEY: sig_peptide
(B) LOCATION: 121..198
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 5.8
seq VKLVTLSVPTSLA/SS

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 237:

```
ATTTGTTCCA AAGGTTCCAA TTATTCAAGA CTGCCTTTGG CTTCTTTTAC AACATGGATG   60

ATTCTATGTT ATGGGCACTG AAACTAAAAG AAACTGTGGA AGGATTGGTA CCTTAGAGAA  120

ATG AAA AAG CAA AAA CAT CAG AAA TTA TGG TGT ATT TCT GTA AAG TTA    168
Met Lys Lys Gln Lys His Gln Lys Leu Trp Cys Ile Ser Val Lys Leu
    -25                 -20                 -15

GTG ACA CTG AGT GTG CCC ACC TCT CTT GCC TCC TCT TTA ACC TCC CCT    216
Val Thr Leu Ser Val Pro Thr Ser Leu Ala Ser Ser Leu Thr Ser Pro
-10                     -5                   1                   5

ACA GGG                                                            222
Thr Gly
```

(2) INFORMATION FOR SEQ ID NO: 238:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 417 base pairs
(B) TYPE: NUCLEIC ACID
(C) STRANDEDNESS: DOUBLE
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Testis

(ix) FEATURE:
(A) NAME/KEY: other
(B) LOCATION: complement(227..414)
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 99
region 94..281
id H53025
est

(ix) FEATURE:
(A) NAME/KEY: other
(B) LOCATION: 131..264
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 97
region 190..323
id H52956
est

(ix) FEATURE:
(A) NAME/KEY: other
(B) LOCATION: 285..318
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 94
region 347..380
id H52956
est

(ix) FEATURE:
(A) NAME/KEY: other
(B) LOCATION: 131..233
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 97
region 191..293
id H53024
est

(ix) FEATURE:
(A) NAME/KEY: other
(B) LOCATION: 227..272
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 93
region 288..333
id H53024
est

(ix) FEATURE:
(A) NAME/KEY: sig_peptide
(B) LOCATION: 184..303
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 5.8
seq VLFALFVAFLLRG/KL

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 238:

AAGTATCTCA CCATTTCTTT CTCTTTCTGA ACCACATTGG GTGCCAACAG AACTTGCTCT 60

```
CTGTTCTCTT TCAAAATTAC CAACATGGAC CCCACCCAAT TCTTCCCTTG GAACTAAGGA  120

ACGCCTGACT GATCATCTGA TACAGCAGTK CCTGAGCAGA ACAAAACAAC AAAAACAGGA  180

CAG ATG GAT GGA ATA CCC ATG TCA ATG AAG AAT GAA ATG CCC ATC TCC     228
    Met Asp Gly Ile Pro Met Ser Met Lys Asn Glu Met Pro Ile Ser
    -40                 -35                 -30

CAA CTA CTG ATG ATC ATC GCC CCC TCC TTG GGA TTT GTG CTC TTC GCA     276
Gln Leu Leu Met Ile Ile Ala Pro Ser Leu Gly Phe Val Leu Phe Ala
-25                 -20                 -15                 -10

TTG TTT GTG GCG TTT CTC CTG AGA GGG AAA CTC ATG GAA ACC TAT TGT     324
Leu Phe Val Ala Phe Leu Leu Arg Gly Lys Leu Met Glu Thr Tyr Cys
                -5                   1               5

TCG CAG AAA CAC ACA AGG CTA GAC TAC ATT GGA GAT AGT AAA AAT GTC     372
Ser Gln Lys His Thr Arg Leu Asp Tyr Ile Gly Asp Ser Lys Asn Val
         10                  15                  20

CTC AAT GAC GTG CAG CAT GGA AGG GAA GAC GAA GAC GGC CAT GGG         417
Leu Asn Asp Val Gln His Gly Arg Glu Asp Glu Asp Gly His Gly
     25                  30                  35
```

(2) INFORMATION FOR SEQ ID NO: 239:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 293 base pairs
(B) TYPE: NUCLEIC ACID
(C) STRANDEDNESS: DOUBLE
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Uterus

(ix) FEATURE:
(A) NAME/KEY: other
(B) LOCATION: 246..293
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 95
region 90..137
id H43824
est

(ix) FEATURE:
(A) NAME/KEY: other
(B) LOCATION: 246..293
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 95
region 93..140
id R73173
est

(ix) FEATURE:
(A) NAME/KEY: other
(B) LOCATION: 246..293

(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 93
region 112..159
id H26792
est

(ix) FEATURE:
(A) NAME/KEY: sig_peptide
(B) LOCATION: 21..191
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 5.7
seq LAICSCLPGPGPA/LP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 239:

```
ACCTCGCTGC TCTTCATCCC ATG GGT GGA TTT TTG CAT CTC CCT GCT CTG TCT    53
                      Met Gly Gly Phe Leu His Leu Pro Ala Leu Ser
                              -55                 -50

TCC TCC TGT CTT TGG ACA TTT CCA CCG ATG TGT GTT CGC ATC TTC TCC     101
Ser Ser Cys Leu Trp Thr Phe Pro Pro Met Cys Val Arg Ile Phe Ser
    -45                 -40                 -35

TAT GTT CCT TTA CCT ATC CTG ACC CCC AAA ACC ATA AAT CTC ATC CCC     149
Tyr Val Pro Leu Pro Ile Leu Thr Pro Lys Thr Ile Asn Leu Ile Pro
-30                 -25                 -20                 -15

GTT CTG GCC ATC TGT TCC TGT CTT CCT GGC CCC GGG CCG GCC CTT CCT     197
Val Leu Ala Ile Cys Ser Cys Leu Pro Gly Pro Gly Pro Ala Leu Pro
                -10                 -5                   1

CTT CCT GCC TTC CCG ACC CTC CTT GTG TCT TGG TAC CAC TGC CCC CCA     245
Leu Pro Ala Phe Pro Thr Leu Leu Val Ser Trp Tyr His Cys Pro Pro
         5                  10                  15

CAG AAG AAG ACA GGC ATG ATG GAC ACG GAT GAT TTC CGC GCC TGC CCG     293
Gln Lys Lys Thr Gly Met Met Asp Thr Asp Asp Phe Arg Ala Cys Pro
    20                  25                  30
```

(2) INFORMATION FOR SEQ ID NO: 240:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 416 base pairs
(B) TYPE: NUCLEIC ACID
(C) STRANDEDNESS: DOUBLE
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Testis

(ix) FEATURE:
(A) NAME/KEY: other
(B) LOCATION: 259..413
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 99

```
                              region 165..319
                              id N46466
                              est

(ix) FEATURE:
     (A) NAME/KEY: other
     (B) LOCATION: 55..147
     (C) IDENTIFICATION METHOD: blastn
     (D) OTHER INFORMATION:  identity 98
                              region 52..144
                              id N46466
                              est

(ix) FEATURE:
     (A) NAME/KEY: other
     (B) LOCATION: 252..338
     (C) IDENTIFICATION METHOD: blastn
     (D) OTHER INFORMATION:  identity 95
                              region 38..124
                              id W86523
                              est

(ix) FEATURE:
     (A) NAME/KEY: other
     (B) LOCATION: 336..413
     (C) IDENTIFICATION METHOD: blastn
     (D) OTHER INFORMATION:  identity 97
                              region 123..200
                              id W86523
                              est

(ix) FEATURE:
     (A) NAME/KEY: other
     (B) LOCATION: complement(322..413)
     (C) IDENTIFICATION METHOD: blastn
     (D) OTHER INFORMATION:  identity 98
                              region 214..305
                              id W86648
                              est

(ix) FEATURE:
     (A) NAME/KEY: other
     (B) LOCATION: complement(276..326)
     (C) IDENTIFICATION METHOD: blastn
     (D) OTHER INFORMATION:  identity 98
                              region 302..352
                              id W86648
                              est

(ix) FEATURE:
     (A) NAME/KEY: sig_peptide
     (B) LOCATION: 264..320
     (C) IDENTIFICATION METHOD: Von Heijne matrix
     (D) OTHER INFORMATION:  score 8
                              seq WGFLCVLFTAVHP/AP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 240:

GTCACACAGC TGGGATGTGG CAGAGSTGGG GTTCCAGCTC CTGYTCCCAT TGCTGGACAG    60
```

```
CTGCCACATC TGGCACCCAA TTTAGGACCC CGCGGGGAGG CCCAAGCCCC GGGGGTGGCG  120

GGGGATCCTA GAGGAAAGTG GCAAGGCCAG GACCCTGGAG CAGAGCCAGA GTAGAAAACT  180

GAGGCTCTGA GAGATGAAGC TACTTGCCAA GGTCACGCAG CACAGTCACA TCCTACTGAA  240

CATCATCCTG TTCTCTGGGT GGA ATG TCA CCA TCG CCC AGG TGG GGA TTT TTG  293
                          Met Ser Pro Ser Pro Arg Trp Gly Phe Leu
                                              -15                -10

TGT GTB TTG TTC ACT GCT GTA CAC CCA GCC CCC AGC ACA GCG CCT GTC    341
Cys Val Leu Phe Thr Ala Val His Pro Ala Pro Ser Thr Ala Pro Val
                 -5                  1               5

CAG GAC AAG TGC CCA GTA AAC ACT TGG GAA GCA ATG CAA GCG TCC TCC    389
Gln Asp Lys Cys Pro Val Asn Thr Trp Glu Ala Met Gln Ala Ser Ser
        10                  15                  20

CAG CAG CTC CTG CAA ACA GAC CCC ATG                                416
Gln Gln Leu Leu Gln Thr Asp Pro Met
    25                  30
```

(2) INFORMATION FOR SEQ ID NO: 241:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 432 base pairs
(B) TYPE: NUCLEIC ACID
(C) STRANDEDNESS: DOUBLE
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Testis

(ix) FEATURE:
(A) NAME/KEY: other
(B) LOCATION: 60..386
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 98
region 7..333
id AA035208
est

(ix) FEATURE:
(A) NAME/KEY: other
(B) LOCATION: 400..429
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 100
region 349..378
id AA035208
est

(ix) FEATURE:
(A) NAME/KEY: other
(B) LOCATION: 77..429
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 99

```
                                    region 1..353
                                    id H64963
                                    est

     (ix) FEATURE:
          (A) NAME/KEY: other
          (B) LOCATION: 50..328
          (C) IDENTIFICATION METHOD: blastn
          (D) OTHER INFORMATION:  identity 98
                                  region 10..288
                                  id R97144
                                  est

     (ix) FEATURE:
          (A) NAME/KEY: other
          (B) LOCATION: 56..393
          (C) IDENTIFICATION METHOD: blastn
          (D) OTHER INFORMATION:  identity 97
                                  region 3..340
                                  id N73170
                                  est

     (ix) FEATURE:
          (A) NAME/KEY: other
          (B) LOCATION: 14..300
          (C) IDENTIFICATION METHOD: blastn
          (D) OTHER INFORMATION:  identity 98
                                  region 2..288
                                  id H13072
                                  est

     (ix) FEATURE:
          (A) NAME/KEY: sig_peptide
          (B) LOCATION: 154..381
          (C) IDENTIFICATION METHOD: Von Heijne matrix
          (D) OTHER INFORMATION:  score 5.3
                                  seq IILASASFSPNFT/QV

     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 241:

AGTAAAAAAA CACTGGAATA AGGAAGGGCT GATGACTTTC AGAAGATGAA GGTAAGTAGA    60

AACCGTTGAT GGGACTGAGA AACCAGAGTK AAAACCTCTT TGGAGCTTCT GAGGACTCAG   120

CTGGAACCAA CGGGCACAGT TGGCAACACC ATC ATG ACA TCA CAA CCT GTT CCC    174
                                     Met Thr Ser Gln Pro Val Pro
                                         -75                 -70

AAT GAG ACC ATC ATA GTG CTC CCA TCA AAT GTC ATC AAC TTC TCC CAA     222
Asn Glu Thr Ile Ile Val Leu Pro Ser Asn Val Ile Asn Phe Ser Gln
            -65                 -60                 -55

GCA GAG AAA CCC GAA CCC ACC AAC CAG GGG CAG GAT AGC CTG AAG AAA     270
Ala Glu Lys Pro Glu Pro Thr Asn Gln Gly Gln Asp Ser Leu Lys Lys
        -50                 -45                 -40

CAT CTA CAC GCA GAR RTC AAA GTT ATT GGG ACT ATC CAG ATC TTG TGT     318
His Leu His Ala Glu Xaa Lys Val Ile Gly Thr Ile Gln Ile Leu Cys
    -35                 -30                 -25
```

```
GGC ATG ATG GTA TTG AGC TTG GGG ATC ATT TTG GCA TCT GCT TCC TTC     366
Gly Met Met Val Leu Ser Leu Gly Ile Ile Leu Ala Ser Ala Ser Phe
    -20                 -15                 -10

TCT CCA AAT TTT ACC CAA GTG ACT TCT ACA CTG TTG AAC TCT GCT TAC     414
Ser Pro Asn Phe Thr Gln Val Thr Ser Thr Leu Leu Asn Ser Ala Tyr
 -5                 1                   5                  10

CCA TTC ATA GGA CCC GGG                                             432
Pro Phe Ile Gly Pro Gly
            15
```

(2) INFORMATION FOR SEQ ID NO: 242:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 437 base pairs
(B) TYPE: NUCLEIC ACID
(C) STRANDEDNESS: DOUBLE
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Testis

(ix) FEATURE:
(A) NAME/KEY: other
(B) LOCATION: 47..230
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 100
region 158..341
id AA040813
est

(ix) FEATURE:
(A) NAME/KEY: other
(B) LOCATION: 229..395
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 99
region 341..507
id AA040813
est

(ix) FEATURE:
(A) NAME/KEY: other
(B) LOCATION: 205..429
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 98
region 111..335
id H84584
est

(ix) FEATURE:
(A) NAME/KEY: other
(B) LOCATION: complement(325..422)
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 96
region 225..322

```
                                   id AA040149
                                   est

     (ix) FEATURE:
          (A) NAME/KEY: other
          (B) LOCATION: complement(215..269)
          (C) IDENTIFICATION METHOD: blastn
          (D) OTHER INFORMATION:  identity 98
                                  region 381..435
                                  id AA040149
                                  est

     (ix) FEATURE:
          (A) NAME/KEY: other
          (B) LOCATION: complement(279..327)
          (C) IDENTIFICATION METHOD: blastn
          (D) OTHER INFORMATION:  identity 100
                                  region 321..369
                                  id AA040149
                                  est

     (ix) FEATURE:
          (A) NAME/KEY: sig_peptide
          (B) LOCATION: 57..329
          (C) IDENTIFICATION METHOD: Von Heijne matrix
          (D) OTHER INFORMATION:  score 4.8
                                  seq IILRLPWLNRSQT/VV

     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 242:

ACGCTTCGTC CTCTGCAGTC AAGACGCTGG GCGCGTCGAG GACTGGGATT TCAAAT ATG     59
                                                              Met

CGT GCA TTA GAG AAT GAT TTT TTC AAT TCT CCC CCA AGA AAA ACT GTT      107
Arg Ala Leu Glu Asn Asp Phe Phe Asn Ser Pro Pro Arg Lys Thr Val
-90                 -85                 -80                 -75

CGG TTT GGT GGA ACT GTG ACA GAA GTC TTG CTG AAG TAC AAA AAG GGT      155
Arg Phe Gly Gly Thr Val Thr Glu Val Leu Leu Lys Tyr Lys Lys Gly
            -70                 -65                 -60

GAA ACA AAT GAC TTT GAG TTG TTG AAG AAC CAG CTG TTA GAT CCA GAC      203
Glu Thr Asn Asp Phe Glu Leu Leu Lys Asn Gln Leu Leu Asp Pro Asp
        -55                 -50                 -45

ATA AAG GAT GAC CAG ATC ATC AAC TGG CTG CTA GAA TTC CGT TCT TCT      251
Ile Lys Asp Asp Gln Ile Ile Asn Trp Leu Leu Glu Phe Arg Ser Ser
    -40                 -35                 -30

GTC ATG TAC TTG ACA AAA GAC TTT GAG CAA CTT ATC AGT ATT ATA TTG      299
Val Met Tyr Leu Thr Lys Asp Phe Glu Gln Leu Ile Ser Ile Ile Leu
    -25                 -20                 -15

AGA TTG CCT TGG TTG AAT AGA AGT CAA ACA GTA GTG GAA GAG TAT TTG      347
Arg Leu Pro Trp Leu Asn Arg Ser Gln Thr Val Val Glu Glu Tyr Leu
-10                  -5                   1               5

GCT TTT CTT GGT AAT CTT GTA TCA GCA GAG ACT GTT TTC CTC AGA CCG      395
Ala Phe Leu Gly Asn Leu Val Ser Ala Glu Thr Val Phe Leu Arg Pro
            10                  15                  20
```

```
TGT CTC AGC ATG ATT GCT TCC CAT TTT GWG CCT CCC GAG CTG          437
Cys Leu Ser Met Ile Ala Ser His Phe Xaa Pro Pro Glu Leu
         25                  30                  35


(2) INFORMATION FOR SEQ ID NO: 243:

      (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 244 base pairs
            (B) TYPE: NUCLEIC ACID
            (C) STRANDEDNESS: DOUBLE
            (D) TOPOLOGY: LINEAR

      (ii) MOLECULE TYPE: CDNA

      (vi) ORIGINAL SOURCE:
            (A) ORGANISM: Homo Sapiens
            (F) TISSUE TYPE: Spleen

      (ix) FEATURE:
            (A) NAME/KEY: other
            (B) LOCATION: 54..242
            (C) IDENTIFICATION METHOD: blastn
            (D) OTHER INFORMATION:  identity 97
                                    region 12..200
                                    id R19497
                                    est

      (ix) FEATURE:
            (A) NAME/KEY: other
            (B) LOCATION: 78..242
            (C) IDENTIFICATION METHOD: blastn
            (D) OTHER INFORMATION:  identity 98
                                    region 1..165
                                    id H75597
                                    est

      (ix) FEATURE:
            (A) NAME/KEY: other
            (B) LOCATION: 84..242
            (C) IDENTIFICATION METHOD: blastn
            (D) OTHER INFORMATION:  identity 98
                                    region 1..159
                                    id H93398
                                    est

      (ix) FEATURE:
            (A) NAME/KEY: other
            (B) LOCATION: 122..243
            (C) IDENTIFICATION METHOD: blastn
            (D) OTHER INFORMATION:  identity 100
                                    region 1..122
                                    id HUM030E11B
                                    est

      (ix) FEATURE:
            (A) NAME/KEY: sig_peptide
            (B) LOCATION: 74..166
            (C) IDENTIFICATION METHOD: Von Heijne matrix
```

(D) OTHER INFORMATION: score 4.8
seq WAFSCGTWLPSRA/EW

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 243:

```
ATAGAAGGGG GTGGGGCCAC GTTTGCGTCC GCGCCATCAG GCCCGAGATA GCGGCGAGGT    60

CCGCTTTCAG TGT ATG GTT TTC CCT GCC AAA CGG TTC TGC TTG GTG CCA      109
               Met Val Phe Pro Ala Lys Arg Phe Cys Leu Val Pro
                   -30                 -25                 -20

TCC ATG GAG GGC GTG CGC TGG GCC TTT TCC TGC GGC ACT TGG CTG CCG     157
Ser Met Glu Gly Val Arg Trp Ala Phe Ser Cys Gly Thr Trp Leu Pro
                -15                 -10                  -5

AGC CGA GCC GAA TGG CTG CTG GCA GTG CGA TCG ATT CAG CCC GAG GAG     205
Ser Arg Ala Glu Trp Leu Leu Ala Val Arg Ser Ile Gln Pro Glu Glu
             1                   5                  10

AAG GAG CGC ATT GGC CAG TTC GTC TTT GCC CGG GAC GGG                 244
Lys Glu Arg Ile Gly Gln Phe Val Phe Ala Arg Asp Gly
     15                  20                  25
```

(2) INFORMATION FOR SEQ ID NO: 244:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 373 base pairs
(B) TYPE: NUCLEIC ACID
(C) STRANDEDNESS: DOUBLE
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Testis

(ix) FEATURE:
(A) NAME/KEY: other
(B) LOCATION: 101..273
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 92
region 159..331
id W57194
est

(ix) FEATURE:
(A) NAME/KEY: sig_peptide
(B) LOCATION: 95..340
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 4.7
seq LTCLADLFHSIAT/XK

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 244:

```
AAGAGGAGAA GGCTGGGTAT GAGGAAACTG CTGTCTTTTC ACTGGATCAG ACGTAAATAT    60
```

```
TAACTGGACC TCTCTTTAGA TTCTTTGCTC AATA ATG AAT TGT TTT CAG GGC ACC  115
                                      Met Asn Cys Phe Gln Gly Thr
                                                  -80

AAT GCC TCT GCT CTG GAA AAA GAC ATT GGT CCA GAG CAG TTT CCA ATC    163
Asn Ala Ser Ala Leu Glu Lys Asp Ile Gly Pro Glu Gln Phe Pro Ile
-75                 -70                 -65                 -60

AAT GAA CAC TAT TTC GGA TTG GTC AAT TTT GGA AAC ACA TGC TAC TGT    211
Asn Glu His Tyr Phe Gly Leu Val Asn Phe Gly Asn Thr Cys Tyr Cys
                -55                 -50                 -45

AAC TCC GTG CTT CAG GCA TTG TAC TCC TGC CGT CCA TTC CGG GAG AAT    259
Asn Ser Val Leu Gln Ala Leu Tyr Ser Cys Arg Pro Phe Arg Glu Asn
            -40                 -35                 -30

GTG TTG GCA TAC AAG GCC CAG CAA AAG AAG AAG GAA AAC TTG CTG ACG    307
Val Leu Ala Tyr Lys Ala Gln Gln Lys Lys Lys Glu Asn Leu Leu Thr
        -25                 -20                 -15

TGC CTG GCG GAC CTT TTC CAC AGC ATT GCC ACA SAG AAG AAG AAG GTT    355
Cys Leu Ala Asp Leu Phe His Ser Ile Ala Thr Xaa Lys Lys Lys Val
    -10                 -5                  1               5

GBR TCA TCC CAC CTG GGG                                            373
Xaa Ser Ser His Leu Gly
                10
```

(2) INFORMATION FOR SEQ ID NO: 245:

(i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 184 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:
- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Testis

(ix) FEATURE:
- (A) NAME/KEY: other
- (B) LOCATION: 73..182
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 93
  region 68..177
  id W60868
  est

(ix) FEATURE:
- (A) NAME/KEY: other
- (B) LOCATION: 62..182
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 96
  region 1..121
  id C17761
  est

(ix) FEATURE:
(A) NAME/KEY: other
(B) LOCATION: complement(150..182)
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 96
region 185..217
id W60944
est

(ix) FEATURE:
(A) NAME/KEY: sig_peptide
(B) LOCATION: 20..67
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 4.6
seq ALRVRXXXFGTRA/CR

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 245:

```
AATTTCCGAS CCGGGCAAG ATG GCA GCG GCG CTG CGC GTG CGT KGT TSA STG     52
                     Met Ala Ala Ala Leu Arg Val Arg Xaa Xaa Xaa
                         -15                 -10

TTC GGG ACG CGG GCC TGC AGG CGC CAT GGT CTT CCT CAC CGC GCA STC     100
Phe Gly Thr Arg Ala Cys Arg Arg His Gly Leu Pro His Arg Ala Xaa
 -5                  1               5                  10

TGG CTG CGG AAT CGC GTC ASC GAC CGC TAC TTT CGG ATC CAG GAG GTG     148
Trp Leu Arg Asn Arg Val Xaa Asp Arg Tyr Phe Arg Ile Gln Glu Val
             15                  20                  25

CTG AAG CAS GCC AGG CAC TTC CGG GGA AGG AAA AGG                     184
Leu Lys Xaa Ala Arg His Phe Arg Gly Arg Lys Arg
         30                  35
```

(2) INFORMATION FOR SEQ ID NO: 246:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 190 base pairs
(B) TYPE: NUCLEIC ACID
(C) STRANDEDNESS: DOUBLE
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Testis

(ix) FEATURE:
(A) NAME/KEY: other
(B) LOCATION: 35..186
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 97
region 1..152
id AA058818
est

(ix) FEATURE:
(A) NAME/KEY: other
(B) LOCATION: 32..135
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 100
region 1..104
id T50012
est

(ix) FEATURE:
(A) NAME/KEY: other
(B) LOCATION: 134..186
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 98
region 102..154
id T50012
est

(ix) FEATURE:
(A) NAME/KEY: other
(B) LOCATION: 56..186
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 96
region 33..163
id H79942
est

(ix) FEATURE:
(A) NAME/KEY: other
(B) LOCATION: 21..135
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 93
region 3..117
id AA058605
est

(ix) FEATURE:
(A) NAME/KEY: other
(B) LOCATION: 134..186
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 98
region 115..167
id AA058605
est

(ix) FEATURE:
(A) NAME/KEY: other
(B) LOCATION: 48..186
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 99
region 1..139
id R37526
est

(ix) FEATURE:
(A) NAME/KEY: sig_peptide
(B) LOCATION: 56..100
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 4.6
seq LLTHNLLSSHVRG/VG

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 246:

```
CTAATCGAAA AGGGGGATTT TCCGGTTCCG GCCTGGCGAG AGTTTGTGCG GCGAC ATG     58
                                                             Met
                                                             -15

AAA CTG CTT ACC CAC AAT CTG CTG AGC TCG CAT GTG CGG GGG GTG GGG   106
Lys Leu Leu Thr His Asn Leu Leu Ser Ser His Val Arg Gly Val Gly
            -10                 -5                   1

TCC CGT GGC TTC CCC CTG CGC CTC CAG GCC ACC GAG GTC CGT ATC TGC   154
Ser Arg Gly Phe Pro Leu Arg Leu Gln Ala Thr Glu Val Arg Ile Cys
        5                  10                  15

CCT GTG GAA TTC AAC CCC AAC TTC GTG GCG CGA CGG                   190
Pro Val Glu Phe Asn Pro Asn Phe Val Ala Arg Arg
    20                  25                  30
```

(2) INFORMATION FOR SEQ ID NO: 247:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 189 base pairs
(B) TYPE: NUCLEIC ACID
(C) STRANDEDNESS: DOUBLE
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Testis

(ix) FEATURE:
(A) NAME/KEY: other
(B) LOCATION: 54..186
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 94
region 45..177
id HSC2KH091
est

(ix) FEATURE:
(A) NAME/KEY: other
(B) LOCATION: 9..52
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 95
region 1..44
id HSC2KH091
est

(ix) FEATURE:
(A) NAME/KEY: other
(B) LOCATION: 82..117
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 97
region 1..36
id AA090704
est

```
(ix) FEATURE:
     (A) NAME/KEY: other
     (B) LOCATION: 129..186
     (C) IDENTIFICATION METHOD: blastn
     (D) OTHER INFORMATION:  identity 93
                             region 36..93
                             id AA126596
                             est

(ix) FEATURE:
     (A) NAME/KEY: other
     (B) LOCATION: 93..131
     (C) IDENTIFICATION METHOD: blastn
     (D) OTHER INFORMATION:  identity 94
                             region 1..39
                             id AA126596
                             est

(ix) FEATURE:
     (A) NAME/KEY: other
     (B) LOCATION: 122..181
     (C) IDENTIFICATION METHOD: blastn
     (D) OTHER INFORMATION:  identity 91
                             region 40..99
                             id AA090640
                             est

(ix) FEATURE:
     (A) NAME/KEY: other
     (B) LOCATION: 88..117
     (C) IDENTIFICATION METHOD: blastn
     (D) OTHER INFORMATION:  identity 96
                             region 8..37
                             id AA090640
                             est

(ix) FEATURE:
     (A) NAME/KEY: other
     (B) LOCATION: 99..186
     (C) IDENTIFICATION METHOD: blastn
     (D) OTHER INFORMATION:  identity 95
                             region 1..88
                             id T36119
                             est

(ix) FEATURE:
     (A) NAME/KEY: sig_peptide
     (B) LOCATION: 7..129
     (C) IDENTIFICATION METHOD: Von Heijne matrix
     (D) OTHER INFORMATION:  score 4.6
                             seq VSAGSLLLPAPQA/EX

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 247:

AACGGG ATG GGA TWC TTC TCA CGG CGC ACG TTC TGT GGG CGG AGT GGG       48
       Met Gly Xaa Phe Ser Arg Arg Thr Phe Cys Gly Arg Ser Gly
           -40                 -35                 -30

CGG AGC TGC CGG GGT CAG TTG GTC CAA GTG TCC CGG CCT GAG GTG TCG       96
```

```
Arg Ser Cys Arg Gly Gln Leu Val Gln Val Ser Arg Pro Glu Val Ser
        -25                 -20                 -15

GCC GGA TCC CTC CTT CTC CCG GCG CCT CAA GCG GAA GAS CAT TCC TCA     144
Ala Gly Ser Leu Leu Leu Pro Ala Pro Gln Ala Glu Xaa His Ser Ser
    -10                 -5                  1                   5

WGR RTT TTG TAT CCA AGG CCC AAA AGT TTG TTA CCC AAG ATG GGG         189
Xaa Xaa Leu Tyr Pro Arg Pro Lys Ser Leu Leu Pro Lys Met Gly
                10                  15                  20
```

(2) INFORMATION FOR SEQ ID NO: 248:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 237 base pairs
(B) TYPE: NUCLEIC ACID
(C) STRANDEDNESS: DOUBLE
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Ovary

(ix) FEATURE:
(A) NAME/KEY: other
(B) LOCATION: 132..235
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 99
region 94..197
id R36207
est

(ix) FEATURE:
(A) NAME/KEY: other
(B) LOCATION: 37..110
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 100
region 1..74
id R36207
est

(ix) FEATURE:
(A) NAME/KEY: other
(B) LOCATION: 41..194
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 94
region 1..154
id AA090796
est

(ix) FEATURE:
(A) NAME/KEY: other
(B) LOCATION: 107..235
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 96
region 15..143
id AA091961

est

(ix) FEATURE:
(A) NAME/KEY: other
(B) LOCATION: 141..193
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 96
region 33..85
id AA091520
est

(ix) FEATURE:
(A) NAME/KEY: other
(B) LOCATION: 190..237
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 97
region 81..128
id AA091520
est

(ix) FEATURE:
(A) NAME/KEY: other
(B) LOCATION: 109..142
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 100
region 2..35
id AA091520
est

(ix) FEATURE:
(A) NAME/KEY: sig_peptide
(B) LOCATION: 1..165
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 4.6
seq CALSLPDAPGASG/GR

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 248:

```
ATG GAA GGA GGC GTT CGT CTA GAT TTG TCG GCT TGC GGG GAG ACT TCA      48
Met Glu Gly Gly Val Arg Leu Asp Leu Ser Ala Cys Gly Glu Thr Ser
-55                 -50                 -45                 -40

GGA GTC GCT GTC TCT GAA CTT CCA GCC TCA GAG ACC GCC GCC CTT GTC      96
Gly Val Ala Val Ser Glu Leu Pro Ala Ser Glu Thr Ala Ala Leu Val
                -35                 -30                 -25

CCC GAG GGC CAT GGG CCG GGT CTC AGG GCT TGT GCC CTC TCG CTT CCT     144
Pro Glu Gly His Gly Pro Gly Leu Arg Ala Cys Ala Leu Ser Leu Pro
            -20                 -15                 -10

GAC GCT CCT GGC GCA TCT GGT GGT CGT CAT CAC CTT ATT CTG GTC CCG     192
Asp Ala Pro Gly Ala Ser Gly Gly Arg His His Leu Ile Leu Val Pro
        -5                   1               5

GGA CAG CAA CAT ACA GGC CTG CCT GCC TCT CAC GTT CAC CCC CAG         237
Gly Gln Gln His Thr Gly Leu Pro Ala Ser His Val His Pro Gln
 10                  15                  20
```

(2) INFORMATION FOR SEQ ID NO: 249:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 216 base pairs
(B) TYPE: NUCLEIC ACID
(C) STRANDEDNESS: DOUBLE
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Ovary

(ix) FEATURE:
(A) NAME/KEY: other
(B) LOCATION: 144..213
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 97
region 1..70
id N53816
est

(ix) FEATURE:
(A) NAME/KEY: other
(B) LOCATION: 21..63
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 100
region 1..43
id T34269
est

(ix) FEATURE:
(A) NAME/KEY: sig_peptide
(B) LOCATION: 163..204
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 4.5
seq TLLSFAALTAAFS/VL

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 249:

```
AAGCGCCGGA HGCGGTGAGG CACAGATGAG TAACGTGAAT TTGTCCGTCT CCGACTTCTG   60

GAGGTAAGGC GGTCGTCAGC CTATCTCTTC TGCTGGCTGG GCTCAATGCC GCGGGTGAGC  120

GTTCGGCCGA GGCTGCTCCT ACCCTTGAGT GATGTGCCTT GA ATG ACG CTG CTT     174
                                               Met Thr Leu Leu

TCA TTC GCT GCT CTC ACG GCT GCT TTC TCC GTC CTC CCC AAG            216
Ser Phe Ala Ala Leu Thr Ala Ala Phe Ser Val Leu Pro Lys
-10                 -5                  1
```

(2) INFORMATION FOR SEQ ID NO: 250:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 269 base pairs
(B) TYPE: NUCLEIC ACID
(C) STRANDEDNESS: DOUBLE

(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Ovary

(ix) FEATURE:
(A) NAME/KEY: other
(B) LOCATION: 46..271
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 98
region 36..261
id HSC3IF011
est

(ix) FEATURE:
(A) NAME/KEY: other
(B) LOCATION: 11..44
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 100
region 2..35
id HSC3IF011
est

(ix) FEATURE:
(A) NAME/KEY: other
(B) LOCATION: 50..271
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 98
region 39..260
id N28442
est

(ix) FEATURE:
(A) NAME/KEY: other
(B) LOCATION: 18..234
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 98
region 1..217
id HUM517C01B
est

(ix) FEATURE:
(A) NAME/KEY: other
(B) LOCATION: 125..215
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 98
region 1..91
id T77607
est

(ix) FEATURE:
(A) NAME/KEY: other
(B) LOCATION: 217..271
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 94
region 92..146
id T77607
est

(ix) FEATURE:
(A) NAME/KEY: sig_peptide
(B) LOCATION: 36..98
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 4.4
seq GLSKLQFAPFSSA/LD

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 250:

```
AGTGGTTGCN GGAAGTTGAG CGGCGGCAAG AAATA ATG GCG GCA GCT ACG GGG       53
                                       Met Ala Ala Ala Thr Gly
                                               -20

GAT CCT GGA CTC TCT AAA CTG CAG TTT GCC CCT TTT AGT AGT GCC TTG     101
Asp Pro Gly Leu Ser Lys Leu Gln Phe Ala Pro Phe Ser Ser Ala Leu
-15                 -10                  -5                   1

GAT GTT GGG TTT TGG CAT GAG TTG ACC CAG AAG AAG CTG AAC GAG TAT     149
Asp Val Gly Phe Trp His Glu Leu Thr Gln Lys Lys Leu Asn Glu Tyr
              5                  10                  15

CGG CTG GAT GAA GCT CCC AAG GAC ATT AAG GGT TAT TAC TAC AAT GGT     197
Arg Leu Asp Glu Ala Pro Lys Asp Ile Lys Gly Tyr Tyr Tyr Asn Gly
        20                  25                  30

GAC TCT GCT GGG MTG CCA GCT CGC TTA ACA TTG GAG TTC AGT GCT TTT     245
Asp Ser Ala Gly Xaa Pro Ala Arg Leu Thr Leu Glu Phe Ser Ala Phe
    35                  40                  45

GAC ATG AGT GCT CCC ACC CCA AGC                                     269
Asp Met Ser Ala Pro Thr Pro Ser
 50                  55
```

(2) INFORMATION FOR SEQ ID NO: 251:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 145 base pairs
(B) TYPE: NUCLEIC ACID
(C) STRANDEDNESS: DOUBLE
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Spleen

(ix) FEATURE:
(A) NAME/KEY: other
(B) LOCATION: 39..143
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 96
region 50..154
id R50695
est

(ix) FEATURE:

```
        (A) NAME/KEY: other
        (B) LOCATION: 3..45
        (C) IDENTIFICATION METHOD: blastn
        (D) OTHER INFORMATION:  identity 90
                                region 15..57
                                id R50695
                                est

    (ix) FEATURE:
        (A) NAME/KEY: other
        (B) LOCATION: 81..143
        (C) IDENTIFICATION METHOD: blastn
        (D) OTHER INFORMATION:  identity 96
                                region 104..166
                                id R94786
                                est

    (ix) FEATURE:
        (A) NAME/KEY: other
        (B) LOCATION: 81..143
        (C) IDENTIFICATION METHOD: blastn
        (D) OTHER INFORMATION:  identity 96
                                region 105..167
                                id T98442
                                est

    (ix) FEATURE:
        (A) NAME/KEY: sig_peptide
        (B) LOCATION: 50..130
        (C) IDENTIFICATION METHOD: Von Heijne matrix
        (D) OTHER INFORMATION:  score 4.4
                                seq LSKSLLLVPSXLS/LL

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 251:

AAGCTTCCCC TCCCCCGGCG CCCTCTGGGG CTCCGAGCCC GGCGGGACC ATG TTC ACC    58
                                                      Met Phe Thr
                                                              -25

AGC ACC GGC TCC AGT GGG CTC TAC AAG GCG CCT CTG TCG AAG AGC CTT     106
Ser Thr Gly Ser Ser Gly Leu Tyr Lys Ala Pro Leu Ser Lys Ser Leu
            -20                 -15                 -10

CTG CTG GTC CCC AGT RCC CTC TCC CTC CTG CSC GCC CAG                 145
Leu Leu Val Pro Ser Xaa Leu Ser Leu Leu Xaa Ala Gln
        -5                   1                   5


(2) INFORMATION FOR SEQ ID NO: 252:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 427 base pairs
        (B) TYPE: NUCLEIC ACID
        (C) STRANDEDNESS: DOUBLE
        (D) TOPOLOGY: LINEAR

    (ii) MOLECULE TYPE: CDNA

    (vi) ORIGINAL SOURCE:
```

(A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Testis

(ix) FEATURE:
(A) NAME/KEY: other
(B) LOCATION: 137..291
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 99
region 138..292
id AA121372
est

(ix) FEATURE:
(A) NAME/KEY: other
(B) LOCATION: 6..91
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 97
region 1..86
id AA121372
est

(ix) FEATURE:
(A) NAME/KEY: other
(B) LOCATION: 318..397
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 98
region 322..401
id AA121372
est

(ix) FEATURE:
(A) NAME/KEY: other
(B) LOCATION: 95..132
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 100
region 94..131
id AA121372
est

(ix) FEATURE:
(A) NAME/KEY: other
(B) LOCATION: 284..313
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 90
region 286..315
id AA121372
est

(ix) FEATURE:
(A) NAME/KEY: other
(B) LOCATION: 2..102
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 98
region 15..115
id T53974
est

(ix) FEATURE:
(A) NAME/KEY: other
(B) LOCATION: 150..258
(C) IDENTIFICATION METHOD: blastn

```
        (D) OTHER INFORMATION:  identity 92
                                region 167..275
                                id T53974
                                est

    (ix) FEATURE:
        (A) NAME/KEY: other
        (B) LOCATION: 95..171
        (C) IDENTIFICATION METHOD: blastn
        (D) OTHER INFORMATION:  identity 97
                                region 111..187
                                id T53974
                                est

    (ix) FEATURE:
        (A) NAME/KEY: other
        (B) LOCATION: 2..102
        (C) IDENTIFICATION METHOD: blastn
        (D) OTHER INFORMATION:  identity 98
                                region 15..115
                                id R09314
                                est

    (ix) FEATURE:
        (A) NAME/KEY: other
        (B) LOCATION: 95..171
        (C) IDENTIFICATION METHOD: blastn
        (D) OTHER INFORMATION:  identity 97
                                region 111..187
                                id R09314
                                est

    (ix) FEATURE:
        (A) NAME/KEY: other
        (B) LOCATION: 150..222
        (C) IDENTIFICATION METHOD: blastn
        (D) OTHER INFORMATION:  identity 90
                                region 167..239
                                id R09314
                                est

    (ix) FEATURE:
        (A) NAME/KEY: sig_peptide
        (B) LOCATION: 179..298
        (C) IDENTIFICATION METHOD: Von Heijne matrix
        (D) OTHER INFORMATION:  score 4.3
                                seq ITLVSAAPGKVIC/EM

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 252:

AAAATCGCGG ACCACCGGGG CTGCCAKCTC GCCTGACTCC CGGCCTCTTG CGCTCCTAGG    60

GGCGGAGAAG GGTGCGGGCT CTTCGCCCTT TGTGTCCTTC TTTCACTAAC TTCTGGACTT   120

TCCAGCTCTT CCGAAGTTCG TTCTTGCGCA AAGCCCAAAG GCTGGAAAAC CGTCCACG     178

ATG ACC AGC ATG ACT CAG TCT CTG CGG GAG GTG ATA AAG GCC ATG ACC     226
Met Thr Ser Met Thr Gln Ser Leu Arg Glu Val Ile Lys Ala Met Thr
-40                 -35                 -30                 -25
```

```
AAG GCT CGC AAT TTT GAG AGA GTT TTG GGA AAG ATT ACT CTT GTC TCT     274
Lys Ala Arg Asn Phe Glu Arg Val Leu Gly Lys Ile Thr Leu Val Ser
                -20                 -15                 -10

GCT GCT CCT GGG AAA GTG ATT TGT GAA ATG AAA GTA GAA GAA GAG CAT     322
Ala Ala Pro Gly Lys Val Ile Cys Glu Met Lys Val Glu Glu Glu His
             -5                   1               5

ACC AAT GCA ATA GGC ACT CTC CAC GGC GGT TTG ACA GCC ACG TTA GTA     370
Thr Asn Ala Ile Gly Thr Leu His Gly Gly Leu Thr Ala Thr Leu Val
     10                  15                  20

GAT AAC ATA TCA ACA ATG GCT CTG CTA TGC ACG GAA AGG GGA GCA CCC     418
Asp Asn Ile Ser Thr Met Ala Leu Leu Cys Thr Glu Arg Gly Ala Pro
 25                  30                  35                  40

GGA GTC AGT                                                         427
Gly Val Ser
```

(2) INFORMATION FOR SEQ ID NO: 253:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 332 base pairs
(B) TYPE: NUCLEIC ACID
(C) STRANDEDNESS: DOUBLE
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Spleen

(ix) FEATURE:
(A) NAME/KEY: other
(B) LOCATION: 2..285
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 98
region 8..291
id T31110
est

(ix) FEATURE:
(A) NAME/KEY: other
(B) LOCATION: 278..331
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 96
region 285..338
id T31110
est

(ix) FEATURE:
(A) NAME/KEY: other
(B) LOCATION: 2..329
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 98
region 6..333
id T08844
est

(ix) FEATURE:
(A) NAME/KEY: other
(B) LOCATION: 2..329
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 98
region 7..334
id T35807
est

(ix) FEATURE:
(A) NAME/KEY: other
(B) LOCATION: 9..331
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 98
region 1..323
id T33763
est

(ix) FEATURE:
(A) NAME/KEY: other
(B) LOCATION: 15..331
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 99
region 1..317
id AA132848
est

(ix) FEATURE:
(A) NAME/KEY: sig_peptide
(B) LOCATION: 75..293
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 4.3
seq DIILSGLVPGSTT/LH

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 253:

```
AAGCGAGCCC AGGCGGCAGT CTTGATTCCC TTTTGGCCAG CAGTTTTTAG GTCTGTCAGT    60

ACTGCACTGC AAGA ATG GCA GAT TTT GGG ATC TCT GCT GGC CAG TTT GTG     110
                Met Ala Asp Phe Gly Ile Ser Ala Gly Gln Phe Val
                            -70                 -65

GCA GTS GTC TGG GAT AAG TCA TCC CCA GTG GAG GCT CTG AAA GGT CTG     158
Ala Val Val Trp Asp Lys Ser Ser Pro Val Glu Ala Leu Lys Gly Leu
    -60                 -55                 -50

GTG GAT AAG CTT CAA GCG TTA ACC GGC AAT GAG GGC CGC GTG TCT GTG     206
Val Asp Lys Leu Gln Ala Leu Thr Gly Asn Glu Gly Arg Val Ser Val
-45                 -40                 -35                 -30

GAA AAC ATC AAG CAG CTG TTG CAA TCT GCC CAC AAA GAA TCC AGC BTT     254
Glu Asn Ile Lys Gln Leu Leu Gln Ser Ala His Lys Glu Ser Ser Xaa
                -25                 -20                 -15

GAC ATT ATT TTG TCA GGT TTA GTC CCA GGA AGC ACC ACT CTG CAC AGT     302
Asp Ile Ile Leu Ser Gly Leu Val Pro Gly Ser Thr Thr Leu His Ser
            -10                 -5                  1

GCT GAG ATT TTG GCT GAA ATC GCC CGG GTG                             332
```

```
Ala Glu Ile Leu Ala Glu Ile Ala Arg Val
      5                   10
```

(2) INFORMATION FOR SEQ ID NO: 254:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 131 base pairs
(B) TYPE: NUCLEIC ACID
(C) STRANDEDNESS: DOUBLE
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Ovary

(ix) FEATURE:
(A) NAME/KEY: other
(B) LOCATION: 36..128
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 100
region 13..105
id AA115592
est

(ix) FEATURE:
(A) NAME/KEY: sig_peptide
(B) LOCATION: 84..125
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 4.2
seq GILLGLLLLGHLT/VR

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 254:

```
AACAGACGCT GGCGGCCACC AGAAGTTTGA GCCTCTTTGG TAGCAGGAGG CTGGAAGAAA    60

GGACAGAAGT AGCTCTGGCT GTG ATG GGG ATC TTA CTG GGC CTG CTA CTC CTG  113
                          Met Gly Ile Leu Leu Gly Leu Leu Leu Leu
                                          -10                 -5

GGG CAC CTA ACA GTG AGA                                            131
Gly His Leu Thr Val Arg
                     1
```

(2) INFORMATION FOR SEQ ID NO: 255:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 486 base pairs
(B) TYPE: NUCLEIC ACID
(C) STRANDEDNESS: DOUBLE
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Testis

(ix) FEATURE:
(A) NAME/KEY: other
(B) LOCATION: 13..53
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 90
region 1..41
id AA063860
est

(ix) FEATURE:
(A) NAME/KEY: sig_peptide
(B) LOCATION: 55..111
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 4.1
seq LLLGQRCSLKVSG/QE

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 255:

```
AAATCTTCAG GGCAGCTCCC AGAGCATGGA TCCCTCCTGA TTCCACTCAG CCCG ATG       57
                                                            Met

TTC CTC ACA GTC AAG CTG CTC CTG GGC CAG AGA TGC AGT CTG AAG GTG      105
Phe Leu Thr Val Lys Leu Leu Leu Gly Gln Arg Cys Ser Leu Lys Val
            -15                 -10                 -5

TCA GGG CAA GAG AGT GTA GCC ACG CTG AAG AGA CTG GTG TCC AGG CGG      153
Ser Gly Gln Glu Ser Val Ala Thr Leu Lys Arg Leu Val Ser Arg Arg
          1               5                  10

CTG AAG GTG CCT GAG GAG CAG CAG CAC CTG CTT TTC CGT GGC CAG CTC      201
Leu Lys Val Pro Glu Glu Gln Gln His Leu Leu Phe Arg Gly Gln Leu
 15                  20                  25                  30

CTG GAG GAT GAC AAG CAC CTC TCT GAC TAC TGC ATT GGG CCC AAT GCC      249
Leu Glu Asp Asp Lys His Leu Ser Asp Tyr Cys Ile Gly Pro Asn Ala
                 35                  40                  45

TCT ATC AAT GTC ATC ATG CAG CCC TTG GAG AAG ATG GCG CTA AAG GAG      297
Ser Ile Asn Val Ile Met Gln Pro Leu Glu Lys Met Ala Leu Lys Glu
            50                  55                  60

GCC CAC CAG CCG CAG ACC CAG CCC CTG TGG CAC CAG CTG GGA CTG GTC      345
Ala His Gln Pro Gln Thr Gln Pro Leu Trp His Gln Leu Gly Leu Val
        65                  70                  75

CTA GCT AAA CAC TTT GAA CCA CAG GAT GCC AAG GCC GTG CTG CAG CTG      393
Leu Ala Lys His Phe Glu Pro Gln Asp Ala Lys Ala Val Leu Gln Leu
    80                  85                  90

CTA AGG CAG GAG CAC GAR GAG CGC CTG CAG AAG ATA AGC CTG GAG CAC      441
Leu Arg Gln Glu His Glu Glu Arg Leu Gln Lys Ile Ser Leu Glu His
 95                 100                 105                 110

CTG GAG CAG CTG GCC CAG TAC CTC CTG GCA GAG GAG CTC ACG TGG          486
Leu Glu Gln Leu Ala Gln Tyr Leu Leu Ala Glu Glu Leu Thr Trp
                115                 120                 125
```

(2) INFORMATION FOR SEQ ID NO: 256:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 411 base pairs
(B) TYPE: NUCLEIC ACID
(C) STRANDEDNESS: DOUBLE
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Testis

(ix) FEATURE:
(A) NAME/KEY: other
(B) LOCATION: complement(195..411)
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 99
region 86..302
id AA062591
est

(ix) FEATURE:
(A) NAME/KEY: sig_peptide
(B) LOCATION: 94..189
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 4.1
seq RLLSSLLLTMSNN/NP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 256:

```
GGCGACGCCG CCATTTTGGA GTCTTCCCTA AGGATCCTCT ACCGGCTTTT CGAGTCAGTG    60

CTGCCGCCGC TGCCCGCGGC TTTGCAGAGC AGG ATG AAT GTG ATA GAC CAC GTG    114
                                     Met Asn Val Ile Asp His Val
                                                 -30

CGG GAC ATG GCG GCC GCG GGG CTG CAC TCC AAC GTG CGG CTC CTC AGC    162
Arg Asp Met Ala Ala Ala Gly Leu His Ser Asn Val Arg Leu Leu Ser
-25                 -20                 -15                 -10

AGC TTG TTA CTT ACA ATG AGT AAT AAC AAC CCT GAG TTA TTC TCC CCA    210
Ser Leu Leu Leu Thr Met Ser Asn Asn Asn Pro Glu Leu Phe Ser Pro
                 -5                   1               5

CCT CAG AAG TAC CAG CTT TTG GTG TAT CAT GCA GAT TCT CTC TTT CAT    258
Pro Gln Lys Tyr Gln Leu Leu Val Tyr His Ala Asp Ser Leu Phe His
        10                  15                  20

GAT AAG GAA TAT CGG AAT GCT GTG AGT AAG TAT ACC ATG GCT TTA CAG    306
Asp Lys Glu Tyr Arg Asn Ala Val Ser Lys Tyr Thr Met Ala Leu Gln
    25                  30                  35

CAG AAG AAA GCG CTA AGT AAA ACT TCA AAA GTG AGA CCT TCA ACT GGA    354
Gln Lys Lys Ala Leu Ser Lys Thr Ser Lys Val Arg Pro Ser Thr Gly
 40                  45                  50                  55
```

```
AAT TCT GCA TCT ACT CCA CAA AGT CAG TGT CTT CCA TCT GAA ATT GAA     402
Asn Ser Ala Ser Thr Pro Gln Ser Gln Cys Leu Pro Ser Glu Ile Glu
                60                  65                  70

GTG AAA TAC                                                         411
Val Lys Tyr
```

(2) INFORMATION FOR SEQ ID NO: 257:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 232 base pairs
(B) TYPE: NUCLEIC ACID
(C) STRANDEDNESS: DOUBLE
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Testis

(ix) FEATURE:
(A) NAME/KEY: other
(B) LOCATION: complement(184..228)
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 100
region 99..143
id AA122158
est

(ix) FEATURE:
(A) NAME/KEY: sig_peptide
(B) LOCATION: 56..178
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 4.1
seq RVLCPLLXAAAAP/KR

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 257:

```
AAGTAGCTCT CTAGGCCTGG GKRCCGGAGG GAGGGAGGCG GGCAGAGKWG GGGAG ATG     58
                                                            Met

GGC ACC CCC AGT CTT TCC ATC CTC CTC ATA GGG GCA CCC GAA TCC CCT     106
Gly Thr Pro Ser Leu Ser Ile Leu Leu Ile Gly Ala Pro Glu Ser Pro
-40                 -35                 -30                 -25

ATT CCT TAT TTC CCC TAT CAC TCA GGC ACT GGC AGG GTC CTT TGC CCA     154
Ile Pro Tyr Phe Pro Tyr His Ser Gly Thr Gly Arg Val Leu Cys Pro
                -20                 -15                 -10

CTC CTG TWG GCC GCT GCG GCT CCA AAG CGA GAT GTG CCT GAG ACA GGT     202
Leu Leu Xaa Ala Ala Ala Ala Pro Lys Arg Asp Val Pro Glu Thr Gly
            -5                  1               5

TTG ACC AGG CAA CTG AAA AGA CAT CCT GGG                             232
Leu Thr Arg Gln Leu Lys Arg His Pro Gly
    10                  15
```

(2) INFORMATION FOR SEQ ID NO: 258:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 216 base pairs
(B) TYPE: NUCLEIC ACID
(C) STRANDEDNESS: DOUBLE
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Testis

(ix) FEATURE:
(A) NAME/KEY: other
(B) LOCATION: 28..211
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 98
region 149..332
id H15076
est

(ix) FEATURE:
(A) NAME/KEY: other
(B) LOCATION: 28..139
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 98
region 147..258
id R18367
est

(ix) FEATURE:
(A) NAME/KEY: other
(B) LOCATION: 138..179
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 92
region 258..299
id R18367
est

(ix) FEATURE:
(A) NAME/KEY: sig_peptide
(B) LOCATION: 46..123
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 3.9
seq HALFVLCLLYAMS/HN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 258:

```
AAATAATTGA TTCCCTGTGT CTGGAATACC TGACCCTTCC TGGAT ATG GTG TAC CAC    57
                                                  Met Val Tyr His
                                                          -25

GCG CTG GAC AGC CCG GAT GAT GAT TAC CAT GCC CTG TTC GTG CTC TGC     105
Ala Leu Asp Ser Pro Asp Asp Asp Tyr His Ala Leu Phe Val Leu Cys
        -20                 -15                 -10
```

```
CTC CTC TAT GCC ATG TCT CAT AAT AAA GGC ATG GAT CCT GAA AAA TTA     153
Leu Leu Tyr Ala Met Ser His Asn Lys Gly Met Asp Pro Glu Lys Leu
     -5                  1               5                  10

GAG CGA ATC CAG CTC CCC GTG CCA AAT GCG GCC GAG AAG ACC ACC TAC     201
Glu Arg Ile Gln Leu Pro Val Pro Asn Ala Ala Glu Lys Thr Thr Tyr
                15                  20                  25

AAC CAC CCG CAT GGG                                                 216
Asn His Pro His Gly
            30
```

(2) INFORMATION FOR SEQ ID NO: 259:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 103 base pairs
(B) TYPE: NUCLEIC ACID
(C) STRANDEDNESS: DOUBLE
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Spleen

(ix) FEATURE:
(A) NAME/KEY: other
(B) LOCATION: complement(2..103)
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 98
region 148..249
id HSB79F042
est

(ix) FEATURE:
(A) NAME/KEY: sig_peptide
(B) LOCATION: 32..73
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 3.8
seq FIVLSMWLCCGFE/IL

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 259:

```
AACTTGGTGA CTCTAGGTGA CTGGTCGACA G ATG TTC ATT GTA CTA TCA ATG      52
                                   Met Phe Ile Val Leu Ser Met
                                                       -10

TGG CTT TGC TGT GGG TTT GAA ATT TTG CAA ACT AAG AGT TGG GTG GCA     100
Trp Leu Cys Cys Gly Phe Glu Ile Leu Gln Thr Lys Ser Trp Val Ala
        -5                   1               5

GGG                                                                 103
Gly
 10
```

(2) INFORMATION FOR SEQ ID NO: 260:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 351 base pairs
(B) TYPE: NUCLEIC ACID
(C) STRANDEDNESS: DOUBLE
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Spleen

(ix) FEATURE:
(A) NAME/KEY: other
(B) LOCATION: complement(184..281)
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 93
region 2..99
id T07232
est

(ix) FEATURE:
(A) NAME/KEY: other
(B) LOCATION: complement(103..170)
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 95
region 113..180
id T07232
est

(ix) FEATURE:
(A) NAME/KEY: other
(B) LOCATION: 42..106
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 96
region 20..84
id AA099117
est

(ix) FEATURE:
(A) NAME/KEY: sig_peptide
(B) LOCATION: 280..324
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 3.8
seq VVILSSXVPLAAM/GV

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 260:

```
AGAAGGCGGG AAAATGGCGG ATTCCTCGGG GCGAGGCGCT GGGAAGCCTG CAACCGGCCC    60

CACAAATTCT AGCAGTGCCA AGAAGAAGGA TAAAAGAGTT CAAGGTAAGC AGTGTCAGGA   120

TCTCTTTAAG GAACATGGTT TTCTTCTTTC ATTACGTGCT TTTGGAGGAA GAAAAAAACA   180

GGCCAGAGAA GGGGGCCTGT GGCTTTACTT CCTTGTAGTC ACACCTGTGG GGATTCTGGG   240

TCTGGCCATC CCAGCCCTGB NGCGAGGGCT GTGTCAGGA ATG GTG GTG GTC ATT      294
                                           Met Val Val Val Ile
```

```
                                                   -15

TTG AGC AGT GYA GTT CCC TTG GCA GCC ATG GGG GTC ATG GGC TGT GTC     342
Leu Ser Ser Xaa Val Pro Leu Ala Ala Met Gly Val Met Gly Cys Val
-10                 -5                  1                   5

CGG GTG TGG                                                          351
Arg Val Trp
```

(2) INFORMATION FOR SEQ ID NO: 261:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 201 base pairs
(B) TYPE: NUCLEIC ACID
(C) STRANDEDNESS: DOUBLE
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Ovary

(ix) FEATURE:
(A) NAME/KEY: other
(B) LOCATION: 16..62
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 97
region 463..509
id AA069619
est

(ix) FEATURE:
(A) NAME/KEY: sig_peptide
(B) LOCATION: 1..45
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 3.8
seq AECSSLLHPSVRG/SI

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 261:

```
ATG TTG GCA GAA TGC AGT TCC TTA CTG CAT CCA TCA GTT AGA GGC TCG      48
Met Leu Ala Glu Cys Ser Ser Leu Leu His Pro Ser Val Arg Gly Ser
-15                 -10                 -5                   1

ATC CCA GAG GCC ACC TGC CGT GTC CTG CCA TGT GGC CCT CTC CAC AAC      96
Ile Pro Glu Ala Thr Cys Arg Val Leu Pro Cys Gly Pro Leu His Asn
            5                   10                  15

ATG GCA GTT TGC TCT TGC AAG GCT AGC AGG AGC TTC TAC TGC AAC TTC     144
Met Ala Val Cys Ser Cys Lys Ala Ser Arg Ser Phe Tyr Cys Asn Phe
        20                  25                  30

AGA TCT CTC CGA CTT GCT GTC TCT GAC TTC TTG ATT CTT TTC CAA AAG     192
Arg Ser Leu Arg Leu Ala Val Ser Asp Phe Leu Ile Leu Phe Gln Lys
    35                  40                  45

GGG CTA GGG                                                         201
```

Gly Leu Gly
50

(2) INFORMATION FOR SEQ ID NO: 262:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 146 base pairs
(B) TYPE: NUCLEIC ACID
(C) STRANDEDNESS: DOUBLE
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Ovary

(ix) FEATURE:
(A) NAME/KEY: other
(B) LOCATION: 76..141
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 90
region 50..115
id R25850
est

(ix) FEATURE:
(A) NAME/KEY: other
(B) LOCATION: 89..141
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 96
region 49..101
id N44651
est

(ix) FEATURE:
(A) NAME/KEY: other
(B) LOCATION: 85..141
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 91
region 38..94
id N31513
est

(ix) FEATURE:
(A) NAME/KEY: sig_peptide
(B) LOCATION: 54..98
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 3.8
seq MARLLGLCAWARK/SV

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 262:

```
AACTCTGTCA CCTCCGCTGG AAGGAGTGGA ACCCAGACTT GCTGGTCTGA TCC ATG      56
                                                           Met
                                                           -15

CAG ATG GCC AGG CTG CTA GGC CTC TGT GCC TGG GCA CGG AAG TCG GTG    104
```

```
Gln Met Ala Arg Leu Leu Gly Leu Cys Ala Trp Ala Arg Lys Ser Val
            -10                 -5                  1

CGG ATG GCC AGC TCC AGG ATG ACC CGC CGG GAC CCG CCA AGG            146
Arg Met Ala Ser Ser Arg Met Thr Arg Arg Asp Pro Pro Arg
        5                   10                  15
```

(2) INFORMATION FOR SEQ ID NO: 263:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 231 base pairs
(B) TYPE: NUCLEIC ACID
(C) STRANDEDNESS: DOUBLE
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Uterus

(ix) FEATURE:
(A) NAME/KEY: other
(B) LOCATION: complement(44..83)
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 97
region 313..352
id R56475
est

(ix) FEATURE:
(A) NAME/KEY: other
(B) LOCATION: complement(73..226)
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 95
region 136..289
id T05392
est

(ix) FEATURE:
(A) NAME/KEY: other
(B) LOCATION: complement(73..226)
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 93
region 161..314
id HUM030E12A
est

(ix) FEATURE:
(A) NAME/KEY: other
(B) LOCATION: complement(72..226)
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 92
region 161..315
id HUM016H07A
est

(ix) FEATURE:
(A) NAME/KEY: other

(B) LOCATION: complement(181..226)
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 97
region 168..213
id H08767
est

(ix) FEATURE:
(A) NAME/KEY: other
(B) LOCATION: complement(39..77)
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 92
region 326..364
id H08767
est

(ix) FEATURE:
(A) NAME/KEY: sig_peptide
(B) LOCATION: 91..219
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 3.8
seq LISVLYLIPKTLT/TN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 263:

```
AACAAAAGGA GAGTTTTATA ATTCACTTTA AAAGGAGATT TGATGGTAAA GTTTAAAGAT    60

TAAAATATTT TGTTCTTCAA TTACAGAGCG ATG ACC CCA CAG TAT CTG CCT CAC   114
                                 Met Thr Pro Gln Tyr Leu Pro His
                                             -40

GGT GGA AAA TAC CAA GTT CTT GGA GAT TAC TCT TTG GCA GTG GTC TTC   162
Gly Gly Lys Tyr Gln Val Leu Gly Asp Tyr Ser Leu Ala Val Val Phe
-35                 -30                 -25                 -20

CCC CTG CAC TTT TCT GAT CTA ATT TCT GTT TTA TAC CTT ATA CCC AAA   210
Pro Leu His Phe Ser Asp Leu Ile Ser Val Leu Tyr Leu Ile Pro Lys
                -15                 -10                  -5

ACA CTT ACT ACC AAC AGC CGG                                       231
Thr Leu Thr Thr Asn Ser Arg
            1
```

(2) INFORMATION FOR SEQ ID NO: 264:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 361 base pairs
(B) TYPE: NUCLEIC ACID
(C) STRANDEDNESS: DOUBLE
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Spleen

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 53..342
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 96
region 19..308
id C18012
est

(ix) FEATURE:
(A) NAME/KEY: other
(B) LOCATION: 123..349
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 96
region 112..338
id AA058608
est

(ix) FEATURE:
(A) NAME/KEY: other
(B) LOCATION: 22..83
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 91
region 12..73
id AA058608
est

(ix) FEATURE:
(A) NAME/KEY: other
(B) LOCATION: 103..331
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 92
region 87..315
id N42002
est

(ix) FEATURE:
(A) NAME/KEY: other
(B) LOCATION: 19..87
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 97
region 1..69
id R13667
est

(ix) FEATURE:
(A) NAME/KEY: other
(B) LOCATION: 139..361
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 100
region 25..247
id AA151008
est

(ix) FEATURE:
(A) NAME/KEY: sig_peptide
(B) LOCATION: 17..85
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 3.7
seq FLPPLXRAFACRG/CQ

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 264:

```
AAGGGGGCGT GGGGCC ATG GTG GTC TTG CGG GCG GGG AAG AAG ACC TTT CTC    52
                  Met Val Val Leu Arg Ala Gly Lys Lys Thr Phe Leu
                              -20                 -15

CCC CCT CTM WGC CGC GCC TTC GCC TGC CGC GGC TGT CAA CTC GCT CCG     100
Pro Pro Leu Xaa Arg Ala Phe Ala Cys Arg Gly Cys Gln Leu Ala Pro
    -10                 -5                   1               5

GAG CGC GGC GCC GAG CGC AGG GAT ACA GCG CCC AGC GGG GTC TCA AGA     148
Glu Arg Gly Ala Glu Arg Arg Asp Thr Ala Pro Ser Gly Val Ser Arg
                10                  15                  20

TTC TGC CCT CCA AGA AAG TCT TGC CAT GAT TGG ATA GGA CCC CCA GAT     196
Phe Cys Pro Pro Arg Lys Ser Cys His Asp Trp Ile Gly Pro Pro Asp
            25                  30                  35

AAA TAT TCA AAC CTT CGA CCT GTT CAC TTT TAC ATA CCT GAA AAT GAA     244
Lys Tyr Ser Asn Leu Arg Pro Val His Phe Tyr Ile Pro Glu Asn Glu
        40                  45                  50

TCT CCA TTG GAA CAA AAG CTT AGA AAA TTA AGA CAA GAA ACA CAA GAA     292
Ser Pro Leu Glu Gln Lys Leu Arg Lys Leu Arg Gln Glu Thr Gln Glu
    55                  60                  65

TGG AAT CAA CAG TTC TGG GCA AAC CAG AAT TTG ACT TTT AGT AAG GAA     340
Trp Asn Gln Gln Phe Trp Ala Asn Gln Asn Leu Thr Phe Ser Lys Glu
 70                  75                  80                  85

AAA GAA GAA TTT ATT CAC TCA                                         361
Lys Glu Glu Phe Ile His Ser
                90
```

(2) INFORMATION FOR SEQ ID NO: 265:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 113 base pairs
(B) TYPE: NUCLEIC ACID
(C) STRANDEDNESS: DOUBLE
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Testis

(ix) FEATURE:
(A) NAME/KEY: other
(B) LOCATION: 11..113
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 99
region 2..104
id N76875
est

(ix) FEATURE:
(A) NAME/KEY: sig_peptide

(B) LOCATION: 15..74
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 3.6
seq AHLCSDSLPESQQ/QD

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 265:

```
AAGAGAGAAC CGCC ATG AAG AGA GAA GGG GGT GCC GCC CAC CTC TGC TCC      50
                Met Lys Arg Glu Gly Gly Ala Ala His Leu Cys Ser
                -20                 -15                 -10

GAC AGC CTC CCG GAG TCC CAG CAG CAA GAC GGC AAC CAC GCA CCC AAC      98
Asp Ser Leu Pro Glu Ser Gln Gln Gln Asp Gly Asn His Ala Pro Asn
             -5                   1               5

TTC TCC AGC CAC GGC                                                  113
Phe Ser Ser His Gly
     10
```

(2) INFORMATION FOR SEQ ID NO: 266:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 342 base pairs
(B) TYPE: NUCLEIC ACID
(C) STRANDEDNESS: DOUBLE
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Testis

(ix) FEATURE:
(A) NAME/KEY: other
(B) LOCATION: 255..343
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 98
region 12..100
id AA026923
est

(ix) FEATURE:
(A) NAME/KEY: sig_peptide
(B) LOCATION: 205..327
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 3.6
seq PYSLAACPCGSQG/GV

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 266:

```
ACCGAGAAGC CCTCACAGAT GCAGATGACT TTGGCCTACA GTTCCCGCTG GACCTGGATG    60

TGAGGGTGAA GGCTGTGCTG CTGGGAGCCA CATTCCTCAT TGACTACATG TTCTTTGAGA   120

AGCGAGGAGG CGCTGGGCCC TCTGCCATCA CCAGTTAGAG GCCACCATGG TGTGAGGAGA   180
```

```
CCATCACCTC GACCAGAACT CCAG ATG GTC ACC TGC CCT GGC CCC TCC TCT      231
                          Met Val Thr Cys Pro Gly Pro Ser Ser
                              -40                 -35

GGG CAG CCC CTT TCC TCC ATG TAC ACT GCA GGG GAC AGA AGG GGG GCC     279
Gly Gln Pro Leu Ser Ser Met Tyr Thr Ala Gly Asp Arg Arg Gly Ala
        -30                 -25                 -20

CCA TCC CTA CCC TAC TCC CTG GCC GCC TGC CCC TGT GGT TCC CAA GGA     327
Pro Ser Leu Pro Tyr Ser Leu Ala Ala Cys Pro Cys Gly Ser Gln Gly
    -15                 -10                  -5

GGG GTA TGT ATG AGA                                                 342
Gly Val Cys Met Arg
  1               5
```

(2) INFORMATION FOR SEQ ID NO: 267:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 420 base pairs
(B) TYPE: NUCLEIC ACID
(C) STRANDEDNESS: DOUBLE
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Spleen

(ix) FEATURE:
(A) NAME/KEY: other
(B) LOCATION: complement(1..300)
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 100
region 1..300
id H13499
est

(ix) FEATURE:
(A) NAME/KEY: other
(B) LOCATION: complement(1..268)
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 100
region 1..268
id W40371
est

(ix) FEATURE:
(A) NAME/KEY: other
(B) LOCATION: complement(1..93)
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 98
region 1..93
id H04223
est

(ix) FEATURE:
(A) NAME/KEY: sig_peptide

(B) LOCATION: 109..162
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 3.5
seq ALEVIVTLSETAA/AM

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 267:

```
AAATCCCTCG TTGAGATTGC AGATACTGTT CCAAAGTATT TGCGTCCTCA CTTGGAAGCA    60

ACTCTACAGC TAAGTCTAAA GTTGTGTGGA GACACTAGCC TCAACAAT ATG CAA CGC    117
                                                     Met Gln Arg

CAG CTT GCC CTT GAA GTG ATC GTC ACC CTC TCT GAG ACT GCA GCT GCT      165
Gln Leu Ala Leu Glu Val Ile Val Thr Leu Ser Glu Thr Ala Ala Ala
-15                 -10                 -5                   1

ATG TTA AGA AAA CAT ACC AAT ATT GTT GCA CAG ACT ATT CCT CAG ATG      213
Met Leu Arg Lys His Thr Asn Ile Val Ala Gln Thr Ile Pro Gln Met
            5                   10                  15

TTA GCA ATG ATG GTT GAT TTG GAA GAA GAT GAG GAC TGG GCA AAT GCA      261
Leu Ala Met Met Val Asp Leu Glu Glu Asp Glu Asp Trp Ala Asn Ala
        20                  25                  30

GAT GAA CTA GAA GAT GAT GAT TTT GAC AGC AAT GCA GTT GCA GGC GAG      309
Asp Glu Leu Glu Asp Asp Asp Phe Asp Ser Asn Ala Val Ala Gly Glu
    35                  40                  45

AGT GCT CTA GAT CGA ATG GCT TGC GGA CTT GGT GGA AAG CTC GTT CTG      357
Ser Ala Leu Asp Arg Met Ala Cys Gly Leu Gly Gly Lys Leu Val Leu
 50                  55                  60                  65

CCG ATG ATC AAG GAA CAC ATT ATG CAA ATG CTT CAA AAT CGT AAG CTG      405
Pro Met Ile Lys Glu His Ile Met Gln Met Leu Gln Asn Arg Lys Leu
                70                  75                  80

TGT CCT TCA ATG CTA                                                  420
Cys Pro Ser Met Leu
            85
```

(2) INFORMATION FOR SEQ ID NO: 268:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 392 base pairs
(B) TYPE: NUCLEIC ACID
(C) STRANDEDNESS: DOUBLE
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Testis

(ix) FEATURE:
(A) NAME/KEY: other
(B) LOCATION: 177..348
(C) IDENTIFICATION METHOD: blastn

(D) OTHER INFORMATION: identity 100
region 266..437
id N32722
est

(ix) FEATURE:
(A) NAME/KEY: other
(B) LOCATION: 52..175
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 94
region 142..265
id N32722
est

(ix) FEATURE:
(A) NAME/KEY: other
(B) LOCATION: 3..41
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 100
region 1..39
id N32722
est

(ix) FEATURE:
(A) NAME/KEY: other
(B) LOCATION: 36..387
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 96
region 12..363
id W32042
est

(ix) FEATURE:
(A) NAME/KEY: other
(B) LOCATION: 177..348
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 100
region 134..305
id R55254
est

(ix) FEATURE:
(A) NAME/KEY: other
(B) LOCATION: 99..175
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 100
region 57..133
id R55254
est

(ix) FEATURE:
(A) NAME/KEY: other
(B) LOCATION: 44..102
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 91
region 1..59
id R55254
est

(ix) FEATURE:
(A) NAME/KEY: other

(B) LOCATION: 356..387
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 90
region 315..346
id R55254
est

(ix) FEATURE:
(A) NAME/KEY: other
(B) LOCATION: 177..334
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 100
region 149..306
id W37647
est

(ix) FEATURE:
(A) NAME/KEY: other
(B) LOCATION: 38..175
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 94
region 11..148
id W37647
est

(ix) FEATURE:
(A) NAME/KEY: other
(B) LOCATION: 38..174
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 95
region 8..144
id R50622
est

(ix) FEATURE:
(A) NAME/KEY: other
(B) LOCATION: 174..295
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 99
region 143..264
id R50622
est

(ix) FEATURE:
(A) NAME/KEY: sig_peptide
(B) LOCATION: 147..374
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 3.5
seq LASASELPLGSRP/AP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 268:

```
AACTTCCTGT GAGCCCGGCG GTGACAACGG CAACATGGCC CGTGAACGGA GCTGAAGTCG    60

ACGACTTCTC CTRGRARMCC CCGACTGAGG CGGAGACGAA GGTGCTGCAG GCGCGACGGG   120

AGCGGCAAGA TCGCATCTCC CGGCTC ATG GGC GAC TAT CTG CTG CGC GGT TAC    173
                             Met Gly Asp Tyr Leu Leu Arg Gly Tyr
                                 -75                 -70
```

```
CGC ATG CTG GGC GAG ACG TGT GCG GAC TGC GGG ACG ATC CTC CTC CAA     221
Arg Met Leu Gly Glu Thr Cys Ala Asp Cys Gly Thr Ile Leu Leu Gln
        -65                 -60                 -55

GAC AAA CAG CGG AAA ATC TAC TGC GTG GCT TGT CAG GAA CTC GAC TCA     269
Asp Lys Gln Arg Lys Ile Tyr Cys Val Ala Cys Gln Glu Leu Asp Ser
    -50                 -45                 -40

GAC GTG GAT AAA GAT AAT CCC GCT CTG AAT GCC CAG GCT GCC CTC TCC     317
Asp Val Asp Lys Asp Asn Pro Ala Leu Asn Ala Gln Ala Ala Leu Ser
-35                 -30                 -25                 -20

CAA GCT CGG GAG CAC CAG CTG GCC TCA GCC TCA GAG CTC CCC CTG GGC     365
Gln Ala Arg Glu His Gln Leu Ala Ser Ala Ser Glu Leu Pro Leu Gly
                -15                 -10                 -5

TCT CGA CCT GCG CCC CAA CCC CAC GGG                                 392
Ser Arg Pro Ala Pro Gln Pro His Gly
             1               5
```

(2) INFORMATION FOR SEQ ID NO: 269:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 234 base pairs
(B) TYPE: NUCLEIC ACID
(C) STRANDEDNESS: DOUBLE
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Ovary

(ix) FEATURE:
(A) NAME/KEY: other
(B) LOCATION: 61..232
(C) IDENTIFICATION METHOD: fasta
(D) OTHER INFORMATION: identity 100
region 1..172
id HSC1R
vrt

(ix) FEATURE:
(A) NAME/KEY: other
(B) LOCATION: 72..232
(C) IDENTIFICATION METHOD: fasta
(D) OTHER INFORMATION: identity 100
region 24..184
id HUMC1R
vrt

(ix) FEATURE:
(A) NAME/KEY: other
(B) LOCATION: 109..232
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 92
region 1..124
id T74375

est

(ix) FEATURE:
(A) NAME/KEY: other
(B) LOCATION: 98..141
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 93
region 1..44
id T64778
est

(ix) FEATURE:
(A) NAME/KEY: sig_peptide
(B) LOCATION: 112..156
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 8.1
seq LLYLLVPALFCRA/GG

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 269:

```
AACTCCACAG AAAACCCTCC CCTCCCTGCT GTGCATGACG CGGGCTCCCT CTGCACACAG   60

TGCACGAAGA CGCTGTCGGG AGAGCCCAGG ATTCAACACG GGCCTTGAGA A ATG TGG   117
                                                         Met Trp
                                                         -15

CTC TTG TAC CTC CTG GTG CCG GCC CTG TTC TGC AGG GCA GGA GGC TCC   165
Leu Leu Tyr Leu Leu Val Pro Ala Leu Phe Cys Arg Ala Gly Gly Ser
            -10                 -5                  1

ATT CCC ATC CCT CAG AAG TTA TTT GGG GAG GTG ACT TCC CCT CTG TTC   213
Ile Pro Ile Pro Gln Lys Leu Phe Gly Glu Val Thr Ser Pro Leu Phe
     5                  10                  15

CCC AAG CCT TAC CCC AAC ACG                                       234
Pro Lys Pro Tyr Pro Asn Thr
 20                 25
```

(2) INFORMATION FOR SEQ ID NO: 270:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 302 base pairs
(B) TYPE: NUCLEIC ACID
(C) STRANDEDNESS: DOUBLE
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Testis

(ix) FEATURE:
(A) NAME/KEY: other
(B) LOCATION: 87..300
(C) IDENTIFICATION METHOD: fasta
(D) OTHER INFORMATION: identity 98
region 1..214

id HSCALICIN
vrt

(ix) FEATURE:
(A) NAME/KEY: sig_peptide
(B) LOCATION: 78..251
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 4
seq LAAVSPLVRSLIS/SN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 270:

```
AAATCTGATC CCACAGGCCT GAGAAAGTCT GCTCTCCAGW ACCTGCTGCT GATCTGTTTC   60

AGCCGACAAG AGGCACC ATG AAA TTG GAA TTC ACG GAG AAA AAC BAC RAT      110
                   Met Lys Leu Glu Phe Thr Glu Lys Asn Xaa Xaa
                               -55                 -50

AGC TTC GTG CTG CAR AAC CTG AAC AGA CAG AGG AAA CGC AAA GAG TAC     158
Ser Phe Val Leu Gln Asn Leu Asn Arg Gln Arg Lys Arg Lys Glu Tyr
    -45                 -40                 -35

TGG GAC ATG GCC CTG AGT GTG GAC AAC CAC GTC TTC TTT GCA CAT CGC     206
Trp Asp Met Ala Leu Ser Val Asp Asn His Val Phe Phe Ala His Arg
-30                 -25                 -20

AAT GTG CTG GCT GCT GTC TCC CCA CTG GTG AGG AGC CTC ATC TCC AGC     254
Asn Val Leu Ala Ala Val Ser Pro Leu Val Arg Ser Leu Ile Ser Ser
-15                 -10                  -5                   1

AAT GAC ATG AAG ACC GCT GAT GAG CTT TTC ATC ACC ATT GAC ACC AAG     302
Asn Asp Met Lys Thr Ala Asp Glu Leu Phe Ile Thr Ile Asp Thr Lys
             5                  10                  15
```

(2) INFORMATION FOR SEQ ID NO: 271:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 125 amino acids
(B) TYPE: AMINO ACID
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Testis

(ix) FEATURE:
(A) NAME/KEY: sig_peptide
(B) LOCATION: -30..-1
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 13.2
seq LLLLSTLVIPSAA/AP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 271:

```
Met Gly Glu Ala Ser Pro Pro Ala Pro Ala Arg Arg His Leu Leu Val
```

```
-30                 -25                 -20                 -15

Leu Leu Leu Leu Leu Ser Thr Leu Val Ile Pro Ser Ala Ala Ala Pro
                -10                 -5                   1

Ile His Asp Ala Asp Ala Gln Glu Ser Ser Leu Gly Leu Thr Gly Leu
         5                  10                  15

Gln Ser Leu Leu Gln Gly Phe Ser Arg Leu Phe Leu Lys Gly Asn Leu
     20                  25                  30

Leu Arg Gly Ile Asp Ser Leu Phe Ser Ala Pro Met Asp Phe Arg Gly
 35                  40                  45                  50

Leu Pro Gly Asn Tyr His Lys Glu Glu Asn Gln Glu His Gln Leu Gly
                 55                  60                  65

Asn Asn Thr Leu Ser Ser Xaa Leu Gln Ile Asp Xaa Met Thr Asp Asn
             70                  75                  80

Lys Thr Gly Glu Val Leu Ile Ser Glu Asn Val Val Ala
         85                  90                  95
```

(2) INFORMATION FOR SEQ ID NO: 272:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 48 amino acids
(B) TYPE: AMINO ACID
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Testis

(ix) FEATURE:
(A) NAME/KEY: sig_peptide
(B) LOCATION: -21..-1
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 12
seq VLVLCVLLLQAQG/GY

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 272:

```
Met Ala Pro Gln Thr Leu Leu Pro Val Leu Val Leu Cys Val Leu Leu
    -20                 -15                 -10

Leu Gln Ala Gln Gly Gly Tyr Arg Asp Lys Met Arg Met Gln Arg Ile
 -5                  1                   5                  10

Lys Val Cys Glu Lys Arg Pro Ser Ile Asp Leu Cys Ile His His Arg
             15                  20                  25
```

(2) INFORMATION FOR SEQ ID NO: 273:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 101 amino acids
(B) TYPE: AMINO ACID
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Testis

(ix) FEATURE:
(A) NAME/KEY: sig_peptide
(B) LOCATION: -19..-1
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 11
seq SLVLLLCLTCSYA/FM

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 273:

```
Met Trp Thr Leu Lys Ser Ser Leu Val Leu Leu Leu Cys Leu Thr Cys
                -15                 -10                 -5

Ser Tyr Ala Phe Met Phe Ser Ser Leu Arg Gln Lys Thr Ser Glu Pro
             1               5                  10

Gln Gly Lys Val Gln Tyr Gly Glu His Phe Arg Ile Arg Gln Asn Leu
    15                  20                  25

Pro Glu His Thr Gln Gly Trp Leu Gly Ser Lys Trp Leu Trp Leu Leu
 30                 35                  40                  45

Xaa Val Val Val Pro Phe Val Ile Leu Gln Cys Gln Arg Asp Ser Glu
                 50                  55                  60

Lys Asn Lys Glu Gln Ser Pro Pro Gly Leu Arg Gly Gly Gln Leu His
             65                  70                  75

Ser Pro Leu Lys Lys
         80
```

(2) INFORMATION FOR SEQ ID NO: 274:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 115 amino acids
(B) TYPE: AMINO ACID
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Testis

(ix) FEATURE:
(A) NAME/KEY: sig_peptide
(B) LOCATION: -16..-1
(C) IDENTIFICATION METHOD: Von Heijne matrix

(D) OTHER INFORMATION: score 10.6
seq LLLLPLLWGGSLQ/EK

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 274:

```
Met Leu Pro Leu Leu Leu Leu Pro Leu Leu Trp Gly Gly Ser Leu Gln
    -15                 -10                 -5

Glu Lys Pro Val Tyr Glu Leu Gln Val Gln Lys Ser Val Thr Val Gln
  1               5                  10                  15

Glu Gly Leu Cys Val Leu Val Pro Cys Ser Phe Ser Tyr Pro Trp Arg
             20                  25                  30

Ser Trp Tyr Ser Ser Pro Pro Leu Tyr Val Tyr Trp Phe Arg Asp Gly
         35                  40                  45

Glu Ile Pro Tyr Tyr Ala Glu Val Val Ala Thr Asn Asn Pro Asp Arg
    50                  55                  60

Arg Val Lys Pro Glu Thr Gln Gly Arg Phe Arg Leu Leu Gly Asp Val
 65                  70                  75                  80

Gln Lys Lys Asn Cys Ser Leu Ser Ile Gly Asp Xaa Arg Met Glu Asp
                 85                  90                  95

Thr Gly Gly
```

(2) INFORMATION FOR SEQ ID NO: 275:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 64 amino acids
(B) TYPE: AMINO ACID
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Ovary

(ix) FEATURE:
(A) NAME/KEY: sig_peptide
(B) LOCATION: -26..-1
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 10.4
seq LLLLLCGPSQDQC/RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 275:

```
Met Glu Thr Gly Ala Leu Arg Arg Pro Gln Leu Leu Pro Leu Leu Leu
    -25                 -20                 -15

Leu Leu Cys Gly Pro Ser Gln Asp Gln Cys Arg Pro Val Leu Gln Asn
-10                 -5                   1                   5

Leu Leu Gln Ser Pro Gly Leu Thr Trp Ser Leu Glu Val Pro Thr Gly
```

10 15 20

Arg Glu Gly Lys Glu Gly Thr Met Arg Val Ser Pro Thr Ala Pro Arg
25 30 35

(2) INFORMATION FOR SEQ ID NO: 276:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 83 amino acids
(B) TYPE: AMINO ACID
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Testis

(ix) FEATURE:
(A) NAME/KEY: sig_peptide
(B) LOCATION: -16..-1
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 10.1
seq LVLTLCTLPLAVA/SA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 276:

Met Glu Arg Leu Val Leu Thr Leu Cys Thr Leu Pro Leu Ala Val Ala
-15 -10 -5

Ser Ala Gly Cys Ala Thr Thr Pro Ala Arg Asn Leu Ser Cys Tyr Gln
1 5 10 15

Cys Phe Lys Val Ser Ser Trp Thr Glu Cys Pro Pro Thr Trp Cys Ser
20 25 30

Pro Leu Asp Gln Val Cys Ile Ser Asn Glu Val Val Val Ser Phe Lys
35 40 45

Trp Ser Val Arg Val Leu Leu Ser Lys Arg Cys Ala Pro Arg Cys Pro
50 55 60

Asn Ser Gly
65

(2) INFORMATION FOR SEQ ID NO: 277:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 120 amino acids
(B) TYPE: AMINO ACID
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Homo Sapiens

(F) TISSUE TYPE: Testis

(ix) FEATURE:
(A) NAME/KEY: sig_peptide
(B) LOCATION: -23..-1
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 9.8
seq FLLFFFLFLLTRG/SL

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 277:

```
Met Met Leu Pro Gln Trp Leu Leu Leu Leu Phe Leu Leu Phe Phe Phe
            -20             -15             -10
Leu Phe Leu Leu Thr Arg Gly Ser Leu Ser Pro Thr Lys Tyr Asn Leu
         -5                  1               5
Leu Glu Leu Lys Glu Xaa Xaa Xaa Gly Asn Gln Asp Cys Glu Thr Gly
 10                  15                  20                  25
Cys Cys Gln Arg Ala Pro Asp Asn Cys Glu Ser His Cys Ala Glu Lys
                 30                  35                  40
Gly Ser Glu Gly Ser Leu Cys Gln Thr Gln Val Phe Phe Gly Gln Tyr
             45                  50                  55
Arg Ala Cys Pro Cys Leu Arg Asn Leu Thr Cys Ile Tyr Ser Lys Asn
         60                  65                  70
Glu Lys Trp Leu Ser Ile Ala Tyr Gly Arg Cys Gln Lys Ile Gly Arg
     75                  80                  85
Gln Lys Leu Ala Arg Lys Cys Ser
 90                  95
```

(2) INFORMATION FOR SEQ ID NO: 278:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 28 amino acids
(B) TYPE: AMINO ACID
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Testis

(ix) FEATURE:
(A) NAME/KEY: sig_peptide
(B) LOCATION: -22..-1
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 9.8
seq LVVFCLALQLVPG/SP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 278:

```
Met Lys Pro Val Leu Pro Leu Gln Xaa Leu Val Val Phe Cys Leu Ala
        -20                 -15                 -10

Leu Gln Leu Val Pro Gly Ser Pro Lys Gln Leu Gly
    -5                  1               5
```

(2) INFORMATION FOR SEQ ID NO: 279:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 40 amino acids
(B) TYPE: AMINO ACID
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Spleen

(ix) FEATURE:
(A) NAME/KEY: sig_peptide
(B) LOCATION: -35..-1
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 9.5
seq LFFSLFSAPLASA/VR

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 279:

```
Met Phe Arg Gln Arg Gln Glu Thr Ala Gln Arg Ser Thr Gln Ser Cys
-35                 -30                 -25                 -20

Arg Cys Pro Arg Asp Gly Leu Phe Phe Ser Leu Phe Ser Ala Pro Leu
                -15                 -10                 -5

Ala Ser Ala Val Arg Ala Ala Xaa
            1               5
```

(2) INFORMATION FOR SEQ ID NO: 280:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 37 amino acids
(B) TYPE: AMINO ACID
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Ovary

(ix) FEATURE:
(A) NAME/KEY: sig_peptide
(B) LOCATION: -26..-1
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 9.4
seq RLLLALPLALVLG/FE

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 280:

Met Gly Ser Ser Ala Cys Glu Ile Ala Val Gly Thr Lys Arg Leu Leu
    -25   -20   -15

Leu Ala Leu Pro Leu Ala Leu Val Leu Gly Phe Glu Gly Ser Ser Val
-10   -5   1   5

Pro Pro Arg Asn Phe
            10

(2) INFORMATION FOR SEQ ID NO: 281:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 56 amino acids
(B) TYPE: AMINO ACID
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Testis

(ix) FEATURE:
(A) NAME/KEY: sig_peptide
(B) LOCATION: -23..-1
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 9.4
seq SLLFICFFGESFC/IC

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 281:

Met Ser Asn Gln Arg Leu Pro Leu Ile Phe Ser Leu Leu Phe Ile Cys
            -20   -15   -10

Phe Phe Gly Glu Ser Phe Cys Ile Cys Asp Gly Thr Val Trp Thr Xaa
        -5   1   5

Val Xaa Trp Glu Ile Leu Pro Glu Glu Val His Tyr Trp Lys Val Lys
10   15   20   25

Gly Ser Pro Ser His Cys Leu Arg
                30

(2) INFORMATION FOR SEQ ID NO: 282:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 amino acids
(B) TYPE: AMINO ACID
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Ovary

(ix) FEATURE:
(A) NAME/KEY: sig_peptide
(B) LOCATION: -16..-1
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 9.2
seq FLSFLLALLSLNC/IP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 282:

```
Met Leu Trp Phe Leu Ser Phe Leu Leu Ala Leu Leu Ser Leu Asn Cys
    -15                 -10                 -5

Ile Pro Ile Gly
  1
```

(2) INFORMATION FOR SEQ ID NO: 283:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 40 amino acids
(B) TYPE: AMINO ACID
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Testis

(ix) FEATURE:
(A) NAME/KEY: sig_peptide
(B) LOCATION: -24..-1
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 9.2
seq ICCVIVLISLSWT/SP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 283:

```
Met Leu Xaa Ile Ser Leu Glu Ile Xaa Ser Phe Ile Cys Cys Val Ile
            -20                 -15                 -10

Val Leu Ile Ser Leu Ser Trp Thr Ser Pro Phe Thr Gly Val Tyr Leu
            -5                   1                   5

Ile Gly Leu Ile Ile Glu Pro Gly
     10                  15
```

(2) INFORMATION FOR SEQ ID NO: 284:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 28 amino acids
(B) TYPE: AMINO ACID

(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Ovary

(ix) FEATURE:
(A) NAME/KEY: sig_peptide
(B) LOCATION: -19..-1
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 9.2
seq ILFILTFFSHTFC/SR

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 284:

```
Met Val Phe Arg Asn Cys Ile Leu Phe Ile Leu Thr Phe Phe Ser His
                -15                 -10                     -5

Thr Phe Cys Ser Arg Gln Asn Lys Ala Gln Pro Trp
             1               5
```

(2) INFORMATION FOR SEQ ID NO: 285:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 51 amino acids
(B) TYPE: AMINO ACID
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Ovary

(ix) FEATURE:
(A) NAME/KEY: sig_peptide
(B) LOCATION: -13..-1
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 9.1
seq MLAACPLSPGCQS/AP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 285:

```
Met Leu Ala Ala Cys Pro Leu Ser Pro Gly Cys Gln Ser Ala Pro Ser
            -10                 -5                   1

Thr Trp Asn His Phe Pro Pro Glu Arg Ile Thr Thr Gly Ala Gly Ser
     5                  10                  15

Leu Leu Lys Pro Gly Gly Gly Leu Trp Pro Arg Thr Val Ser Leu Pro
 20                 25                  30                  35

Ser Pro Ala
```

(2) INFORMATION FOR SEQ ID NO: 286:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 76 amino acids
(B) TYPE: AMINO ACID
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Spleen

(ix) FEATURE:
(A) NAME/KEY: sig_peptide
(B) LOCATION: -19..-1
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 9.1
seq FLTLITHCTVSWA/QS

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 286:

```
Met Ala Trp Ser Pro Leu Phe Leu Thr Leu Ile Thr His Cys Thr Val
                -15                 -10                 -5

Ser Trp Ala Gln Ser Val Leu Thr Gln Pro Pro Ser Val Ser Glu Ala
             1                   5                  10

Pro Arg Gln Arg Val Thr Ile Ser Cys Phe Gly Ser Ser Ser Asn Ile
     15                  20                  25

Gly Arg Asn Ala Val Asn Trp Tyr Gln Gln Leu Pro Gly Arg Ser Pro
 30                  35                  40                  45

Arg Leu Leu Ile Phe Tyr Asn Asn Leu Pro Ala Ser
                50                  55
```

(2) INFORMATION FOR SEQ ID NO: 287:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 21 amino acids
(B) TYPE: AMINO ACID
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Testis

(ix) FEATURE:
(A) NAME/KEY: sig_peptide
(B) LOCATION: -18..-1
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 9.1
seq LVSLCSWSPPLTS/SP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 287:

```
Met Leu Lys Ser Val Leu Val Ser Leu Cys Ser Trp Ser Pro Pro Leu
            -15                 -10                 -5

Thr Ser Ser Pro Arg
         1
```

(2) INFORMATION FOR SEQ ID NO: 288:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 44 amino acids
(B) TYPE: AMINO ACID
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Testis

(ix) FEATURE:
(A) NAME/KEY: sig_peptide
(B) LOCATION: -22..-1
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 9
seq FILAALSLSTTFS/LQ

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 288:

```
Met Thr Ser Lys Xaa Ile Leu Val Ser Phe Ile Leu Ala Ala Leu Ser
        -20                 -15                 -10

Leu Ser Thr Thr Phe Ser Leu Gln Pro Tyr Gln Gln Lys Val Leu Leu
    -5                       1               5                  10

Val Ser Phe Asp Gly Phe Arg Trp Asp Tyr Leu Tyr
                15                  20
```

(2) INFORMATION FOR SEQ ID NO: 289:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 24 amino acids
(B) TYPE: AMINO ACID
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Ovary

(ix) FEATURE:
(A) NAME/KEY: sig_peptide
(B) LOCATION: -20..-1

(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 8.9
seq LAVXLGLATAVSA/GP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 289:

```
Met Lys Ser Leu Ser Leu Xaa Leu Ala Val Xaa Leu Gly Leu Ala Thr
-20                 -15                 -10                  -5

Ala Val Ser Ala Gly Pro Ala Trp
                1
```

(2) INFORMATION FOR SEQ ID NO: 290:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 80 amino acids
(B) TYPE: AMINO ACID
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Ovary

(ix) FEATURE:
(A) NAME/KEY: sig_peptide
(B) LOCATION: -21..-1
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 8.8
seq LLWALLFMQSLWP/QL

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 290:

```
Met Trp Ala Met Glu Ser Gly His Leu Leu Trp Ala Leu Leu Phe Met
    -20                 -15                 -10

Gln Ser Leu Trp Pro Gln Leu Thr Asp Gly Ala Thr Arg Val Tyr Tyr
 -5                  1               5                  10

Leu Gly Ile Arg Asp Val Gln Trp Asn Tyr Ala Pro Lys Gly Arg Asn
            15                  20                  25

Val Ile Thr Asn Gln Pro Leu Asp Ser Asp Ile Val Ala Ser Ser Phe
        30                  35                  40

Leu Lys Ser Asp Lys Asn Arg Ile Gly Gly Thr Thr Arg Arg Pro Trp
    45                  50                  55
```

(2) INFORMATION FOR SEQ ID NO: 291:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 49 amino acids
(B) TYPE: AMINO ACID
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Testis

(ix) FEATURE:
(A) NAME/KEY: sig_peptide
(B) LOCATION: -20..-1
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 8.8
seq LLVMGSLPSASWS/LP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 291:

```
Met Ala Gln Thr Trp Ala Xaa Leu Leu Val Met Gly Ser Leu Pro Ser
-20                 -15                 -10                  -5

Ala Ser Trp Ser Leu Pro Cys Leu Ser Trp Glu Ser Leu Leu Lys Ala
                1               5                   10

Ala Ala Cys Ser Glu Leu Asp Gly Arg Asn Val Gly Asn Thr Pro Thr
        15                  20                  25

Arg
```

(2) INFORMATION FOR SEQ ID NO: 292:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 24 amino acids
(B) TYPE: AMINO ACID
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Ovary

(ix) FEATURE:
(A) NAME/KEY: sig_peptide
(B) LOCATION: -22..-1
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 8.7
seq LITLLYVWPVINA/CQ

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 292:

```
Met Lys Cys Gly Phe Leu Ala Tyr Leu Leu Ile Thr Leu Leu Tyr Val
        -20                 -15                 -10

Trp Pro Val Ile Asn Ala Cys Gln
    -5                  1
```

(2) INFORMATION FOR SEQ ID NO: 293:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 36 amino acids
(B) TYPE: AMINO ACID
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Testis

(ix) FEATURE:
(A) NAME/KEY: sig_peptide
(B) LOCATION: -25..-1
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 8.5
seq LKVLLLPLAPAAA/QD

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 293:

```
Met Arg Lys Pro Ala Ala Gly Phe Leu Pro Ser Leu Leu Lys Val Leu
-25                 -20                 -15                 -10

Leu Leu Pro Leu Ala Pro Ala Ala Ala Gln Asp Ser Thr Gln Ala Ser
                -5                   1               5

Thr Pro Gly Arg
        10
```

(2) INFORMATION FOR SEQ ID NO: 294:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 54 amino acids
(B) TYPE: AMINO ACID
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Spleen

(ix) FEATURE:
(A) NAME/KEY: sig_peptide
(B) LOCATION: -17..-1
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 8.4
seq LLFLTSVVPFVLA/PR

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 294:

```
Met Arg Gln Ser Leu Leu Phe Leu Thr Ser Val Val Pro Phe Val Leu
    -15                 -10                 -5

Ala Pro Arg Pro Pro Asp Asp Pro Gly Phe Gly Pro His Gln Arg Leu
```

1 5 10 15

Glu Lys Leu Asp Ser Leu Leu Ser Asp Tyr Asp Ile Leu Ser Leu Ser
20 25 30

Asn Ile Gln Gln Gln Xaa
35

(2) INFORMATION FOR SEQ ID NO: 295:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 38 amino acids
(B) TYPE: AMINO ACID
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Ovary

(ix) FEATURE:
(A) NAME/KEY: sig_peptide
(B) LOCATION: -25..-1
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 8.1
seq SVLLGLLALMATA/AV

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 295:

Met Glu Leu Ser Gln Met Ser Glu Leu Met Gly Leu Ser Val Leu Leu
-25 -20 -15 -10

Gly Leu Leu Ala Leu Met Ala Thr Ala Ala Val Ala Arg Gly Trp Leu
-5 1 5

Arg Ala Gly Glu Val Arg
10

(2) INFORMATION FOR SEQ ID NO: 296:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 103 amino acids
(B) TYPE: AMINO ACID
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Testis

(ix) FEATURE:
(A) NAME/KEY: sig_peptide
(B) LOCATION: -65..-1
(C) IDENTIFICATION METHOD: Von Heijne matrix

(D) OTHER INFORMATION: score 8
seq LTLIGCLVTGVES/KI

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 296:

```
Met Gln Asp Ala Pro Leu Ser Cys Leu Ser Pro Thr Lys Trp Ser Ser
-65                 -60                 -55                 -50

Val Ser Ser Ala Asp Ser Thr Glu Lys Ser Ala Ser Ala Ala Gly Thr
                -45                 -40                 -35

Arg Asn Leu Pro Phe Gln Phe Cys Leu Arg Gln Ala Leu Arg Met Lys
            -30                 -25                 -20

Ala Ala Gly Ile Leu Thr Leu Ile Gly Cys Leu Val Thr Gly Val Glu
        -15                 -10                 -5

Ser Lys Ile Tyr Thr Arg Cys Lys Leu Ala Lys Ile Phe Ser Arg Ala
    1               5                   10                  15

Gly Leu Asp Asn Xaa Arg Gly Phe Ser Leu Gly Xaa Trp Ile Cys Met
                20                  25                  30

Ala Tyr Tyr Glu Ser Gly Trp
            35
```

(2) INFORMATION FOR SEQ ID NO: 297:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 132 amino acids
(B) TYPE: AMINO ACID
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Spleen

(ix) FEATURE:
(A) NAME/KEY: sig_peptide
(B) LOCATION: -96..-1
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 7.6
seq ALCGLCLLCPRAA/RV

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 297:

```
Met Ala Leu Ala Phe Cys Leu Cys Met Ala Glu Ala Ile Leu Leu Phe
    -95                 -90                 -85

Ser Pro Glu His Ser Leu Phe Phe Phe Cys Ser Arg Lys Ala Arg Ile
-80                 -75                 -70                 -65

Arg Leu His Trp Ala Gly Gln Thr Leu Ala Ile Leu Cys Ala Ala Leu
                -60                 -55                 -50
```

Gly Leu Gly Phe Ile Ile Ser Ser Arg Thr Arg Ser Glu Leu Pro His
-45 -40 -35

Leu Val Ser Trp His Ser Trp Val Gly Ala Leu Thr Leu Leu Ala Thr
-30 -25 -20

Ala Val Gln Ala Leu Cys Gly Leu Cys Leu Leu Cys Pro Arg Ala Ala
-15 -10 -5

Arg Val Ser Arg Val Ala Arg Leu Lys Leu Tyr His Leu Thr Cys Gly
1 5 10 15

Leu Val Val Tyr Leu Met Ala Thr Val Thr Val Leu Leu Gly Met Tyr
20 25 30

Ser Val Trp Phe
35

(2) INFORMATION FOR SEQ ID NO: 298:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 100 amino acids
(B) TYPE: AMINO ACID
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Spleen

(ix) FEATURE:
(A) NAME/KEY: sig_peptide
(B) LOCATION: -57..-1
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 7.5
seq LLHRLASFHRVWS/FP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 298:

Met Leu Arg Phe Pro Thr Cys Phe Pro Ser Xaa Arg Val Xaa Gly Xaa
-55 -50 -45

Lys Gln Leu Pro Gln Glu Ile Ile Xaa Leu Val Trp Ser Pro Xaa Arg
-40 -35 -30

Asp Xaa Ile Xaa Leu Ala Asn Thr Ala Gly Glu Val Leu Leu His Arg
-25 -20 -15 -10

Leu Ala Ser Phe His Arg Val Trp Ser Phe Pro Pro Asn Glu Asn Thr
-5 1 5

Gly Xaa Glu Val Thr Cys Leu Ala Trp Arg Pro Asp Gly Lys Leu Leu
10 15 20

Ala Phe Ala Leu Ala Asp Thr Lys Lys Ile Val Leu Cys Asp Val Glu
25 30 35

Lys Pro Glu Ser
40

(2) INFORMATION FOR SEQ ID NO: 299:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 130 amino acids
(B) TYPE: AMINO ACID
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Spleen

(ix) FEATURE:
(A) NAME/KEY: sig_peptide
(B) LOCATION: -42..-1
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 7.5
seq LALVVALVAERFA/RR

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 299:

```
Met Phe Met Val Leu Glu Val Val Val Ser Arg Val Thr Ser Ser Leu
        -40                 -35                 -30

Ala Met Leu Ser Asp Ser Phe His Met Leu Ser Asp Val Leu Ala Leu
    -25                 -20                 -15

Val Val Ala Leu Val Ala Glu Arg Phe Ala Arg Arg Thr His Ala Thr
-10                 -5                   1                   5

Gln Lys Asn Thr Phe Gly Trp Ile Arg Ala Glu Val Met Gly Ala Leu
            10                  15                  20

Val Asn Ala Ile Phe Leu Thr Gly Leu Cys Phe Ala Ile Leu Leu Glu
        25                  30                  35

Ala Ile Glu Arg Phe Ile Glu Pro His Glu Met Gln Gln Pro Leu Val
    40                  45                  50

Val Xaa Trp Gly Arg Ala Trp Xaa Ala Ala Gly Gln Arg Ala Gly Ala
 55                  60                  65                  70

Leu Pro Leu Pro Pro Ser Gln Arg Leu Gln Pro Gly Leu Arg Pro Arg
                75                  80                  85

Pro Trp
```

(2) INFORMATION FOR SEQ ID NO: 300:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 79 amino acids
(B) TYPE: AMINO ACID

(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Testis

(ix) FEATURE:
(A) NAME/KEY: sig_peptide
(B) LOCATION: -39..-1
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 7.5
seq LLLLLGLIVLVNI/GI

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 300:

```
Met Glu Asn Gln Leu Trp His Asn Thr Val Arg Cys Cys Asn Gln Tyr
                -35                 -30                 -25

Gln Glu Ser Pro His Asp Ala Glu Asp Ile Leu Leu Leu Leu Leu Gly
            -20                 -15                 -10

Leu Ile Val Leu Val Asn Ile Gly Ile Asn Val Ala Thr Met Met Trp
        -5                   1               5

His Gly Leu Gln Asn Ala Leu Asp Lys Met Ile Asp Trp Ala Thr Gln
 10                 15                  20                  25

Lys Ile Ala Val Phe Phe Ala Val Phe Val Ala Ala Ala Ala Arg
                30                  35                  40
```

(2) INFORMATION FOR SEQ ID NO: 301:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 52 amino acids
(B) TYPE: AMINO ACID
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Ovary

(ix) FEATURE:
(A) NAME/KEY: sig_peptide
(B) LOCATION: -18..-1
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 7.5
seq ITLLTLSPNSVCC/CP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 301:

```
Met Leu Ser Xaa Lys Ile Thr Leu Leu Thr Leu Ser Pro Asn Ser Val
            -15                 -10                 -5
```

```
Cys Cys Cys Pro Ser Ala Thr Leu Gly Ala Ser Asn His Ser His Leu
        1               5                  10

Trp Arg Ser Thr Ser Arg His Gly Ile Ser Phe Pro Trp Ala Phe Leu
 15                 20                  25                  30

Leu Ile Asn Gly
```

(2) INFORMATION FOR SEQ ID NO: 302:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 52 amino acids
(B) TYPE: AMINO ACID
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Testis

(ix) FEATURE:
(A) NAME/KEY: sig_peptide
(B) LOCATION: -18..-1
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 7.4
seq GWLVLCVLAISLA/SM

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 302:

```
Met Glu Gly Pro Arg Gly Trp Leu Val Leu Cys Val Leu Ala Ile Ser
            -15                 -10                 -5

Leu Ala Ser Met Val Thr Glu Asp Leu Cys Arg Ala Pro Asp Gly Lys
        1               5                  10

Lys Gly Glu Ala Gly Xaa Pro Gly Arg Arg Gly Arg Pro Gly Leu Lys
 15                 20                  25                  30

Gly Glu Gln Arg
```

(2) INFORMATION FOR SEQ ID NO: 303:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 108 amino acids
(B) TYPE: AMINO ACID
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Testis

(ix) FEATURE:
(A) NAME/KEY: sig_peptide

(B) LOCATION: -20..-1
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 7.3
seq LAVFMLLAQLVSG/NW

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 303:

```
Met Lys Ser Leu Leu Phe Thr Leu Ala Val Phe Met Leu Leu Ala Gln
-20                 -15                 -10                  -5

Leu Val Ser Gly Asn Trp Tyr Val Lys Lys Cys Leu Asn Asp Val Gly
                 1               5                  10

Ile Cys Lys Lys Lys Cys Lys Pro Glu Glu Met His Val Lys Asn Gly
         15                  20                  25

Trp Ala Met Cys Gly Lys Gln Arg Asp Cys Cys Val Pro Ala Asp Arg
    30                  35                  40

Arg Ala Asn Tyr Pro Val Phe Cys Val Gln Thr Lys Thr Thr Arg Ile
 45                 50                  55                  60

Ser Thr Val Thr Ala Thr Thr Ala Thr Thr Thr Leu Met Met Thr Thr
                 65                  70                  75

Ala Ser Met Ser Ser Met Ala Pro Thr Arg Phe Ser
             80                  85
```

(2) INFORMATION FOR SEQ ID NO: 304:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 18 amino acids
(B) TYPE: AMINO ACID
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Ovary

(ix) FEATURE:
(A) NAME/KEY: sig_peptide
(B) LOCATION: -16..-1
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 7.3
seq LILLFSLLISIVC/MI

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 304:

```
Met Leu Lys Leu Ile Leu Leu Phe Ser Leu Leu Ile Ser Ile Val Cys
    -15                 -10                  -5

Met Ile
  1
```

(2) INFORMATION FOR SEQ ID NO: 305:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 34 amino acids
(B) TYPE: AMINO ACID
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Testis

(ix) FEATURE:
(A) NAME/KEY: sig_peptide
(B) LOCATION: -26..-1
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 7.1
seq LASLQWSLTLAWC/GS

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 305:

```
Met Thr Pro Trp Cys Leu Ala Cys Leu Gly Arg Arg Pro Leu Ala Ser
    -25                 -20                 -15

Leu Gln Trp Ser Leu Thr Leu Ala Trp Cys Gly Ser Gly Ser His Trp
-10                 -5                      1               5

Thr Glu
```

(2) INFORMATION FOR SEQ ID NO: 306:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 55 amino acids
(B) TYPE: AMINO ACID
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Spleen

(ix) FEATURE:
(A) NAME/KEY: sig_peptide
(B) LOCATION: -26..-1
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 6.9
seq LWVLLLCAHVVTL/LV

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 306:

```
Met Thr Met Arg His Asn Trp Thr Pro Asp Leu Ser Pro Leu Trp Val
    -25                 -20                 -15

Leu Leu Leu Cys Ala His Val Val Thr Leu Leu Val Arg Ala Thr Pro
```

```
-10                 -5                  1               5

Val Ser Gln Thr Thr Thr Ala Ala Thr Ala Ser Val Arg Ser Thr Lys
            10                  15                  20

Asp Pro Cys Pro Ser Gln Arg
        25
```

(2) INFORMATION FOR SEQ ID NO: 307:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 35 amino acids
(B) TYPE: AMINO ACID
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Testis

(ix) FEATURE:
(A) NAME/KEY: sig_peptide
(B) LOCATION: -20..-1
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 6.9
seq LFCATLSCMPATS/AP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 307:

```
Met Thr Gly Asn Asn Arg Asp Leu Phe Cys Ala Thr Leu Ser Cys Met
-20                 -15                 -10                  -5

Pro Ala Thr Ser Ala Pro His Met Lys Leu Pro Asp Ile Ser Phe His
                 1                   5                  10

Leu Pro Gly
     15
```

(2) INFORMATION FOR SEQ ID NO: 308:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 37 amino acids
(B) TYPE: AMINO ACID
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Ovary

(ix) FEATURE:
(A) NAME/KEY: sig_peptide
(B) LOCATION: -26..-1
(C) IDENTIFICATION METHOD: Von Heijne matrix

(D) OTHER INFORMATION: score 6.9
seq LWVLLLCAHVVTL/LV

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 308:

```
Met Thr Met Arg His Asn Trp Thr Pro Asp Leu Ser Pro Leu Trp Val
    -25                 -20                 -15

Leu Leu Leu Cys Ala His Val Val Thr Leu Leu Val Arg Ala Thr Pro
-10                 -5                  1               5

Val Ser Gln Pro Thr
            10
```

(2) INFORMATION FOR SEQ ID NO: 309:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 85 amino acids
(B) TYPE: AMINO ACID
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Testis

(ix) FEATURE:
(A) NAME/KEY: sig_peptide
(B) LOCATION: -20..-1
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 6.9
seq LYLLGMLVPGGLG/YD

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 309:

```
Met Lys Pro Leu Leu Glu Thr Leu Tyr Leu Leu Gly Met Leu Val Pro
-20                 -15                 -10                 -5

Gly Gly Leu Gly Tyr Asp Arg Ser Leu Ala Gln His Arg Gln Glu Ile
                1               5                   10

Val Asp Lys Ser Val Ser Pro Trp Ser Leu Glu Thr Tyr Ser Tyr Asn
        15                  20                  25

Ile Tyr His Pro Met Gly Glu Ile Tyr Glu Trp Met Arg Glu Ile Ser
    30                  35                  40

Glu Lys Tyr Lys Glu Val Val Thr Gln His Phe Leu Gly Val Thr Tyr
45                  50                  55                  60

Glu Thr Gln Pro Ala
                65
```

(2) INFORMATION FOR SEQ ID NO: 310:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 72 amino acids
(B) TYPE: AMINO ACID
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Spleen

(ix) FEATURE:
(A) NAME/KEY: sig_peptide
(B) LOCATION: -65..-1
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 6.8
seq LLFLISLAAHLSQ/WT

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 310:

```
Met Asn Gln Ala Asp Pro Arg Leu Arg Ala Val Cys Leu Trp Thr Leu
-65                 -60                 -55                 -50

Thr Ser Ala Ala Met Ser Arg Gly Asp Asn Cys Thr Asp Leu Leu Ala
                -45                 -40                 -35

Leu Gly Ile Pro Ser Ile Thr Gln Ala Trp Gly Leu Trp Val Leu Leu
            -30                 -25                 -20

Gly Ala Val Thr Leu Leu Phe Leu Ile Ser Leu Ala Ala His Leu Ser
        -15                 -10                 -5

Gln Trp Thr Arg Gly Arg Ser Gly
     1               5
```

(2) INFORMATION FOR SEQ ID NO: 311:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 45 amino acids
(B) TYPE: AMINO ACID
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Spleen

(ix) FEATURE:
(A) NAME/KEY: sig_peptide
(B) LOCATION: -42..-1
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION:. score 6.8
seq LLSILSSLTMVIC/RH

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 311:

```
Met His Arg Gln Ile Ser Phe Leu Leu Leu Arg Lys Pro Arg Lys Asn
    -40                 -35                 -30

Trp Phe Cys Gln Asn His Val Asn Leu Arg Lys Arg Tyr Leu Leu Ser
    -25                 -20                 -15

Ile Leu Ser Ser Leu Thr Met Val Ile Cys Arg His Gly
-10                 -5                  1
```

(2) INFORMATION FOR SEQ ID NO: 312:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 52 amino acids
(B) TYPE: AMINO ACID
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Testis

(ix) FEATURE:
(A) NAME/KEY: sig_peptide
(B) LOCATION: -43..-1
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 6.8
seq ALSAXTFVSFLHA/AP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 312:

```
Met Lys Gln Trp Leu Cys Trp Val Leu Arg Leu Glu Gly Arg Gln Gly
            -40                 -35                 -30

Leu Gly Val Gly Glu Pro Arg Gly Leu Arg Leu Cys Leu Gly Ala Leu
        -25                 -20                 -15

Ser Ala Xaa Thr Phe Val Ser Phe Leu His Ala Ala Pro His Ser His
    -10                 -5                  1                   5

Pro Ala Leu Gly
```

(2) INFORMATION FOR SEQ ID NO: 313:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 69 amino acids
(B) TYPE: AMINO ACID
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Ovary

(ix) FEATURE:
(A) NAME/KEY: sig_peptide
(B) LOCATION: -66..-1
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 6.8
seq LLFFLFPILFIRS/QH

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 313:

```
Met Arg Leu Gly Leu Cys Phe Trp Val Pro His Arg Gly Glu Met Ser
    -65                 -60                 -55

Phe Ser Ser His Tyr Ser Arg Gly Thr Trp Tyr Gln Trp Asp Leu Ser
-50                 -45                 -40                 -35

Leu Leu Met Leu Thr Leu Ile Ser Trp Phe Arg Trp Cys Leu Pro Ala
                -30                 -25                 -20

Val Ser Thr Val Glu Leu Leu Phe Phe Leu Phe Pro Ile Leu Phe Ile
            -15                 -10                 -5

Arg Ser Gln His Arg
        1
```

(2) INFORMATION FOR SEQ ID NO: 314:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 108 amino acids
(B) TYPE: AMINO ACID
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Ovary

(ix) FEATURE:
(A) NAME/KEY: sig_peptide
(B) LOCATION: -101..-1
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 6.6
seq IIIVITITSACSA/CI

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 314:

```
Met Asp Phe Trp Glu Glu Tyr Arg Arg Gly Asp Val Pro Phe Ser Trp
    -100                -95                 -90

Cys Pro Ile Arg Ser Tyr Leu Met Ser Val Cys Pro Val Thr Gly Lys
-85                 -80                 -75                 -70

Val Asn Leu Asn His Leu Val Lys Val Ala Ser Ala Arg Phe Leu His
                -65                 -60                 -55

Gln Val Thr Ile Phe Pro Phe Leu Tyr Ser Val Lys Ala Asn Tyr Cys
            -50                 -45                 -40
```

```
Phe Leu Asn Phe Asp Val Pro Gln Tyr Ala Trp Glu Ile His Ser Phe
        -35                 -30                 -25

Ala Ala Pro Ser Ile Leu Ile Val Ile Ile Ile Val Ile Thr Ile Thr
    -20                 -15                 -10

Ser Ala Cys Ser Ala Cys Ile Val Leu Asn Thr Cys
 -5                  1               5
```

(2) INFORMATION FOR SEQ ID NO: 315:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 97 amino acids
(B) TYPE: AMINO ACID
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Testis

(ix) FEATURE:
(A) NAME/KEY: sig_peptide
(B) LOCATION: -27..-1
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 6.5
seq SLSLSTVWNWIQA/SF

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 315:

```
Met Ser Thr Ser Ser Ser Ser Ser Trp Asp Asn Leu Leu Glu Ser Leu
        -25                 -20                 -15

Ser Leu Ser Thr Val Trp Asn Trp Ile Gln Ala Ser Phe Leu Gly Glu
    -10                  -5                   1               5

Thr Ser Ala Pro Gln Gln Thr Ser Leu Gly Leu Leu Asp Asn Leu Ala
                 10                  15                  20

Pro Ala Val Gln Ile Ile Leu Arg Ile Ser Phe Leu Ile Leu Leu Gly
             25                  30                  35

Ile Gly Ile Tyr Ala Leu Trp Lys Arg Ser Ile Gln Ser Ile Gln Lys
        40                  45                  50

Thr Leu Leu Phe Val Ile Thr Leu Tyr Lys Leu Tyr Lys Lys Gly Ser
    55                  60                  65

Ala
 70
```

(2) INFORMATION FOR SEQ ID NO: 316:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 92 amino acids
(B) TYPE: AMINO ACID
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Spleen

(ix) FEATURE:
(A) NAME/KEY: sig_peptide
(B) LOCATION: -26..-1
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 6.5
seq LALGSAGLLWCLA/GF

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 316:

```
Met Val Phe Ala Thr Ile Gly Phe Ser Leu Lys Ser Gly Leu Ala Leu
    -25                 -20                 -15

Gly Ser Ala Gly Leu Leu Trp Cys Leu Ala Gly Phe Phe Gly Tyr Asp
-10                 -5                  1                   5

Thr Gln Gln Pro Thr Ala Pro Asn Ala Ile Glu Gly Tyr Arg Val Met
            10                  15                  20

Ser Ser Phe Gly Val Gly Ala Leu Phe Ala Ala Cys Thr Ile Cys Leu
        25                  30                  35

Leu Ala Xaa Lys Leu Asn Lys Gln Thr Thr Leu Lys Met Ala Asp Asp
    40                  45                  50

Leu Ala Gln Arg Arg Gln Gln Ala Asp Leu Ala Pro
 55                 60                  65
```

(2) INFORMATION FOR SEQ ID NO: 317:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 39 amino acids
(B) TYPE: AMINO ACID
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Testis

(ix) FEATURE:
(A) NAME/KEY: sig_peptide
(B) LOCATION: -14..-1
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 6.4
seq VLLLSGSVSVGVC/CA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 317:

```
Met Val Leu Leu Leu Ser Gly Ser Val Ser Val Gly Val Cys Cys Ala
                -10                 -5                   1

Tyr Leu Cys Ile Ser Ile Ser Lys Thr Pro Thr Ala Cys Ala Leu Tyr
        5                   10                  15

Gly Leu Tyr Leu Pro Phe Phe
    20                  25
```

(2) INFORMATION FOR SEQ ID NO: 318:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 48 amino acids
(B) TYPE: AMINO ACID
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Uterus

(ix) FEATURE:
(A) NAME/KEY: sig_peptide
(B) LOCATION: -29..-1
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 6.4
seq GLCXLCXVXNVFA/GS

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 318:

```
Met Cys Ser Gln Lys Arg Ala Val Ser Asn Gln Gly Leu Met Asp Leu
                -25                 -20                 -15

Gly Leu Cys Xaa Leu Cys Xaa Val Xaa Asn Val Phe Ala Gly Ser Met
            -10                 -5                   1

Pro Gly Lys Ser His Cys His Ser Pro Phe Ser Ile Asn Gln Gly Arg
    5                   10                  15
```

(2) INFORMATION FOR SEQ ID NO: 319:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 43 amino acids
(B) TYPE: AMINO ACID
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Ovary

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
(B) LOCATION: -14..-1
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 6.4
seq LIVLTLHSPSCDT/AQ

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 319:

```
Met Leu Ile Val Leu Thr Leu His Ser Pro Ser Cys Asp Thr Ala Gln
                -10                 -5                   1

Glu Glu Met Gly Arg Val Pro Thr Thr Pro Lys Cys Arg Trp Lys Leu
        5                   10                  15

Gly Leu Ser Met Cys Ser Leu Leu Thr Pro Gly
    20                  25
```

(2) INFORMATION FOR SEQ ID NO: 320:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 124 amino acids
(B) TYPE: AMINO ACID
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Testis

(ix) FEATURE:
(A) NAME/KEY: sig_peptide
(B) LOCATION: -62..-1
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 6.4
seq SVLWLGALGLTIQ/AV

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 320:

```
Met Thr Arg Leu Cys Leu Pro Arg Pro Glu Ala Arg Glu Asp Pro Ile
        -60                 -55                 -50

Pro Val Pro Pro Arg Gly Leu Gly Ala Gly Glu Gly Ser Gly Ser Pro
    -45                 -40                 -35

Val Arg Pro Pro Val Ser Thr Trp Gly Pro Ser Trp Ala Gln Leu Leu
-30                 -25                 -20                 -15

Asp Ser Val Leu Trp Leu Gly Ala Leu Gly Leu Thr Ile Gln Ala Val
                -10                 -5                   1

Phe Ser Thr Thr Gly Pro Ala Leu Leu Leu Leu Leu Val Ser Phe Leu
        5                   10                  15

Thr Phe Asp Leu Leu His Arg Pro Ala Val Thr Leu Cys His Ser Ala
    20                  25                  30
```

Asn Phe Ser Pro Gly Ala Arg Val Arg Gly Pro Val Lys Val Leu Asp
35 40 45 50

Ser Arg Arg Leu Tyr Ser Cys Lys Trp Val Gln Ser
55 60

(2) INFORMATION FOR SEQ ID NO: 321:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 35 amino acids
(B) TYPE: AMINO ACID
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Uterus

(ix) FEATURE:
(A) NAME/KEY: sig_peptide
(B) LOCATION: -15..-1
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 6.4
seq LTCLFLSLISTYP/SC

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 321:

Met Val Leu Thr Cys Leu Phe Leu Ser Leu Ile Ser Thr Tyr Pro Ser
-15 -10 -5 1

Cys Ile Thr Leu Phe Leu Ser Lys Ile Pro Asn Pro Leu Ser Ser Leu
5 10 15

Pro Ser Leu
20

(2) INFORMATION FOR SEQ ID NO: 322:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 37 amino acids
(B) TYPE: AMINO ACID
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Testis

(ix) FEATURE:
(A) NAME/KEY: sig_peptide
(B) LOCATION: -18..-1
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 6.3
seq FSFSLQLLSSSST/NP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 322:

```
Met Leu Ile Pro Val Phe Ser Phe Ser Leu Gln Leu Leu Ser Ser Ser
            -15                 -10                 -5

Ser Thr Asn Pro Val Asn Ser Thr Phe Gln Met Pro Phe Glu Ser Ser
        1               5                   10

His Xaa Thr Thr Arg
 15
```

(2) INFORMATION FOR SEQ ID NO: 323:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 64 amino acids
(B) TYPE: AMINO ACID
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Spleen

(ix) FEATURE:
(A) NAME/KEY: sig_peptide
(B) LOCATION: -47..-1
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 6.3
seq LLLLESVSGLLQP/RT

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 323:

```
Met Ala Ala Ala Xaa Leu Ser Gly Pro Ser Ala Gly Ser Ala Ala Gly
    -45                 -40                 -35

Val Pro Gly Gly Thr Gly Gly Leu Ser Ala Val Ser Ser Gly Pro Arg
    -30                 -25                 -20

Leu Arg Leu Leu Leu Leu Glu Ser Val Ser Gly Leu Leu Gln Pro Arg
-15                 -10                 -5                   1

Thr Gly Ser Ala Val Ala Pro Val His Pro Pro Asn Arg Ser Ala Arg
            5                   10                  15
```

(2) INFORMATION FOR SEQ ID NO: 324:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 21 amino acids
(B) TYPE: AMINO ACID
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Ovary

(ix) FEATURE:
(A) NAME/KEY: sig_peptide
(B) LOCATION: -15..-1
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 6.2
seq NWLFLFVFTFCNC/FF

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 324:

```
Met His Asn Trp Leu Phe Leu Phe Val Phe Thr Phe Cys Asn Cys Phe
-15                 -10                  -5                   1

Phe Lys Asn Asn Gly
            5
```

(2) INFORMATION FOR SEQ ID NO: 325:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 36 amino acids
(B) TYPE: AMINO ACID
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Uterus

(ix) FEATURE:
(A) NAME/KEY: sig_peptide
(B) LOCATION: -17..-1
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 6.2
seq CFYFLSTALGSQA/DS

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 325:

```
Met His Val Glu Cys Phe Tyr Phe Leu Ser Thr Ala Leu Gly Ser Gln
    -15                 -10                  -5

Ala Asp Ser Trp Val Ser Gly Leu Gln Gln Ala Gly Leu Leu Pro Ala
      1              5                  10                  15

Ile Gly Tyr Arg
```

(2) INFORMATION FOR SEQ ID NO: 326:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 59 amino acids
(B) TYPE: AMINO ACID
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Ovary

(ix) FEATURE:
(A) NAME/KEY: sig_peptide
(B) LOCATION: -19..-1
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 6.1
seq LALLWSLPASDLG/RS

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 326:

```
Met Ser Pro Gly Ser Ala Leu Ala Leu Leu Trp Ser Leu Pro Ala Ser
            -15                 -10                 -5

Asp Leu Gly Arg Ser Val Ile Ala Gly Leu Trp Pro His Thr Gly Val
            1                5                  10

Leu Ile His Leu Glu Thr Ser Gln Ser Phe Leu Gln Gly Gln Leu Thr
    15                  20                  25

Lys Ser Ile Phe Pro Leu Cys Cys Thr Ser Leu
30                  35                  40
```

(2) INFORMATION FOR SEQ ID NO: 327:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 37 amino acids
(B) TYPE: AMINO ACID
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Spleen

(ix) FEATURE:
(A) NAME/KEY: sig_peptide
(B) LOCATION: -13..-1
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 6.1
seq MALALGSIPSSIA/SS

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 327:

```
Met Ala Leu Ala Leu Gly Ser Ile Pro Ser Ser Ile Ala Ser Ser Trp
        -10                 -5                  1

Val His Val Ser His Phe Cys Pro Cys Leu Leu His Thr Thr Leu Pro
    5                   10                  15

Gln Ser Thr Pro Lys
```

20

(2) INFORMATION FOR SEQ ID NO: 328:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 26 amino acids
(B) TYPE: AMINO ACID
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Ovary

(ix) FEATURE:
(A) NAME/KEY: sig_peptide
(B) LOCATION: -16..-1
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 6.1
seq FLFCTLFSLVVHP/SH

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 328:

```
Met Leu Ala Phe Leu Phe Cys Thr Leu Phe Ser Leu Val Val His Pro
    -15                 -10                     -5

Ser His Ile Asp Leu Lys Cys Ser Phe Tyr
  1               5                 10
```

(2) INFORMATION FOR SEQ ID NO: 329:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 106 amino acids
(B) TYPE: AMINO ACID
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Spleen

(ix) FEATURE:
(A) NAME/KEY: sig_peptide
(B) LOCATION: -36..-1
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 6
seq LLYTLQTISSLSG/CF

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 329:

```
Met Ala Gln Met Pro Leu Thr Gly Ser Tyr Gln Asp Leu Glu Tyr Phe
    -35                 -30                     -25
```

Leu Glu Cys Met Phe Leu His Leu Leu Tyr Thr Leu Gln Thr Ile Ser
-20 -15 -10 -5

Ser Leu Ser Gly Cys Phe Lys Gln Phe Phe Phe Gln Leu Asn Cys Phe
1 5 10

Cys Trp Gly Glu Ile Leu Trp His Ser Ser Phe Leu His Ser Gly Ser
15 20 25

Cys Leu Leu Val Leu Leu Ile Lys Lys Lys Lys Ile Tyr Leu Gln Ser
30 35 40

Xaa Xaa Ile Tyr Thr Gly Tyr Xaa Ile Asp Xaa Xaa Xaa Leu Xaa Xaa
45 50 55 60

Phe Ser Ile Pro Leu Ser Phe Ile Gln Phe
65 70

(2) INFORMATION FOR SEQ ID NO: 330:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 amino acids
(B) TYPE: AMINO ACID
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Ovary

(ix) FEATURE:
(A) NAME/KEY: sig_peptide
(B) LOCATION: -15..-1
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 6
seq LLMGLWVRTVLQG/KE

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 330:

Met Ala Leu Leu Met Gly Leu Trp Val Arg Thr Val Leu Gln Gly Lys
-15 -10 -5 1

Glu Ala Ser Gly
5

(2) INFORMATION FOR SEQ ID NO: 331:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 27 amino acids
(B) TYPE: AMINO ACID
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Uterus

(ix) FEATURE:
(A) NAME/KEY: sig_peptide
(B) LOCATION: -19..-1
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 6
seq LAILIXSLKLTIG/IQ

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 331:

```
Met Ile Asn His Leu Tyr Leu Ala Ile Leu Ile Xaa Ser Leu Lys Leu
                -15                 -10                 -5

Thr Ile Gly Ile Gln Lys Arg Phe Gly Pro Pro
            1               5
```

(2) INFORMATION FOR SEQ ID NO: 332:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 69 amino acids
(B) TYPE: AMINO ACID
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Ovary

(ix) FEATURE:
(A) NAME/KEY: sig_peptide
(B) LOCATION: -50..-1
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 6
seq LLYLCSFPLPGTS/LF

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 332:

```
Met Gly Arg Gln Gly Thr Leu Glu Ile Glu Gly Ile Leu Cys Val Ile
-50                 -45                 -40                 -35

Thr Trp Leu Glu Ala Asn Leu Gly Lys Gln Lys Asp Glu Asn His Tyr
                -30                 -25                 -20

Tyr Lys Lys Leu Ser Leu Leu Tyr Leu Cys Ser Phe Pro Leu Pro Gly
            -15                 -10                 -5

Thr Ser Leu Phe Leu Leu Cys Ser Phe Ser Tyr Leu Thr Gln Arg Leu
        1               5                   10

Ser Gln Gly Gly Gly
 15
```

(2) INFORMATION FOR SEQ ID NO: 333:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 74 amino acids
(B) TYPE: AMINO ACID
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Testis

(ix) FEATURE:
(A) NAME/KEY: sig_peptide
(B) LOCATION: -39..-1
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 5.9
seq SAWWCVLLEWSQG/AS

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 333:

```
Met Glu Leu Thr Asn Lys Gln Thr Gly Thr Asp Arg His Glu Gln Val
                -35                 -30                 -25

Leu Arg Arg Val Lys Gln Asp Lys Arg Ile Ser Ala Trp Trp Cys Val
            -20                 -15                 -10

Leu Leu Glu Trp Ser Gln Gly Ala Ser Leu Arg Arg Gln His Arg Gly
        -5                   1               5

Glu Thr Ser Pro Lys Ser Gly Glu Arg Leu Ser Arg Gln Arg Glu Gln
 10                 15                  20                  25

Gln Lys Pro Gln Met Ser Asp Lys Ser Leu
                30                  35
```

(2) INFORMATION FOR SEQ ID NO: 334:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 70 amino acids
(B) TYPE: AMINO ACID
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Testis

(ix) FEATURE:
(A) NAME/KEY: sig_peptide
(B) LOCATION: -22..-1
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 5.9
seq VLGLLFSISDTWA/PA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 334:

```
Met Ala Lys Arg Gln Asn Pro Thr Ser Val Leu Gly Leu Leu Phe Ser
    -20                 -15                 -10

Ile Ser Asp Thr Trp Ala Pro Ala Val Ser Ser Trp Lys Ala Glu Ala
     -5                  1               5                  10

Lys Asp Gly Ala Asp Gln Glu Asp Ala Arg Xaa Xaa Ser Gln Arg Ser
                 15                  20                  25

Pro Xaa Ser Thr Ala Gly Ser Gln Glu Pro Tyr Phe Trp Phe Val Trp
             30                  35                  40

Val Glu Gly Glu Gly Arg
         45
```

(2) INFORMATION FOR SEQ ID NO: 335:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 42 amino acids
(B) TYPE: AMINO ACID
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Testis

(ix) FEATURE:
(A) NAME/KEY: sig_peptide
(B) LOCATION: -25..-1
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 5.9
seq FCLSLQIFRVSLA/LA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 335:

```
Met Asn Val Leu Pro Phe Ser Tyr Tyr Tyr Ile Leu Phe Cys Leu Ser
-25                 -20                 -15                 -10

Leu Gln Ile Phe Arg Val Ser Leu Ala Leu Ala Xaa Thr His Glu Val
                 -5                   1               5

Pro Val Ser Thr His Thr Asn Xaa Leu His
     10                  15
```

(2) INFORMATION FOR SEQ ID NO: 336:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 58 amino acids
(B) TYPE: AMINO ACID
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Ovary

(ix) FEATURE:
(A) NAME/KEY: sig_peptide
(B) LOCATION: -29..-1
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 5.9
seq FSYISXFLSPVCG/CS

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 336:

```
Met Lys Cys Leu Lys Val Asn Pro Phe Leu Phe Leu Val Phe Asn Phe
            -25                 -20                 -15

Phe Ser Tyr Ile Ser Xaa Phe Leu Ser Pro Val Cys Gly Cys Ser Val
        -10                 -5                  1

Cys Asn Leu Lys His Trp Glu Asn Glu Leu Leu Phe Pro Ser Pro His
    5                   10                  15

Phe Leu Pro Tyr Lys Phe Xaa Phe Leu Phe
20                  25
```

(2) INFORMATION FOR SEQ ID NO: 337:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 51 amino acids
(B) TYPE: AMINO ACID
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Testis

(ix) FEATURE:
(A) NAME/KEY: sig_peptide
(B) LOCATION: -33..-1
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 5.8
seq XLCLGMALCPRQA/TR

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 337:

```
Met Ser Trp Thr Val Pro Val Val Arg Ala Ser Gln Arg Val Ser Ser
        -30                 -25                 -20

Val Gly Ala Asn Xaa Leu Cys Leu Gly Met Ala Leu Cys Pro Arg Gln
    -15                 -10                 -5

Ala Thr Arg Ile Pro Leu Asn Gly Thr Trp Leu Phe Thr Pro Val Ser
    1               5                   10                  15
```

Lys Met Ala

(2) INFORMATION FOR SEQ ID NO: 338:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 21 amino acids
(B) TYPE: AMINO ACID
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Ovary

(ix) FEATURE:
(A) NAME/KEY: sig_peptide
(B) LOCATION: -15..-1
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 5.8
seq FLXLMTLTTHVHS/SA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 338:

```
Met Gly Phe Leu Xaa Leu Met Thr Leu Thr Thr His Val His Ser Ser
-15                 -10                 -5                   1

Ala Lys Pro Asn Gly
            5
```

(2) INFORMATION FOR SEQ ID NO: 339:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 22 amino acids
(B) TYPE: AMINO ACID
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Ovary

(ix) FEATURE:
(A) NAME/KEY: sig_peptide
(B) LOCATION: -16..-1
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 5.7
seq RVLLLAQLFLGSG/KT

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 339:

```
Met Leu Phe Arg Val Leu Leu Leu Ala Gln Leu Phe Leu Gly Ser Gly
    -15                 -10                 -5
```

```
Lys Thr Leu Arg Thr Pro
  1               5
```

(2) INFORMATION FOR SEQ ID NO: 340:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 55 amino acids
(B) TYPE: AMINO ACID
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Ovary

(ix) FEATURE:
(A) NAME/KEY: sig_peptide
(B) LOCATION: -32..-1
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 5.7
seq SLPLSTSAPPLRG/LR

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 340:

```
Met Arg Val Pro Glu Asp Leu Ala Ser Lys Ile Leu Leu Pro Gly Cys
        -30                 -25                 -20

Ala Pro Gly Ser Leu Pro Leu Ser Thr Ser Ala Pro Pro Leu Arg Gly
    -15                 -10                 -5

Leu Arg Leu Lys Glu His Pro Gly Arg Gly Pro Ser Ser Pro Lys Ala
  1               5                  10                  15

Ala Cys Pro Glu Thr Pro Ala
            20
```

(2) INFORMATION FOR SEQ ID NO: 341:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 40 amino acids
(B) TYPE: AMINO ACID
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Ovary

(ix) FEATURE:
(A) NAME/KEY: sig_peptide
(B) LOCATION: -31..-1
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 5.7
seq SDLCLCQCILARA/HD

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 341:

```
Met Phe Pro His Xaa Glu Thr Gln Val Lys Cys Phe Trp Gln Gly Leu
    -30                 -25                 -20

Arg Arg Ser Asp Leu Cys Leu Cys Gln Cys Ile Leu Ala Arg Ala His
-15                 -10                 -5                    1

Asp Gly Asp Leu Tyr Leu Phe Phe
            5
```

(2) INFORMATION FOR SEQ ID NO: 342:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 64 amino acids
(B) TYPE: AMINO ACID
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Testis

(ix) FEATURE:
(A) NAME/KEY: sig_peptide
(B) LOCATION: -20..-1
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 5.6
seq LAVFMXLAQLVSG/NW

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 342:

```
Met Lys Ser Leu Leu Phe Thr Leu Ala Val Phe Met Xaa Leu Ala Gln
-20                 -15                 -10                  -5

Leu Val Ser Gly Asn Trp Tyr Val Lys Lys Cys Leu Asn Xaa Phe Gly
                1                   5                   10

Ile Cys Lys Xaa Lys Cys Lys Pro Glu Glu Met His Val Lys Asn Gly
        15                  20                  25

Trp Xaa Met Cys Gly Lys Gln Arg Asp Cys Cys Val Pro Ala Asn Gly
    30                  35                  40
```

(2) INFORMATION FOR SEQ ID NO: 343:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 48 amino acids
(B) TYPE: AMINO ACID
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Testis

(ix) FEATURE:
(A) NAME/KEY: sig_peptide
(B) LOCATION: -23..-1
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 5.6
seq LLNVACCIPFSSS/LF

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 343:

```
Met His Leu Tyr Ser Cys Ser Cys Met Arg Leu Leu Asn Val Ala Cys
            -20                 -15                 -10

Cys Ile Pro Phe Ser Ser Ser Leu Phe Pro His Ile Leu Phe Lys Ser
         -5                  1               5

Leu Asn Tyr Ser Leu Thr Ser Phe Leu Lys Ala Val Arg Gly Arg Trp
 10                  15                  20                  25
```

(2) INFORMATION FOR SEQ ID NO: 344:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 21 amino acids
(B) TYPE: AMINO ACID
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Testis

(ix) FEATURE:
(A) NAME/KEY: sig_peptide
(B) LOCATION: -16..-1
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 5.5
seq PLVLSPLSYQCSS/QG

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 344:

```
Met Arg Ala Pro Leu Val Leu Ser Pro Leu Ser Tyr Gln Cys Ser Ser
    -15                 -10                  -5

Gln Gly His Ile Trp
  1               5
```

(2) INFORMATION FOR SEQ ID NO: 345:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 39 amino acids
(B) TYPE: AMINO ACID

(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Testis

(ix) FEATURE:
(A) NAME/KEY: sig_peptide
(B) LOCATION: -36..-1
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 5.5
seq FTSMCILFHCLLS/FQ

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 345:

```
Met Gln Val Pro His Leu Arg Val Trp Thr Gln Val Xaa Asp Thr Phe
    -35                 -30                 -25

Ile Gly Tyr Arg Asn Leu Gly Phe Thr Ser Met Cys Ile Leu Phe His
-20                 -15                 -10                  -5

Cys Leu Leu Ser Phe Gln Arg
                 1
```

(2) INFORMATION FOR SEQ ID NO: 346:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 46 amino acids
(B) TYPE: AMINO ACID
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Testis

(ix) FEATURE:
(A) NAME/KEY: sig_peptide
(B) LOCATION: -36..-1
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 5.4
seq LWLMHQSFQKSNS/SS

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 346:

```
Met Gln Lys Leu Met Ala Val Pro Met Ile Thr Arg Ala Gln Gly Gly
    -35                 -30                 -25

Asp Thr Cys Thr Arg Gln Ile Leu Trp Leu Met His Gln Ser Phe Gln
-20                 -15                 -10                  -5

Lys Ser Asn Ser Ser Ser Thr Ser Tyr Cys Ser Ala Gln Gly
                 1               5                  10
```

(2) INFORMATION FOR SEQ ID NO: 347:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 54 amino acids
(B) TYPE: AMINO ACID
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Ovary

(ix) FEATURE:
(A) NAME/KEY: sig_peptide
(B) LOCATION: -45..-1
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 5.4
seq AHRSLCLWPACLC/AR

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 347:

```
Met Cys Xaa Ala Gly Phe Xaa Asp His Pro Arg Ala Ala Arg His Ala
-45                 -40                 -35                 -30

Arg Thr Ser Arg His Pro Leu Pro Trp Val Cys Val Ser Gln Xaa Pro
                -25                 -20                 -15

Ala His Arg Ser Leu Cys Leu Trp Pro Ala Cys Leu Cys Ala Arg Val
            -10                 -5                  1

Leu Pro Pro Ala Pro Gly
    5
```

(2) INFORMATION FOR SEQ ID NO: 348:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 22 amino acids
(B) TYPE: AMINO ACID
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Testis

(ix) FEATURE:
(A) NAME/KEY: sig_peptide
(B) LOCATION: -18..-1
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 5.4
seq ILVSFILAALSLS/TT

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 348:

```
Met Thr Ser Lys Phe Ile Leu Val Ser Phe Ile Leu Ala Ala Leu Ser
            -15                 -10                     -5

Leu Ser Thr Thr Ile Gly
         1
```

(2) INFORMATION FOR SEQ ID NO: 349:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 18 amino acids
(B) TYPE: AMINO ACID
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Ovary

(ix) FEATURE:
(A) NAME/KEY: sig_peptide
(B) LOCATION: -15..-1
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 5.4
seq LLIFILTVHHTPS/LP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 349:

```
Met His Leu Leu Ile Phe Ile Leu Thr Val His His Thr Pro Ser Leu
-15                 -10                 -5                    1

Pro Ser
```

(2) INFORMATION FOR SEQ ID NO: 350:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 amino acids
(B) TYPE: AMINO ACID
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Ovary

(ix) FEATURE:
(A) NAME/KEY: sig_peptide
(B) LOCATION: -16..-1
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 5.3
seq SSLMVQLISQVYS/CM

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 350:

Met Leu Ser Ser Ser Leu Met Val Gln Leu Ile Ser Gln Val Tyr Ser
    -15   -10   -5

Cys Met Arg Arg
  1

(2) INFORMATION FOR SEQ ID NO: 351:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 30 amino acids
(B) TYPE: AMINO ACID
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Testis

(ix) FEATURE:
(A) NAME/KEY: sig_peptide
(B) LOCATION: -14..-1
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 5.3
seq FSYILCMLFCLFS/QD

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 351:

Met Phe Ser Tyr Ile Leu Cys Met Leu Phe Cys Leu Phe Ser Gln Asp
                -10   -5   1

Lys Phe Leu Glu Val Thr Leu Leu Cys Glu Arg Tyr Met Leu
        5   10   15

(2) INFORMATION FOR SEQ ID NO: 352:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 45 amino acids
(B) TYPE: AMINO ACID
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Uterus

(ix) FEATURE:
(A) NAME/KEY: sig_peptide
(B) LOCATION: -19..-1
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 5.2
seq VTLAFSLLVLSES/AV

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 352:

```
Met Leu Phe Leu Tyr Tyr Val Thr Leu Ala Phe Ser Leu Leu Val Leu
                -15                 -10                 -5

Ser Glu Ser Ala Val Leu Lys Arg Arg Glu Ile Phe Xaa Thr Gly Leu
            1                   5                   10

Gly Cys Val Thr Gly Leu Gly Cys Val Thr Gly Leu Arg
    15                  20                  25
```

(2) INFORMATION FOR SEQ ID NO: 353:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 31 amino acids
(B) TYPE: AMINO ACID
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Spleen

(ix) FEATURE:
(A) NAME/KEY: sig_peptide
(B) LOCATION: -14..-1
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 5.2
seq LLSGLWLSSVKEC/DD

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 353:

```
Met Leu Leu Ser Gly Leu Trp Leu Ser Ser Val Lys Glu Cys Asp Asp
                -10                 -5                  1

Trp Arg Ala Asp Gly Cys Leu Pro Ser Ile Val His Pro Leu Arg
        5                   10                  15
```

(2) INFORMATION FOR SEQ ID NO: 354:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 41 amino acids
(B) TYPE: AMINO ACID
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Testis

(ix) FEATURE:
(A) NAME/KEY: sig_peptide
(B) LOCATION: -18..-1
(C) IDENTIFICATION METHOD: Von Heijne matrix

(D) OTHER INFORMATION: score 5.2
seq VFCFSWLMSSSSP/SI

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 354:

```
Met Val Ala Phe Ser Val Phe Cys Phe Ser Trp Leu Met Ser Ser Ser
            -15                 -10                     -5

Ser Pro Ser Ile Phe Trp Ser His Phe Tyr Ser Pro Phe Lys Asp Leu
        1               5                   10

Ser Lys Met Tyr Asn Tyr Val Ser Pro
 15                 20
```

(2) INFORMATION FOR SEQ ID NO: 355:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 42 amino acids
(B) TYPE: AMINO ACID
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Spleen

(ix) FEATURE:
(A) NAME/KEY: sig_peptide
(B) LOCATION: -16..-1
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 5.1
seq LALGIGPPGCLQG/SP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 355:

```
Met Val Pro Leu Ala Leu Gly Ile Gly Pro Pro Gly Cys Leu Gln Gly
    -15                 -10                     -5

Ser Pro Ser Gln Trp Leu Val Arg Ala Pro Gly Ala Gln Leu Ser Pro
  1                 5                   10                  15

Ile Gly Val Ala Thr Glu Arg Glu Gln Arg
            20                  25
```

(2) INFORMATION FOR SEQ ID NO: 356:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 41 amino acids
(B) TYPE: AMINO ACID
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Uterus

(ix) FEATURE:
(A) NAME/KEY: sig_peptide
(B) LOCATION: -32..-1
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 5.1
seq LLWFCTAMRPGGA/GL

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 356:

```
Met Asn Leu Cys Met Gly Val Leu Leu Lys Val Gly Thr Ser Arg Arg
        -30                 -25                 -20

Cys Leu Cys Leu Leu Trp Phe Cys Thr Ala Met Arg Pro Gly Gly Ala
    -15                 -10                 -5

Gly Leu Pro Asn Ala Thr Pro Glu Trp
  1               5
```

(2) INFORMATION FOR SEQ ID NO: 357:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 16 amino acids
(B) TYPE: AMINO ACID
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Uterus

(ix) FEATURE:
(A) NAME/KEY: sig_peptide
(B) LOCATION: -14..-1
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 5.1
seq SLAKSLFLRVARG/LG

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 357:

```
Met Ser Leu Ala Lys Ser Leu Phe Leu Arg Val Ala Arg Gly Leu Gly
                -10                 -5                    1
```

(2) INFORMATION FOR SEQ ID NO: 358:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 94 amino acids
(B) TYPE: AMINO ACID
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Ovary

(ix) FEATURE:
(A) NAME/KEY: sig_peptide
(B) LOCATION: -18..-1
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 5.1
seq FLPSATLLLSAES/FF

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 358:

```
Met Arg Leu Pro Pro Phe Leu Pro Ser Ala Thr Leu Leu Leu Ser Ala
        -15                 -10                 -5

Glu Ser Phe Phe Arg Ser Val Ser Glu Tyr Pro Ser Leu Pro Ser Pro
         1               5                  10

Ser Ala Gly Gly Pro Gly Cys Val Ser Gly Lys Trp Gly Ser Gly Ser
 15                 20                  25                  30

Asn Gly Pro Leu Ser Ser Leu Ser Cys Ser Leu Cys Arg Lys Pro Leu
                35                  40                  45

Leu His Ser Thr Ala Leu Ser Ser Ser Arg Pro Phe Phe Ser Pro Gly
            50                  55                  60

Phe Pro Cys Gln Ile Ser Pro Arg Ser Gly Leu His Pro Leu
        65                  70                  75
```

(2) INFORMATION FOR SEQ ID NO: 359:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 51 amino acids
(B) TYPE: AMINO ACID
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Ovary

(ix) FEATURE:
(A) NAME/KEY: sig_peptide
(B) LOCATION: -49..-1
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 5
seq PLLLLLREELVTG/AV

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 359:

```
Met Ser Asp Arg Lys Arg Thr Lys Phe Ser Tyr Val Gln Leu Pro Cys
            -45                 -40                 -35

Pro Ile Ser Leu Leu Pro Arg Ser Phe Lys Arg Gly Gln Ile Pro Gly
```

-30 -25 -20

Pro Ser Ala Pro Pro Leu Leu Leu Leu Leu Arg Glu Glu Leu Val Thr
-15 -10 -5

Gly Ala Val
1

(2) INFORMATION FOR SEQ ID NO: 360:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 79 amino acids
(B) TYPE: AMINO ACID
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Ovary

(ix) FEATURE:
(A) NAME/KEY: sig_peptide
(B) LOCATION: -41..-1
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 5
seq FCFFPAFLVXVXS/QP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 360:

Met Thr Pro Leu Gly Ser Gly Pro Pro Arg Glu Ala Ser Ile Ala Gln
-40 -35 -30

Val Arg Gly Phe Ser Arg Thr Phe Phe Arg Val Ala Phe Cys Phe Phe
-25 -20 -15 -10

Pro Ala Phe Leu Val Xaa Val Xaa Ser Gln Pro Ser Gly Phe Ser Thr
-5 1 5

Thr Glu Thr Leu Cys Ala Gln Asp Phe Ser Asp Val Ile Phe Leu Arg
10 15 20

Arg Ala Asp Thr Arg Arg Trp Lys Lys Lys Gln Leu Arg Arg Arg
25 30 35

(2) INFORMATION FOR SEQ ID NO: 361:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 amino acids
(B) TYPE: AMINO ACID
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Homo Sapiens

(F) TISSUE TYPE: Testis

(ix) FEATURE:
(A) NAME/KEY: sig_peptide
(B) LOCATION: -15..-1
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 5
seq CSALFPLLSLLSC/KE

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 361:

```
Met Arg Cys Ser Ala Leu Phe Pro Leu Leu Ser Leu Leu Ser Cys Lys
-15                 -10                 -5                   1

Glu Arg Xaa Trp Cys Leu Ser Thr Leu Glu Asp Ala Ala Thr Xaa Arg
            5                   10                  15

His Leu Gly Ser Arg Glu Gln Pro Ser Gly Asp Ala Glu Pro Val Glu
        20                  25                  30

Val Trp
    35
```

(2) INFORMATION FOR SEQ ID NO: 362:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 35 amino acids
(B) TYPE: AMINO ACID
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Ovary

(ix) FEATURE:
(A) NAME/KEY: sig_peptide
(B) LOCATION: -21..-1
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 5
seq IISLLKLCSFCFI/KD

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 362:

```
Met Leu Tyr Asp Gln Tyr Tyr Leu Ile Ile Ser Leu Leu Lys Leu Cys
    -20                 -15                 -10

Ser Phe Cys Phe Ile Lys Asp Phe Lys Ala Ser Asn Ile Thr Leu Val
-5                  1                   5                   10

Val Ile Leu
```

(2) INFORMATION FOR SEQ ID NO: 363:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 75 amino acids
(B) TYPE: AMINO ACID
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Uterus

(ix) FEATURE:
(A) NAME/KEY: sig_peptide
(B) LOCATION: -65..-1
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 5
seq LCSFLSLRFCTLS/FM

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 363:

```
Met Ala Asn Cys Phe Leu Ser His Lys Ser Gln Thr Ile Leu Ile Ser
-65                 -60                 -55                 -50

Lys Pro Ala Leu Thr Gln Ser His Phe Thr Ser Pro Ala Gly Leu Phe
                -45                 -40                 -35

Leu Thr Val Glu Lys Ser His Leu Leu Thr Arg Leu Phe Phe His Trp
            -30                 -25                 -20

Leu Ser Leu Val Leu Cys Ser Phe Leu Ser Leu Arg Phe Cys Thr Leu
        -15                 -10                 -5

Ser Phe Met Cys Ser Phe Ala Leu Phe His Leu
    1               5                   10
```

(2) INFORMATION FOR SEQ ID NO: 364:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 93 amino acids
(B) TYPE: AMINO ACID
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Testis

(ix) FEATURE:
(A) NAME/KEY: sig_peptide
(B) LOCATION: -18..-1
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 5
seq LTYLLFLPDWAAV/FE

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 364:

```
Met His Gly Ala Gly Leu Thr Tyr Leu Leu Phe Leu Pro Asp Trp Ala
            -15                 -10                 -5

Ala Val Phe Glu Leu Tyr Asn Cys Glu Asp Glu Arg Cys Tyr Leu Asp
        1               5                   10

Leu Ala Arg Leu Arg Gly Val His Tyr Ile Thr Trp Arg Arg Gln Asn
 15                 20                  25                  30

Lys Val Phe Pro Gln Asp Lys Gly His His Pro Thr Leu Gly Glu His
                35                  40                  45

Pro Lys Phe Thr Asn Tyr Ser Phe Asp Val Glu Glu Phe Met Tyr Leu
            50                  55                  60

Val Leu Gln Ala Ala Asp His Val Leu Gln His Pro Gly
        65                  70                  75
```

(2) INFORMATION FOR SEQ ID NO: 365:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 41 amino acids
(B) TYPE: AMINO ACID
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Ovary

(ix) FEATURE:
(A) NAME/KEY: sig_peptide
(B) LOCATION: -15..-1
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 4.9
seq CLSATLAFSGSFL/AP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 365:

```
Met Cys Cys Leu Ser Ala Thr Leu Ala Phe Ser Gly Ser Phe Leu Ala
-15                 -10                 -5                  1

Pro His Leu Ile Phe Cys Cys Phe Ser His Leu Asn Val Ile Ile Leu
            5                   10                  15

Leu Ser Ser Leu Ser Pro Ile His Gly
        20                  25
```

(2) INFORMATION FOR SEQ ID NO: 366:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 45 amino acids
(B) TYPE: AMINO ACID
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Ovary

(ix) FEATURE:
(A) NAME/KEY: sig_peptide
(B) LOCATION: -39..-1
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 4.9
seq SGLRGLLLQEALG/AV

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 366:

```
Met Ala Glu Leu Asp Leu Met Ala Pro Gly Pro Leu Pro Arg Ala Thr
                -35                 -30                 -25

Ala Gln Pro Pro Ala Pro Leu Ser Pro Asp Ser Gly Leu Arg Gly Leu
            -20                 -15                 -10

Leu Leu Gln Glu Ala Leu Gly Ala Val Pro Asp Pro Arg
        -5                  1               5
```

(2) INFORMATION FOR SEQ ID NO: 367:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 56 amino acids
(B) TYPE: AMINO ACID
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Ovary

(ix) FEATURE:
(A) NAME/KEY: sig_peptide
(B) LOCATION: -28..-1
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 4.9
seq FLVACPLFGVCLX/FF

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 367:

```
Met Thr Leu Thr His Gly Asn Asn Ile Leu His Leu Ala Asn Phe Phe
            -25                 -20                 -15

Leu Val Ala Cys Pro Leu Phe Gly Val Cys Leu Xaa Phe Phe Ile Leu
        -10                 -5                  1

Arg Phe Arg Leu Tyr Ile Gln Gly Pro Asn Val Thr Gln Val Ile Leu
5                   10                  15                  20

His Leu Ser Gln Gly Thr Leu Ser
                25
```

(2) INFORMATION FOR SEQ ID NO: 368:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 16 amino acids
(B) TYPE: AMINO ACID
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Ovary

(ix) FEATURE:
(A) NAME/KEY: sig_peptide
(B) LOCATION: -14..-1
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 4.9
seq VLRWLPWPRGSHS/DS

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 368:

```
Met Val Leu Arg Trp Leu Pro Trp Pro Arg Gly Ser His Ser Asp Ser
                -10                 -5                   1
```

(2) INFORMATION FOR SEQ ID NO: 369:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 39 amino acids
(B) TYPE: AMINO ACID
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Uterus

(ix) FEATURE:
(A) NAME/KEY: sig_peptide
(B) LOCATION: -24..-1
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 4.8
seq FSFLGTLFHKSNS/ED

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 369:

```
Met Lys Ala Arg Leu Ser Gly Asn Leu Ile Cys Phe Ser Phe Leu Gly
                -20                 -15                 -10

Thr Leu Phe His Lys Ser Asn Ser Glu Asp Ser Ser Val Gly Lys Gly
            -5                   1               5

Asp Trp Lys Lys Lys Asn Lys
```

10 15

(2) INFORMATION FOR SEQ ID NO: 370:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 37 amino acids
(B) TYPE: AMINO ACID
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Ovary

(ix) FEATURE:
(A) NAME/KEY: sig_peptide
(B) LOCATION: -16..-1
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 4.8
seq VCLVPQTPSLCLG/KG

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 370:

```
Met Ser His Val Cys Leu Val Pro Gln Thr Pro Ser Leu Cys Leu Gly
    -15                 -10                 -5

Lys Gly Thr Pro Arg Ser Arg Ser Ala Pro Phe Gln Ser Ser Gly Pro
  1               5                  10                  15

His Arg Leu Cys Ala
            20
```

(2) INFORMATION FOR SEQ ID NO: 371:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 68 amino acids
(B) TYPE: AMINO ACID
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Spleen

(ix) FEATURE:
(A) NAME/KEY: sig_peptide
(B) LOCATION: -29..-1
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 4.8
seq VLTSVNLFIGING/SV

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 371:

```
Met Tyr Pro Ala Ser Phe Val Phe Lys Ile Pro Ser Thr Ala Tyr Val
                -25                 -20                 -15

Val Leu Thr Ser Val Asn Leu Phe Ile Gly Ile Asn Gly Ser Val Ala
            -10                 -5                  1

Thr Phe Val Leu Glu Leu Phe Thr Asp Asn Lys Leu Asn Asn Ile Asn
     5                  10                  15

Asp Ile Leu Lys Ser Val Phe Leu Ile Phe Pro His Phe Cys Leu Gly
 20                 25                  30                  35

Arg Gly Gln Thr
```

(2) INFORMATION FOR SEQ ID NO: 372:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 42 amino acids
(B) TYPE: AMINO ACID
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Testis

(ix) FEATURE:
(A) NAME/KEY: sig_peptide
(B) LOCATION: -30..-1
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 4.8
seq RSSLWVTAPLVSA/CP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 372:

```
Met Ser Ser Ser Arg Lys Asp His Leu Gly Ala Xaa Ala Gln Ser Pro
-30                 -25                 -20                 -15

Ser Arg Ser Ser Leu Trp Val Thr Ala Pro Leu Val Ser Ala Cys Pro
                -10                 -5                  1

Thr Cys Ser Pro Ala Thr His Pro Thr Gly
         5                  10
```

(2) INFORMATION FOR SEQ ID NO: 373:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 56 amino acids
(B) TYPE: AMINO ACID
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Homo Sapiens

(F) TISSUE TYPE: Spleen

(ix) FEATURE:
(A) NAME/KEY: sig_peptide
(B) LOCATION: -19..-1
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 4.8
seq ATYLVQSSACCPA/IV

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 373:

```
Met Ala Ser Pro Ala Ala Ala Thr Tyr Leu Val Gln Ser Ser Ala Cys
                -15                 -10                     -5

Cys Pro Ala Ile Val Arg His Leu Cys Gln Xaa Tyr Arg Ser Met Pro
             1               5                  10

Val Phe Leu Asp Pro Ala Xaa Ile Ala Thr Leu Glu Gly Ile Ser Trp
     15                  20                  25

Arg Leu Pro Ser Ala Pro Ser Asp
 30                  35
```

(2) INFORMATION FOR SEQ ID NO: 374:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 69 amino acids
(B) TYPE: AMINO ACID
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Testis

(ix) FEATURE:
(A) NAME/KEY: sig_peptide
(B) LOCATION: -61..-1
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 4.7
seq LLPCNLHXSWLHS/SP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 374:

```
Met Asn Ala Ala Ile Asn Thr Gly Pro Ala Pro Ala Val Thr Lys Thr
    -60                 -55                 -50

Glu Thr Glu Val Gln Asn Pro Asp Val Leu Trp Asp Leu Asp Ile Pro
-45                 -40                 -35                 -30

Glu Ala Arg Ser His Ala Asp Gln Asp Ser Asn Pro Xaa Ala Glu Ala
                -25                 -20                 -15

Leu Leu Pro Cys Asn Leu His Xaa Ser Trp Leu His Ser Ser Pro Arg
            -10                 -5                   1
```

```
Pro Asp Pro His Ser
    5
```

(2) INFORMATION FOR SEQ ID NO: 375:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 61 amino acids
(B) TYPE: AMINO ACID
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Testis

(ix) FEATURE:
(A) NAME/KEY: sig_peptide
(B) LOCATION: -43..-1
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 4.7
seq GIFLVIFCSESFS/LL

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 375:

```
Met Ile Asn Leu Leu Val Gly Asn Cys Ile Tyr Leu Leu Gly Ala Ile
            -40                 -35                 -30

Arg Ala Ser Cys Met Cys Arg Xaa Met Ser Phe Ala Lys Phe Gly Ile
        -25                 -20                 -15

Phe Leu Val Ile Phe Cys Ser Glu Ser Phe Ser Leu Leu Leu Trp Asn
    -10                 -5                   1               5

Phe Ser Ser Ile Tyr Val Lys Thr Phe Trp Pro Val Gly
                10                  15
```

(2) INFORMATION FOR SEQ ID NO: 376:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 52 amino acids
(B) TYPE: AMINO ACID
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Spleen

(ix) FEATURE:
(A) NAME/KEY: sig_peptide
(B) LOCATION: -19..-1
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 4.7
seq LRFLLRDPGCLLA/QP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 376:

```
Met Leu Cys Cys Gly Pro Leu Arg Phe Leu Leu Arg Asp Pro Gly Cys
                -15                 -10                 -5

Leu Leu Ala Gln Pro Glu Leu Ala Phe Trp Gly Pro Ala Ser Phe Ile
            1               5                   10

Ser Gly Gly Leu Val Val Val Ser Glu Thr Pro His Pro Ser Phe Pro
    15                  20                  25

Leu Asp Pro Pro
30
```

(2) INFORMATION FOR SEQ ID NO: 377:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 26 amino acids
(B) TYPE: AMINO ACID
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Spleen

(ix) FEATURE:
(A) NAME/KEY: sig_peptide
(B) LOCATION: -19..-1
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 4.7
seq ILLRMTVLPTLWT/RR

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 377:

```
Met Arg Lys Thr Ser Phe Ile Leu Leu Arg Met Thr Val Leu Pro Thr
                -15                 -10                     -5

Leu Trp Thr Arg Arg Arg Val Gln Leu Val
            1               5
```

(2) INFORMATION FOR SEQ ID NO: 378:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 41 amino acids
(B) TYPE: AMINO ACID
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Ovary

(ix) FEATURE:
(A) NAME/KEY: sig_peptide
(B) LOCATION: -23..-1
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 4.6
seq VRVGLVLVXRALC/LX

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 378:

```
Met Trp Trp Lys Pro Ala Pro Glu Glu Gly Val Arg Val Gly Leu Val
            -20                 -15                 -10

Leu Val Xaa Arg Ala Leu Cys Leu Xaa Val Leu Ser Arg Phe Met Phe
        -5                  1               5

Xaa Asn Pro Gly Leu Gly Gly Met Gly
 10                  15
```

(2) INFORMATION FOR SEQ ID NO: 379:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 27 amino acids
(B) TYPE: AMINO ACID
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Testis

(ix) FEATURE:
(A) NAME/KEY: sig_peptide
(B) LOCATION: -14..-1
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 4.6
seq FNFLLGNSSCVYQ/RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 379:

```
Met Phe Asn Phe Leu Leu Gly Asn Ser Ser Cys Val Tyr Gln Arg Pro
                -10                 -5                   1

Ile Arg Leu Lys Leu Ile Ile Phe Pro Ser Gly
        5                   10
```

(2) INFORMATION FOR SEQ ID NO: 380:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 119 amino acids
(B) TYPE: AMINO ACID
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Testis

(ix) FEATURE:
(A) NAME/KEY: sig_peptide
(B) LOCATION: -42..-1
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 4.6
seq LDPAVSLSAPAFA/SA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 380:

```
Met Lys Arg Gly Ala Phe Ser Asn Leu Asn Asp Ser Gln Leu Ser Ala
        -40                 -35                 -30

Ser Phe Leu Gln Pro Ser Leu Gln Ala Asn Cys Pro Ala Leu Asp Pro
    -25                 -20                 -15

Ala Val Ser Leu Ser Ala Pro Ala Phe Ala Ser Ala Leu Arg Ser Met
-10                 -5                  1                   5

Lys Ser Ser Gln Ala Ala Arg Lys Asp Asp Phe Leu Arg Ser Leu Ser
            10                  15                  20

Asp Gly Asp Ser Gly Thr Ser Glu His Ile Ser Ala Val Val Thr Ser
        25                  30                  35

Pro Arg Ile Ser Cys His Gly Ala Ala Ile Pro Xaa Ala Xaa Ala Xaa
    40                  45                  50

Xaa Xaa Gly Cys Ser Cys Xaa Thr Glu Arg Xaa Leu Xaa Xaa Pro Pro
55                  60                  65                  70

Ser Leu Leu Ser Leu Glu Ala
                75
```

(2) INFORMATION FOR SEQ ID NO: 381:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 80 amino acids
(B) TYPE: AMINO ACID
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Testis

(ix) FEATURE:
(A) NAME/KEY: sig_peptide
(B) LOCATION: -24..-1
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 4.6
seq FFIFCSLNTLLLG/GV

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 381:

```
Met Lys Ser Ala Lys Leu Gly Phe Leu Leu Arg Phe Phe Ile Phe Cys
            -20                 -15                 -10

Ser Leu Asn Thr Leu Leu Leu Gly Gly Val Asn Lys Ile Ala Glu Lys
            -5                   1               5

Ile Cys Gly Asp Leu Lys Asp Pro Cys Lys Leu Asp Met Asn Phe Gly
    10                  15                  20

Ser Cys Tyr Glu Val His Phe Arg Tyr Phe Tyr Asn Arg Thr Ser Lys
25                  30                  35                  40

Arg Cys Glu Thr Phe Val Phe Ser Ser Cys Asn Gly Asn Leu Asn Gly
                45                  50                  55
```

(2) INFORMATION FOR SEQ ID NO: 382:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 40 amino acids
(B) TYPE: AMINO ACID
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Testis

(ix) FEATURE:
(A) NAME/KEY: sig_peptide
(B) LOCATION: -15..-1
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 4.6
seq ILFPLHSVIGSHP/QC

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 382:

```
Met Asp Ile Leu Phe Pro Leu His Ser Val Ile Gly Ser His Pro Gln
-15                 -10                 -5                   1

Cys Leu Pro Glu Arg Xaa Thr Ala Arg Met Ile Lys Leu Lys Trp Gly
            5                   10                  15

Asn Gly Ser Gly Ser Asp Phe Gly
        20                  25
```

(2) INFORMATION FOR SEQ ID NO: 383:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 52 amino acids
(B) TYPE: AMINO ACID
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Testis

(ix) FEATURE:
(A) NAME/KEY: sig_peptide
(B) LOCATION: -27..-1
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 4.6
seq FGILILLSQRQWS/KN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 383:

```
Met Leu Lys Val Phe Arg Ala Xaa His Pro Lys Ile Cys His Phe Gly
    -25                 -20                 -15

Ile Leu Ile Leu Leu Ser Gln Arg Gln Trp Ser Lys Asn Arg Cys Arg
-10                 -5                   1               5

Glu Gly Cys Leu Thr Thr Leu Phe Leu Phe Glu Ala Glu His Lys Ser
                10                  15                  20

Ser Leu Val Lys
            25
```

(2) INFORMATION FOR SEQ ID NO: 384:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 45 amino acids
(B) TYPE: AMINO ACID
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Uterus

(ix) FEATURE:
(A) NAME/KEY: sig_peptide
(B) LOCATION: -34..-1
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 4.6
seq LXWRKLAASWTLS/QE

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 384:

```
Met Leu Val Arg Asn Ala Arg Arg Gly Ser Arg Gly Arg Ser Pro Trp
                -30                 -25                 -20

Trp Arg Ala Gly Cys Leu Xaa Trp Arg Lys Leu Ala Ala Ser Trp Thr
            -15                 -10                 -5

Leu Ser Gln Glu Ile Phe Arg Gly Ser Arg Lys Gly Ser
     1                   5                  10
```

(2) INFORMATION FOR SEQ ID NO: 385:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 52 amino acids
(B) TYPE: AMINO ACID
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Ovary

(ix) FEATURE:
(A) NAME/KEY: sig_peptide
(B) LOCATION: -29..-1
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 4.5
seq FTLGLGYPIPTRL/QP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 385:

```
Met Thr Lys Gly His His His Gln His Pro Leu His Pro His Pro Leu
                -25                 -20                 -15

Phe Thr Leu Gly Leu Gly Tyr Pro Ile Pro Thr Arg Leu Gln Pro Cys
            -10                 -5                   1

Thr Leu Ser Ser Asp Pro Leu Leu Asp Ile Thr Cys Ser Leu Arg Ser
     5                  10                  15

Pro Ser Ser Gly
 20
```

(2) INFORMATION FOR SEQ ID NO: 386:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 25 amino acids
(B) TYPE: AMINO ACID
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Spleen

(ix) FEATURE:
(A) NAME/KEY: sig_peptide
(B) LOCATION: -23..-1
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 4.5
seq RLHILFIVCLARG/KG

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 386:

Met Thr Tyr His Xaa Ile Gln Phe Ser Glu Arg Leu His Ile Leu Phe
-20 -15 -10

Ile Val Cys Leu Ala Arg Gly Lys Gly
-5 1

(2) INFORMATION FOR SEQ ID NO: 387:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 74 amino acids
(B) TYPE: AMINO ACID
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Ovary

(ix) FEATURE:
(A) NAME/KEY: sig_peptide
(B) LOCATION: -46..-1
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 4.5
seq LIYCGLSQPLTLG/VT

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 387:

Met Ser Gln Phe Pro Leu Cys Ser Pro Pro Trp Lys Pro Leu Val Lys
-45 -40 -35

Val Ser Arg Asn Leu Lys Ile Arg Met Ser Ile Pro Trp Pro Leu Ser
-30 -25 -20 -15

Val Leu Ile Tyr Cys Gly Leu Ser Gln Pro Leu Thr Leu Gly Val Thr
-10 -5 1

Ser Pro Ser Phe Pro Gln Asn Ser Phe Phe Pro Trp Leu Pro Glu His
5 10 15

Pro Thr His Leu Val Ser Ser Thr Pro Gln
20 25

(2) INFORMATION FOR SEQ ID NO: 388:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 140 amino acids
(B) TYPE: AMINO ACID
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Homo Sapiens

(F) TISSUE TYPE: Testis

(ix) FEATURE:
(A) NAME/KEY: sig_peptide
(B) LOCATION: -25..-1
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 4.4
seq AMGFLLMFDLTSQ/QS

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 388:

```
Met Phe Arg Ser Leu Thr Thr Ala Phe Phe Arg Asp Ala Met Gly Phe
-25                 -20                 -15                 -10

Leu Leu Met Phe Asp Leu Thr Ser Gln Gln Ser Phe Leu Asn Val Arg
                -5                   1               5

Asn Trp Met Ser Gln Leu Gln Ala Asn Ala Tyr Cys Glu Asn Pro Asp
        10                  15                  20

Ile Val Leu Ile Gly Asn Lys Ala Asp Leu Pro Asp Gln Arg Glu Val
    25                  30                  35

Asn Glu Arg Gln Ala Arg Glu Leu Ala Asp Lys Tyr Gly Ile Pro Tyr
 40                 45                  50                  55

Phe Glu Thr Ser Ala Ala Thr Gly Gln Asn Val Glu Lys Ala Val Glu
                60                  65                  70

Thr Leu Leu Asp Leu Ile Met Xaa Arg Met Glu Gln Cys Val Glu Lys
            75                  80                  85

Thr Gln Ile Pro Asp Thr Val Asn Gly Gly Asn Ser Gly Asn Leu Asp
        90                  95                 100

Gly Glu Ser His Gln Arg Arg Asn Val Ser Ala Arg
    105                 110                 115
```

(2) INFORMATION FOR SEQ ID NO: 389:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 45 amino acids
(B) TYPE: AMINO ACID
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Testis

(ix) FEATURE:
(A) NAME/KEY: sig_peptide
(B) LOCATION: -37..-1
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 4.4
seq LSYASSALSPCLX/AP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 389:

```
Met Val Leu Thr Thr Leu Pro Leu Pro Ser Ala Asn Ser Pro Val Asn
    -35                 -30                 -25

Met Pro Thr Thr Gly Pro Asn Ser Leu Ser Tyr Ala Ser Ser Ala Leu
    -20                 -15                 -10

Ser Pro Cys Leu Xaa Ala Pro Lys Ser Pro Arg Leu Gly
 -5                  1               5
```

(2) INFORMATION FOR SEQ ID NO: 390:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 55 amino acids
(B) TYPE: AMINO ACID
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Testis

(ix) FEATURE:
(A) NAME/KEY: sig_peptide
(B) LOCATION: -30..-1
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 4.3
seq LLPTLPWLPSTRL/LS

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 390:

```
Met Gln Arg Asn Ala Thr Phe Ile His Leu Gln Leu Ala Ile Arg Pro
-30                 -25                 -20                 -15

Ser Leu Leu Pro Thr Leu Pro Trp Leu Pro Ser Thr Arg Leu Leu Ser
                -10                 -5                   1

Pro Thr Pro Leu Gly Gln Leu Arg Gly Pro Pro Gly Xaa Gln Arg Ala
         5                  10                  15

Met Pro Thr Ala His Leu Arg
     20                  25
```

(2) INFORMATION FOR SEQ ID NO: 391:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 amino acids
(B) TYPE: AMINO ACID
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Ovary

(ix) FEATURE:
(A) NAME/KEY: sig_peptide
(B) LOCATION: -15..-1
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 4.3
seq ILFCFHSFHPLFQ/DT

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 391:

```
Met Asn Ile Leu Phe Cys Phe His Ser Phe His Pro Leu Phe Gln Asp
-15                 -10                  -5                   1

Thr Ile Glu Phe
              5
```

(2) INFORMATION FOR SEQ ID NO: 392:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 58 amino acids
(B) TYPE: AMINO ACID
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Spleen

(ix) FEATURE:
(A) NAME/KEY: sig_peptide
(B) LOCATION: -20..-1
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 4.3
seq FNFLFLVQLCILA/CD

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 392:

```
Met Leu Thr Asn Arg Asn Tyr Phe Asn Phe Leu Phe Leu Val Gln Leu
-20                 -15                 -10                  -5

Cys Ile Leu Ala Cys Asp Asn Ala Tyr Leu Gln Ser Cys Pro Leu Thr
                  1               5                  10

Ser Lys Thr Pro Leu Leu Gln Thr His Ser Ala Leu Phe Tyr Asn Ser
         15                  20                  25

Thr Tyr Gly Ile Phe Leu Leu Leu Gly Val
     30                  35
```

(2) INFORMATION FOR SEQ ID NO: 393:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 58 amino acids
(B) TYPE: AMINO ACID
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Testis

(ix) FEATURE:
(A) NAME/KEY: sig_peptide
(B) LOCATION: -26..-1
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 4.3
seq ALCRFVGMQPCTA/QT

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 393:

```
Met Lys Leu Asn Pro Gly Gln Val Pro Thr Trp Trp Glu Ala Leu Cys
    -25                 -20                 -15

Arg Phe Val Gly Met Gln Pro Cys Thr Ala Gln Thr Gly Leu Leu Pro
-10                 -5                  1                   5

His Gly Thr His Asn Thr Arg Glu Arg Gln Arg Asp Pro Ser Ala Gln
            10                  15                  20

Lys Asn Thr Arg Arg Phe Ser Pro Val Gly
        25                  30
```

(2) INFORMATION FOR SEQ ID NO: 394:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 30 amino acids
(B) TYPE: AMINO ACID
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Spleen

(ix) FEATURE:
(A) NAME/KEY: sig_peptide
(B) LOCATION: -27..-1
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 4.3
seq LCLNLCPCSSSLL/SP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 394:

```
Met Leu Ala Gly Phe Arg Arg Ser Ala Pro Ala Ser Gln Ser Leu Cys
        -25                 -20                 -15

Leu Asn Leu Cys Pro Cys Ser Ser Ser Leu Leu Ser Pro Ala
```

-10 -5 1

(2) INFORMATION FOR SEQ ID NO: 395:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 25 amino acids
(B) TYPE: AMINO ACID
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Testis

(ix) FEATURE:
(A) NAME/KEY: sig_peptide
(B) LOCATION: -18..-1
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 4.3
seq SFYLLFFLNDVPP/CP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 395:

```
Met Lys Glu Gly Ala Ser Phe Tyr Leu Leu Phe Phe Leu Asn Asp Val
            -15                 -10                 -5

Pro Pro Cys Pro Pro His Thr Pro Gly
         1               5
```

(2) INFORMATION FOR SEQ ID NO: 396:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 32 amino acids
(B) TYPE: AMINO ACID
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Spleen

(ix) FEATURE:
(A) NAME/KEY: sig_peptide
(B) LOCATION: -29..-1
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 4.3
seq ETLLLKLSSQSRT/NR

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 396:

```
Met Gly Leu Glu Cys Cys Cys Pro Pro His Asn Leu Arg Val Tyr Ile
                -25                 -20                 -15
```

```
Glu Thr Leu Leu Leu Lys Leu Ser Ser Gln Ser Arg Thr Asn Arg Leu
            -10                     -5                   1
```

(2) INFORMATION FOR SEQ ID NO: 397:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 34 amino acids
(B) TYPE: AMINO ACID
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Testis

(ix) FEATURE:
(A) NAME/KEY: sig_peptide
(B) LOCATION: -21..-1
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 4.2
seq VLSIAASLLQCRL/AV

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 397:

```
Met Gln Leu Cys Pro Phe Thr Ser Val Leu Ser Ile Ala Ala Ser Leu
    -20                 -15                 -10

Leu Gln Cys Arg Leu Ala Val Val Thr Glu Thr Ile Trp Pro Pro Gln
 -5                  1               5                   10

Xaa Trp
```

(2) INFORMATION FOR SEQ ID NO: 398:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 72 amino acids
(B) TYPE: AMINO ACID
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Testis

(ix) FEATURE:
(A) NAME/KEY: sig_peptide
(B) LOCATION: -44..-1
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 4.2
seq QLLFKLNSTWCRA/LQ

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 398:

```
Met Asp Val Thr Cys Cys Phe Asp Ala Val Glu Gly Ser Asp Phe Arg
                -40                 -35                 -30

Val Cys Cys His Gly Cys Val Ser Trp Leu Cys Leu Gln Met Leu Gln
            -25                 -20                 -15

Leu Leu Phe Lys Leu Asn Ser Thr Trp Cys Arg Ala Leu Gln Ser Glu
        -10                  -5                   1

Thr Ser Leu Ala Ser Arg Arg Leu Trp Met Trp Val Ser His Leu Xaa
  5                  10                  15                  20

Glu Phe Phe Thr Val Thr Pro Trp
                 25
```

(2) INFORMATION FOR SEQ ID NO: 399:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 26 amino acids
(B) TYPE: AMINO ACID
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Ovary

(ix) FEATURE:
(A) NAME/KEY: sig_peptide
(B) LOCATION: -22..-1
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 4.2
seq HCFCFTLFSYSSS/FF

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 399:

```
Met Arg Gln Gly Pro Gly Ala Pro Leu His Cys Phe Cys Phe Thr Leu
        -20                 -15                 -10

Phe Ser Tyr Ser Ser Ser Phe Phe Phe Phe
     -5                   1
```

(2) INFORMATION FOR SEQ ID NO: 400:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 23 amino acids
(B) TYPE: AMINO ACID
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Testis

(ix) FEATURE:
(A) NAME/KEY: sig_peptide
(B) LOCATION: -15..-1
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 4.2
seq ITLLGIWLTXRLQ/FP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 400:

```
Met His Ile Thr Leu Leu Gly Ile Trp Leu Thr Xaa Arg Leu Gln Phe
-15                 -10                  -5                   1

Pro Arg Ser Gly Arg Ala Gly
            5
```

(2) INFORMATION FOR SEQ ID NO: 401:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 24 amino acids
(B) TYPE: AMINO ACID
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Spleen

(ix) FEATURE:
(A) NAME/KEY: sig_peptide
(B) LOCATION: -17..-1
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 4.2
seq SWVCLLSAGTAFE/DY

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 401:

```
Met Leu Tyr Gly Ser Trp Val Cys Leu Leu Ser Ala Gly Thr Ala Phe
        -15                 -10                  -5

Glu Asp Tyr His Leu Gly Gly Thr
     1               5
```

(2) INFORMATION FOR SEQ ID NO: 402:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 amino acids
(B) TYPE: AMINO ACID
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Uterus

(ix) FEATURE:
(A) NAME/KEY: sig_peptide
(B) LOCATION: -32..-1
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 4.2
seq XXXXFLLGRRVVG/ES

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 402:

Met Leu Phe Phe Pro Leu Leu Ser Phe Arg Phe Leu Pro Ser Glu Ser
-30 -25 -20

Leu Leu Lys Xaa Xaa Xaa Xaa Phe Leu Leu Gly Arg Arg Val Val Gly
-15 -10 -5

Glu Ser Xaa Phe Ile Phe Thr Cys Gly Asn Leu Leu Leu Ile Trp Pro
1 5 10 15

Tyr Gly

(2) INFORMATION FOR SEQ ID NO: 403:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 25 amino acids
(B) TYPE: AMINO ACID
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Testis

(ix) FEATURE:
(A) NAME/KEY: sig_peptide
(B) LOCATION: -16..-1
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 4.2
seq WAILGCWGTLSRG/HL

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 403:

Met Pro Val Trp Ala Ile Leu Gly Cys Trp Gly Thr Leu Ser Arg Gly
-15 -10 -5

His Leu Pro Val Ser Leu Asp Pro Lys
1 5

(2) INFORMATION FOR SEQ ID NO: 404:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 40 amino acids
(B) TYPE: AMINO ACID
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Ovary

(ix) FEATURE:
(A) NAME/KEY: sig_peptide
(B) LOCATION: -38..-1
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 4.1
seq GILCGSLPGPSLC/PP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 404:

```
Met Gly Met Ser Gly Lys Lys His Phe Pro Leu Ser Trp Asp His Ile
            -35                 -30                 -25

Gln Gly Ser Thr Glu Ala Thr Ser Gln Gly Ile Leu Cys Gly Ser Leu
        -20                 -15                 -10

Pro Gly Pro Ser Leu Cys Pro Pro
     -5                  1
```

(2) INFORMATION FOR SEQ ID NO: 405:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 74 amino acids
(B) TYPE: AMINO ACID
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Testis

(ix) FEATURE:
(A) NAME/KEY: sig_peptide
(B) LOCATION: -37..-1
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 4
seq PLSLDCGHSLCRA/CI

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 405:

```
Met Ala Ser Lys Ile Leu Leu Asn Val Gln Glu Glu Val Thr Cys Pro
        -35                 -30                 -25

Ile Cys Leu Glu Leu Leu Thr Glu Pro Leu Ser Leu Asp Cys Gly His
    -20                 -15                 -10

Ser Leu Cys Arg Ala Cys Ile Thr Val Ser Asn Lys Glu Ala Val Thr
 -5                  1               5                  10

Ser Met Gly Gly Lys Ser Ser Cys Pro Val Cys Gly Ile Ser Xaa Ser
```

15 20 25

Xaa Glu His Leu Gln Ala Asn Gln His Arg
30 35

(2) INFORMATION FOR SEQ ID NO: 406:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 31 amino acids
(B) TYPE: AMINO ACID
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Testis

(ix) FEATURE:
(A) NAME/KEY: sig_peptide
(B) LOCATION: -14..-1
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 4
seq YYMVCLFFRLIFS/EH

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 406:

Met Tyr Tyr Met Val Cys Leu Phe Phe Arg Leu Ile Phe Ser Glu His
-10 -5 1

Leu Pro Ile Ile Gly Thr Val Thr Ser His Lys Thr Gly Thr Gly
5 10 15

(2) INFORMATION FOR SEQ ID NO: 407:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 48 amino acids
(B) TYPE: AMINO ACID
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Ovary

(ix) FEATURE:
(A) NAME/KEY: sig_peptide
(B) LOCATION: -36..-1
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 4
seq KLAGLWSPGLVPA/AP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 407:

```
Met Gly Ala Gly Gly Xaa Arg Glu Ile Arg Ala Ala Ala Ala Ser Trp
    -35                 -30                 -25

Leu Arg Ala Ala Glu His Ser Lys Leu Ala Gly Leu Trp Ser Pro Gly
-20                 -15                 -10                  -5

Leu Val Pro Ala Ala Pro Arg Thr Glu Asn Tyr Thr Ile Gly Pro Leu
                  1                   5                  10
```

(2) INFORMATION FOR SEQ ID NO: 408:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 80 amino acids
(B) TYPE: AMINO ACID
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Testis

(ix) FEATURE:
(A) NAME/KEY: sig_peptide
(B) LOCATION: -60..-1
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 4
seq LVRRTLLVAALRA/WM

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 408:

```
Met Gly Ser Lys Cys Cys Lys Gly Gly Pro Asp Glu Asp Ala Val Glu
-60                 -55                 -50                 -45

Arg Gln Arg Arg Gln Lys Leu Leu Leu Ala Gln Leu His His Arg Lys
                -40                 -35                 -30

Arg Val Lys Ala Ala Gly Gln Ile Gln Ala Trp Trp Arg Gly Val Leu
            -25                 -20                 -15

Val Arg Arg Thr Leu Leu Val Ala Ala Leu Arg Ala Trp Met Ile Gln
        -10                  -5                   1

Cys Trp Trp Arg Thr Leu Val Gln Arg Arg Ile Arg Gln Arg Arg Gln
  5                 10                  15                  20
```

(2) INFORMATION FOR SEQ ID NO: 409:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 30 amino acids
(B) TYPE: AMINO ACID
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Ovary

(ix) FEATURE:
(A) NAME/KEY: sig_peptide
(B) LOCATION: -26..-1
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 4
seq SIHSWQLLTSAQP/QQ

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 409:

```
Met Gln Gln Gly His Pro His Leu Ser Ala Gly Thr Leu Ser Ile His
    -25                 -20                 -15

Ser Trp Gln Leu Leu Thr Ser Ala Gln Pro Gln Gln Ala Gly
-10                  -5                  1
```

(2) INFORMATION FOR SEQ ID NO: 410:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 58 amino acids
(B) TYPE: AMINO ACID
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Ovary

(ix) FEATURE:
(A) NAME/KEY: sig_peptide
(B) LOCATION: -49..-1
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 4
seq ATCCLSLFQWCAV/LR

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 410:

```
Met Ser Arg Tyr Glu Xaa Gly Ser Ser Leu Leu Pro Phe Pro Asp His
            -45                 -40                 -35

Phe Ser Val Tyr Ser Phe Lys Xaa Xaa Ser Phe Phe Glu Ala Tyr Ser
        -30                 -25                 -20

Ile Ser Asp Tyr Ala Thr Cys Cys Leu Ser Leu Phe Gln Trp Cys Ala
    -15                 -10                  -5

Val Leu Arg Phe Leu Ser Leu Pro Leu Pro
    1               5
```

(2) INFORMATION FOR SEQ ID NO: 411:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 29 amino acids
(B) TYPE: AMINO ACID
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Ovary

(ix) FEATURE:
(A) NAME/KEY: sig_peptide
(B) LOCATION: -24..-1
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 3.9
seq LLLHHYLLLFITT/SR

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 411:

```
Met Ile Tyr Phe Ile Lys Ile Asn Asn Lys Leu Leu Leu Leu His His
                -20                 -15                 -10

Tyr Leu Leu Leu Phe Ile Thr Thr Ser Arg Pro Thr Gly
            -5                   1               5
```

(2) INFORMATION FOR SEQ ID NO: 412:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 34 amino acids
(B) TYPE: AMINO ACID
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Ovary

(ix) FEATURE:
(A) NAME/KEY: sig_peptide
(B) LOCATION: -27..-1
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 3.9
seq LSWALCLSQSGYY/HP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 412:

```
Met Glu Leu Leu Tyr Leu Lys Val Lys Arg Gly Gln Lys Asp Leu Ser
    -25                 -20                 -15

Trp Ala Leu Cys Leu Ser Gln Ser Gly Tyr Tyr His Pro Ser His Pro
    -10                 -5                   1               5

His Trp
```

(2) INFORMATION FOR SEQ ID NO: 413:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 41 amino acids
(B) TYPE: AMINO ACID
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Ovary

(ix) FEATURE:
(A) NAME/KEY: sig_peptide
(B) LOCATION: -14..-1
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 3.9
seq TLAVTLSALGATG/LF

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 413:

```
Met Thr Leu Ala Val Thr Leu Ser Ala Leu Gly Ala Thr Gly Leu Phe
                -10                 -5                   1

Lys Glu Ala Cys Asp Leu Thr Phe Leu Asn Ile Gly Gln Ile Thr Ser
         5                  10                  15

Xaa Leu Lys Gln Ser Gly Gly Pro Gln
     20                  25
```

(2) INFORMATION FOR SEQ ID NO: 414:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 72 amino acids
(B) TYPE: AMINO ACID
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Uterus

(ix) FEATURE:
(A) NAME/KEY: sig_peptide
(B) LOCATION: -41..-1
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 3.9
seq CRCLITLPRSCRP/ST

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 414:

```
Met Leu Gly Pro Pro Leu Gln Pro Gly Ser His Gly Lys Val Leu Ala
    -40                 -35                 -30

Pro Gln Gly Ser Ser Gly Leu Thr Pro Pro Phe Pro Cys Arg Cys Leu
```

-25 -20 -15 -10

Ile Thr Leu Pro Arg Ser Cys Arg Pro Ser Thr Ser Val Pro Arg Xaa
-5 1 5

Ala Ser Thr Arg Ser Ser Gln Arg Pro Xaa Ser Ser Cys Trp Arg Ser
10 15 20

Ser Cys Ser Thr Thr Ala Thr Met
25 30

(2) INFORMATION FOR SEQ ID NO: 415:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 48 amino acids
(B) TYPE: AMINO ACID
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Testis

(ix) FEATURE:
(A) NAME/KEY: sig_peptide
(B) LOCATION: -27..-1
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 3.8
seq QLXLILVHFPAYS/VE

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 415:

Met Gly Asn Val Cys Ser Cys Cys Leu Arg Ala Arg Tyr Gln Gln Leu
-25 -20 -15

Xaa Leu Ile Leu Val His Phe Pro Ala Tyr Ser Val Glu Asp Gln Arg
-10 -5 1 5

Val Asp Pro Gly Val Pro Gly Glu Ser Thr Val Cys His His Asn Arg
10 15 20

(2) INFORMATION FOR SEQ ID NO: 416:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 41 amino acids
(B) TYPE: AMINO ACID
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Spleen

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
(B) LOCATION: -21..-1
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 3.8
seq PRCVISCIHGVWC/EE

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 416:

```
Met Leu Tyr Gly Leu Gly Ser Gly Pro Arg Cys Val Ile Ser Cys Ile
    -20                 -15                 -10

His Gly Val Trp Cys Glu Glu Gly Asp Gly Ser Leu Pro Arg Leu His
 -5                  1               5                  10

Val Ala Leu Met Ile Pro Ala Leu Gly
            15                  20
```

(2) INFORMATION FOR SEQ ID NO: 417:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 79 amino acids
(B) TYPE: AMINO ACID
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Testis

(ix) FEATURE:
(A) NAME/KEY: sig_peptide
(B) LOCATION: -42..-1
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 3.8
seq VTPLDSCPPSAHS/AP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 417:

```
Met His Arg Ile Met Thr Leu Leu His Leu Lys Ala Leu Gln Gln Leu
    -40                 -35                 -30

Gln Asn Lys Ile His Val Pro Arg Met Leu Pro Gly Pro Val Thr Pro
    -25                 -20                 -15

Leu Asp Ser Cys Pro Pro Ser Ala His Ser Ala Pro Ser Leu Leu Thr
-10                 -5                   1               5

Ser Gln Leu Pro Leu Gln His Thr Asn Ala Pro Pro Pro His Gly Leu
            10                  15                  20

Ser Leu Arg Arg Ala Leu His Trp Ile Ala Leu Pro Leu Met Gly
        25                  30                  35
```

(2) INFORMATION FOR SEQ ID NO: 418:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 19 amino acids
(B) TYPE: AMINO ACID
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Ovary

(ix) FEATURE:
(A) NAME/KEY: sig_peptide
(B) LOCATION: -13..-1
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 3.8
seq MLFLVLFYSAIFL/FT

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 418:

```
Met Leu Phe Leu Val Leu Phe Tyr Ser Ala Ile Phe Leu Phe Thr Leu
            -10                  -5                  1

Thr Phe Phe
    5
```

(2) INFORMATION FOR SEQ ID NO: 419:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 16 amino acids
(B) TYPE: AMINO ACID
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Ovary

(ix) FEATURE:
(A) NAME/KEY: sig_peptide
(B) LOCATION: -14..-1
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 3.8
seq VSLCVAALFPLQA/YG

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 419:

```
Met Val Ser Leu Cys Val Ala Ala Leu Phe Pro Leu Gln Ala Tyr Gly
                -10                 -5                  1
```

(2) INFORMATION FOR SEQ ID NO: 420:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 22 amino acids
(B) TYPE: AMINO ACID
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Testis

(ix) FEATURE:
(A) NAME/KEY: sig_peptide
(B) LOCATION: -17..-1
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 3.7
seq LFYIPSILTLLLA/CR

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 420:

```
Met Ser Ser Asn Leu Phe Tyr Ile Pro Ser Ile Leu Thr Leu Leu Leu
        -15                 -10                 -5

Ala Cys Arg Gln Thr Gly
     1               5
```

(2) INFORMATION FOR SEQ ID NO: 421:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 40 amino acids
(B) TYPE: AMINO ACID
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Ovary

(ix) FEATURE:
(A) NAME/KEY: sig_peptide
(B) LOCATION: -35..-1
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 3.7
seq IKQFILCLGTCRG/EM

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 421:

```
Met Gly Leu Leu Arg Lys Cys Phe Pro Val Met Leu Gly Gly Asn Thr
-35                 -30                 -25                 -20

His Ile Gln Ile Thr Cys Ile Lys Gln Phe Ile Leu Cys Leu Gly Thr
                -15                 -10                 -5

Cys Arg Gly Glu Met Leu Thr Arg
             1               5
```

(2) INFORMATION FOR SEQ ID NO: 422:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 31 amino acids
(B) TYPE: AMINO ACID
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Ovary

(ix) FEATURE:
(A) NAME/KEY: sig_peptide
(B) LOCATION: -14..-1
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 3.7
seq MLPLFCSPWESGG/RT

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 422:

```
Met Met Leu Pro Leu Phe Cys Ser Pro Trp Glu Ser Gly Gly Arg Thr
                -10                 -5                   1

Val Lys Gln Ser Glu Gly Xaa Cys Xaa Phe Gln Ala Pro His Gly
         5                  10                  15
```

(2) INFORMATION FOR SEQ ID NO: 423:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 38 amino acids
(B) TYPE: AMINO ACID
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Uterus

(ix) FEATURE:
(A) NAME/KEY: sig_peptide
(B) LOCATION: -15..-1
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 3.7
seq KLLSDLSVDSARC/KP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 423:

```
Met Ala Lys Leu Leu Ser Asp Leu Ser Val Asp Ser Ala Arg Cys Lys
-15                 -10                 -5                   1

Pro Gly Asn Asn Leu Thr Lys Ser Leu Leu Asn Ile His Asp Lys Gln
             5                  10                  15
```

```
Leu Gln His Asp Pro Arg
        20
```

(2) INFORMATION FOR SEQ ID NO: 424:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 73 amino acids
(B) TYPE: AMINO ACID
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Testis

(ix) FEATURE:
(A) NAME/KEY: sig_peptide
(B) LOCATION: -18..-1
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 3.7
seq VCWGHLLPARVST/RS

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 424:

```
Met Cys Gly Tyr Trp Val Cys Trp Gly His Leu Leu Pro Ala Arg Val
            -15                 -10                 -5

Ser Thr Arg Ser Ser Glu Gln Pro Arg Val Thr Pro Arg Asp Glu Asp
         1               5                  10

Ala Met Met Ser Ala Ser Leu Leu Thr Trp Arg Tyr Val Thr Phe Met
 15                  20                  25                  30

Val Pro Met Pro Leu Ser Pro Cys Arg Ser Val Trp Val Cys Phe Arg
                 35                  40                  45

Gln Lys Ile Leu Glu Tyr Val Xaa Ala
            50                  55
```

(2) INFORMATION FOR SEQ ID NO: 425:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 34 amino acids
(B) TYPE: AMINO ACID
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Uterus

(ix) FEATURE:
(A) NAME/KEY: sig_peptide
(B) LOCATION: -24..-1

(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 3.7
seq AILGLSTFLNLLS/IN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 425:

```
Met Lys Leu Ser Cys Ala Gly Cys Ala Asp Thr Ala Ile Leu Gly Leu
                -20                 -15                 -10

Ser Thr Phe Leu Asn Leu Leu Ser Ile Asn Leu Leu Gly Met Ile Ser
            -5                   1               5

Phe Ser
    10
```

(2) INFORMATION FOR SEQ ID NO: 426:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 58 amino acids
(B) TYPE: AMINO ACID
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Spleen

(ix) FEATURE:
(A) NAME/KEY: sig_peptide
(B) LOCATION: -21..-1
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 3.7
seq FSLGSCPAGPLSA/CV

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 426:

```
Met Ile Pro Phe Ser Gly Thr Val Phe Ser Leu Gly Ser Cys Pro Ala
    -20                 -15                 -10

Gly Pro Leu Ser Ala Cys Val Pro Asp His Gly Ser Leu Gln Tyr Pro
 -5                  1               5                  10

Leu Thr Ile Tyr Gln Gln Asp Cys Xaa Thr His Xaa Cys Pro Arg Cys
            15                  20                  25

Leu Ser Leu Pro Leu Gln His Pro Arg Gln
        30                  35
```

(2) INFORMATION FOR SEQ ID NO: 427:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 97 amino acids
(B) TYPE: AMINO ACID
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Testis

(ix) FEATURE:
(A) NAME/KEY: sig_peptide
(B) LOCATION: -35..-1
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 3.7
seq PAVSLSAPAFASA/LR

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 427:

```
Met Ile Pro Ser Ser Gln Pro Arg Phe Xaa Asn Pro Ala Cys Lys Gln
-35                 -30                 -25                 -20

Thr Val Leu Leu Xaa Asp Pro Ala Val Ser Leu Ser Ala Pro Ala Phe
                -15                 -10                  -5

Ala Ser Ala Leu Arg Ser Met Xaa Ser Ser Gln Ala Ala Arg Lys Asp
              1               5                  10

Asp Phe Leu Arg Ser Leu Ser Asp Gly Asp Ser Gly Thr Ser Glu His
     15                  20                  25

Ile Ser Ala Val Val Thr Ser Pro Arg Ile Ser Cys His Gly Ala Ala
 30                  35                  40                  45

Ile Pro Thr Ala Arg Ala Leu Cys Leu Xaa Cys Ser Cys Cys Thr Glu
                 50                  55                  60

Arg
```

(2) INFORMATION FOR SEQ ID NO: 428:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 22 amino acids
(B) TYPE: AMINO ACID
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Ovary

(ix) FEATURE:
(A) NAME/KEY: sig_peptide
(B) LOCATION: -15..-1
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 3.6
seq PTFLLISDSFLTS/QP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 428:

Met Ala Pro Thr Phe Leu Leu Ile Ser Asp Ser Phe Leu Thr Ser Gln
-15 -10 -5 1

Pro Ser Phe Phe Phe Phe
5

(2) INFORMATION FOR SEQ ID NO: 429:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 48 amino acids
(B) TYPE: AMINO ACID
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Testis

(ix) FEATURE:
(A) NAME/KEY: sig_peptide
(B) LOCATION: -19..-1
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 3.6
seq LSLLGIKIQWCLS/EN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 429:

Met Ile Ser Leu Ile Val Leu Ser Leu Leu Gly Ile Lys Ile Gln Trp
-15 -10 -5

Cys Leu Ser Glu Asn Thr Leu Phe Cys Asp Ser Asp Tyr Leu Leu Ser
1 5 10

Pro Lys Ala Pro Ile Glu Pro Leu Ser Phe Asn Leu Thr Thr Gln Gly
15 20 25

(2) INFORMATION FOR SEQ ID NO: 430:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 45 amino acids
(B) TYPE: AMINO ACID
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Ovary

(ix) FEATURE:
(A) NAME/KEY: sig_peptide
(B) LOCATION: -43..-1
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 3.6

seq LLYFNTFLPRKVA/RV

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 430:

```
Met Ala Cys Asp Ser Phe Leu Lys Asp Ala Leu Pro Gln Glu Leu Ser
            -40                 -35                 -30

Gln Leu Xaa Phe Leu Phe Pro Leu Val Asp Met Arg Glu Asp Leu Leu
        -25                 -20                 -15

Tyr Phe Asn Thr Phe Leu Pro Arg Lys Val Ala Arg Val
    -10                 -5                   1
```

(2) INFORMATION FOR SEQ ID NO: 431:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 68 amino acids
(B) TYPE: AMINO ACID
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Uterus

(ix) FEATURE:
(A) NAME/KEY: sig_peptide
(B) LOCATION: -53..-1
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 3.6
seq FLILHFFPQQIRK/KI

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 431:

```
Met Leu Leu Leu Asn Glu Asn Leu Lys Ala Glu Ile Gln Lys Asn Glu
            -50                 -45                 -40

Ala Gln Gly Ser Cys Ile Leu Phe Leu Phe Cys Phe Glu Ser Gln Asn
        -35                 -30                 -25

Met Arg Ser Lys Ser Ile Phe Pro Phe Leu Ile Leu His Phe Phe Pro
    -20                 -15                 -10

Gln Gln Ile Arg Lys Lys Ile Val Val Leu Leu Leu Gly Leu Asn Ser
-5                   1               5                  10

Gln Lys Ala Gly
            15
```

(2) INFORMATION FOR SEQ ID NO: 432:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 40 amino acids
(B) TYPE: AMINO ACID

(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Spleen

(ix) FEATURE:
(A) NAME/KEY: sig_peptide
(B) LOCATION: -26..-1
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 3.5
seq LLPFTFLSLKAFL/QX

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 432:

```
Met Ile Ser Lys Tyr Val His Tyr Ser Leu Thr Asp Leu Leu Leu Pro
    -25                 -20                 -15

Phe Thr Phe Leu Ser Leu Lys Ala Phe Leu Gln Xaa Arg Val Leu Met
-10                 -5                  1                   5

Ser Leu Pro Gln His Lys Pro Trp
            10
```

(2) INFORMATION FOR SEQ ID NO: 433:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 51 amino acids
(B) TYPE: AMINO ACID
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Testis

(ix) FEATURE:
(A) NAME/KEY: sig_peptide
(B) LOCATION: -27..-1
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 3.5
seq CSLLSSFCALHFG/LK

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 433:

```
Met Ala Arg Thr Met Gly Val Pro Arg Ala Cys Lys Ala Phe Cys Ser
    -25                 -20                 -15

Leu Leu Ser Ser Phe Cys Ala Leu His Phe Gly Leu Lys Lys Gln Tyr
    -10                 -5                  1                   5

Gly Thr Ser Tyr Leu His Ala Cys Ala Tyr Ala Ser Pro Leu Thr Trp
                10                  15                  20
```

Gly Pro Trp

(2) INFORMATION FOR SEQ ID NO: 434:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 29 amino acids
(B) TYPE: AMINO ACID
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Testis

(ix) FEATURE:
(A) NAME/KEY: sig_peptide
(B) LOCATION: -15..-1
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 3.5
seq LCFLLPHHRLQEA/RX

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 434:

```
Met Ile Leu Cys Phe Leu Leu Pro His His Arg Leu Gln Glu Ala Arg
-15                 -10                     -5                   1

Xaa Ile Gln Val Leu Lys Xaa Leu Pro Arg Glu Lys Leu
            5                   10
```

(2) INFORMATION FOR SEQ ID NO: 435:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 83 amino acids
(B) TYPE: AMINO ACID
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Spleen

(ix) FEATURE:
(A) NAME/KEY: sig_peptide
(B) LOCATION: -26..-1
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 3.5
seq QCFFVCFSPKIYG/VI

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 435:

```
Met Gln Asp Tyr Val Ser His Ala Val Arg Arg His Cys Gln Cys Phe
    -25                 -20                     -15
```

```
Phe Val Cys Phe Ser Pro Lys Ile Tyr Gly Val Ile Thr Trp Thr Val
-10                 -5                  1               5

Leu Ile Thr Gly Ala Arg Val Leu Ser Glu Pro Gln Arg Leu Trp Val
            10                  15                  20

Arg Leu Asp Asp Ile Thr Ala Asn Ala Ala Cys Gly Tyr Arg Lys Gln
        25                  30                  35

Glu Pro Arg Lys Thr Phe Glu Asn Asn Trp Glu Asn Leu Tyr Thr Asp
    40                  45                  50

Trp Asn Trp
 55
```

(2) INFORMATION FOR SEQ ID NO: 436:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 35 amino acids
(B) TYPE: AMINO ACID
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Testis

(ix) FEATURE:
(A) NAME/KEY: sig_peptide
(B) LOCATION: -31..-1
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 3.5
seq VLLNLALSHFNNC/GL

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 436:

```
Met Glu Phe Ala His Ala Ala Glu Cys Val Ser Phe Ala Leu Asn Glu
    -30                 -25                 -20

Thr His Val Leu Leu Asn Leu Ala Leu Ser His Phe Asn Asn Cys Gly
-15                 -10                 -5                  1

Leu Ala Val
```

(2) INFORMATION FOR SEQ ID NO: 437:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 48 amino acids
(B) TYPE: AMINO ACID
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Homo Sapiens

(F) TISSUE TYPE: Ovary

(ix) FEATURE:
(A) NAME/KEY: sig_peptide
(B) LOCATION: -30..-1
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 3.5
seq LLAASWLPRDAPC/EA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 437:

```
Met Gly Asn Gln Gly Phe Pro Tyr Leu Ser Pro Ser Leu Ser Val Gln
-30                 -25                 -20                 -15

Asp Leu Leu Ala Ala Ser Trp Leu Pro Arg Asp Ala Pro Cys Glu Ala
                -10                 -5                   1

Pro Pro Gly Leu Pro Ser Gln Thr Met Leu Cys Ala Pro Gly Pro Arg
         5                  10                  15
```

(2) INFORMATION FOR SEQ ID NO: 438:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 43 amino acids
(B) TYPE: AMINO ACID
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Ovary

(ix) FEATURE:
(A) NAME/KEY: sig_peptide
(B) LOCATION: -22..-1
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 3.5
seq AQLASPLLPGATP/VA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 438:

```
Met Lys Tyr Gln Met Val Ser Gly Ser Ala Gln Leu Ala Ser Pro Leu
    -20                 -15                 -10

Leu Pro Gly Ala Thr Pro Val Ala Gly Thr Ile Leu Lys Ser Leu Leu
    -5                   1               5                  10

Leu Arg Thr Val Lys Met Met Arg Val Tyr Gly
                15                  20
```

(2) INFORMATION FOR SEQ ID NO: 439:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 35 amino acids

(B) TYPE: AMINO ACID
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Testis

(ix) FEATURE:
(A) NAME/KEY: sig_peptide
(B) LOCATION: -21..-1
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 12.7
seq ILFLLSWSGPLQG/QQ

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 439:

```
Met Gly Pro Ser Thr Pro Leu Leu Ile Leu Phe Leu Leu Ser Trp Ser
    -20                 -15                 -10

Gly Pro Leu Gln Gly Gln Gln His His Leu Val Glu Tyr Met Glu Arg
 -5                  1                   5                  10

Arg His Gly
```

(2) INFORMATION FOR SEQ ID NO: 440:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 29 amino acids
(B) TYPE: AMINO ACID
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Ovary

(ix) FEATURE:
(A) NAME/KEY: sig_peptide
(B) LOCATION: -20..-1
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 7.4
seq LVFCVGLLTMAKA/ES

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 440:

```
Met Ala Ser Leu Gly His Ile Leu Val Phe Cys Val Gly Leu Leu Thr
-20                 -15                 -10                  -5

Met Ala Lys Ala Glu Ser Pro Lys Glu His Asp Pro Arg
                 1                   5
```

(2) INFORMATION FOR SEQ ID NO: 441:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 47 amino acids
(B) TYPE: AMINO ACID
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Testis

(ix) FEATURE:
(A) NAME/KEY: sig_peptide
(B) LOCATION: -23..-1
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 7.3
seq ALSLLLVSGSLLP/GP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 441:

```
Met Ser Gly Ser Ser Leu Pro Ser Ala Leu Ala Leu Ser Leu Leu Leu
            -20                 -15                 -10

Val Ser Gly Ser Leu Leu Pro Gly Pro Gly Ala Ala Gln Asn Glu Pro
        -5                   1               5

Arg Ile Val Thr Ser Glu Glu Val Ile Ile Arg Asp Ser Pro Val
 10                  15                  20
```

(2) INFORMATION FOR SEQ ID NO: 442:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 65 amino acids
(B) TYPE: AMINO ACID
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Ovary

(ix) FEATURE:
(A) NAME/KEY: sig_peptide
(B) LOCATION: -57..-1
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 7.1
seq VGLAVVSLGGSRG/SG

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 442:

```
Met Met Glu Val Val Val Gly Asn Gly Val Val Ala Leu Arg Gly Ile
    -55                 -50                 -45

Pro Pro Arg Thr Ser Arg Lys Ser Ser Arg Lys Thr Arg Phe Cys Gly
    -40                 -35                 -30
```

```
Glu Arg Gly Ser Lys Gln Ser Gly Lys Cys Ser Pro Val Gly Leu Ala
-25                 -20                 -15                 -10

Val Val Ser Leu Gly Gly Ser Arg Gly Ser Gly Lys Gly Leu Gly Arg
                 -5                   1               5

Leu
```

(2) INFORMATION FOR SEQ ID NO: 443:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 58 amino acids
(B) TYPE: AMINO ACID
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Testis

(ix) FEATURE:
(A) NAME/KEY: sig_peptide
(B) LOCATION: -16..-1
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 6.7
seq CFSLVLLLTSIWT/TR

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 443:

```
Met Ala Arg Cys Phe Ser Leu Val Leu Leu Leu Thr Ser Ile Trp Thr
    -15                 -10                     -5

Thr Arg Leu Leu Val Gln Gly Ser Leu Arg Ala Glu Glu Leu Ser Ile
  1                 5                  10                  15

Gln Val Ser Cys Arg Xaa Met Gly Ile Thr Leu Val Ser Lys Lys Ala
             20                  25                  30

Asn Gln Gln Leu Asn Phe Thr Glu Ala Lys
         35                  40
```

(2) INFORMATION FOR SEQ ID NO: 444:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 136 amino acids
(B) TYPE: AMINO ACID
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Spleen

(ix) FEATURE:
(A) NAME/KEY: sig_peptide
(B) LOCATION: -21..-1
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 5.6
seq CLSCLLIPLALWS/II

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 444:

```
Met Gly Ser Arg Lys Cys Gly Gly Cys Leu Ser Cys Leu Leu Ile Pro
    -20                 -15                 -10

Leu Ala Leu Trp Ser Ile Ile Val Asn Ile Leu Leu Tyr Phe Pro Asn
 -5                   1               5                  10

Gly Gln Thr Ser Tyr Ala Ser Ser Asn Lys Leu Thr Asn Tyr Val Trp
             15                  20                  25

Tyr Phe Glu Gly Ile Cys Phe Ser Gly Ile Met Met Leu Ile Val Thr
         30                  35                  40

Thr Val Leu Leu Val Leu Glu Asn Asn Asn Asn Tyr Lys Cys Cys Gln
     45                  50                  55

Ser Glu Asn Cys Ser Lys Lys Tyr Val Thr Leu Leu Ser Ile Ile Phe
 60                  65                  70                  75

Ser Ser Leu Gly Ile Ala Phe Ser Gly Tyr Cys Leu Val Ile Ser Ala
                 80                  85                  90

Leu Gly Leu Val Gln Gly Pro Tyr Cys Arg Thr Leu Asp Gly Trp Glu
             95                 100                 105

Tyr Ala Phe Glu Gly Thr Ala Gly
        110                 115
```

(2) INFORMATION FOR SEQ ID NO: 445:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 82 amino acids
(B) TYPE: AMINO ACID
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Uterus

(ix) FEATURE:
(A) NAME/KEY: sig_peptide
(B) LOCATION: -21..-1
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 5.6
seq CLSCLLIPLALWS/II

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 445:

```
Met Gly Ser Arg Lys Cys Gly Gly Cys Leu Ser Cys Leu Leu Ile Pro
    -20                 -15                 -10

Leu Ala Leu Trp Ser Ile Ile Val Asn Ile Leu Leu Tyr Phe Pro Asn
 -5                     1               5                   10

Gly Gln Thr Ser Tyr Ala Ser Ser Asn Lys Leu Thr Asn Tyr Val Trp
            15                  20                  25

Tyr Phe Glu Gly Ile Cys Phe Ser Gly Ile Met Met Leu Ile Val Thr
        30                  35                  40

Thr Val Leu Leu Val Leu Glu Asn Asn Asn Asn Tyr Lys Cys Cys Gln
    45                  50                  55

Ser Gly
 60
```

(2) INFORMATION FOR SEQ ID NO: 446:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 24 amino acids
(B) TYPE: AMINO ACID
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Testis

(ix) FEATURE:
(A) NAME/KEY: sig_peptide
(B) LOCATION: -17..-1
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 5.3
seq ILFGVSFVFLTHC/TI

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 446:

```
Met Met Val Met Ile Leu Phe Gly Val Ser Phe Val Phe Leu Thr His
        -15                 -10                 -5

Cys Thr Ile Gln Ser Ser Cys Gly
    1               5
```

(2) INFORMATION FOR SEQ ID NO: 447:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 34 amino acids
(B) TYPE: AMINO ACID
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Testis

(ix) FEATURE:
(A) NAME/KEY: sig_peptide
(B) LOCATION: -19..-1
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 4.4
seq VLVSLPHPHPALT/CC

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 447:

```
Met Ser Asn Thr His Thr Val Leu Val Ser Leu Pro His Pro His Pro
            -15                 -10                  -5

Ala Leu Thr Cys Cys His Leu Gly Xaa Pro His Pro Val Arg Ala Pro
            1               5                  10

Arg Pro
    15
```

(2) INFORMATION FOR SEQ ID NO: 448:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 125 amino acids
(B) TYPE: AMINO ACID
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Testis

(ix) FEATURE:
(A) NAME/KEY: sig_peptide
(B) LOCATION: -106..-1
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 4.1
seq IITLACVPMTSFT/RN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 448:

```
Met Xaa Val Tyr Arg Leu Gln Thr Gln Glu Lys Pro Asn Thr Thr Val
    -105                -100                -95

Gln Val Pro Ala Phe Leu Gln Glu Leu Val Asp Arg Asp Asn Ser Lys
-90                 -85                 -80                 -75

Phe Glu Glu Trp Cys Ile Glu Met Ala Glu Met Arg Xaa Lys Val Trp
                -70                 -65                 -60

Ile Lys Glu Lys Gln Asn Thr Lys Arg Leu Arg Ser Cys Thr Lys Gly
            -55                 -50                 -45

Tyr Leu Leu Glu Leu Ser Pro Met Ser Leu Ser Leu Trp Asn Gly Cys
```

```
    -40                     -35                       -30

Lys Ser Gly Trp Met Asn Gln Gln Xaa Pro Asn Leu Leu Ile Ile Thr
    -25                     -20                     -15

Leu Ala Cys Val Pro Met Thr Ser Phe Thr Arg Asn Lys Ile Ser Ile
-10                 -5                       1               5

Met Lys Arg Ile Ser Glu Tyr Ala Ala Asp Ile Phe Tyr
            10                  15
```

(2) INFORMATION FOR SEQ ID NO: 449:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 27 amino acids
(B) TYPE: AMINO ACID
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Testis

(ix) FEATURE:
(A) NAME/KEY: sig_peptide
(B) LOCATION: -21..-1
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 3.9
seq LIAVVIIILLIFT/SV

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 449:

```
Met Phe Pro Val Leu Gly Trp Ile Leu Ile Ala Val Val Ile Ile Ile
    -20                 -15                 -10

Leu Leu Ile Phe Thr Ser Val Thr Arg Cys Leu
 -5                     1               5
```

(2) INFORMATION FOR SEQ ID NO: 450:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 65 amino acids
(B) TYPE: AMINO ACID
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Testis

(ix) FEATURE:
(A) NAME/KEY: sig_peptide
(B) LOCATION: -19..-1
(C) IDENTIFICATION METHOD: Von Heijne matrix

(D) OTHER INFORMATION: score 3.9
seq SVCLCPCLNKGQS/EN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 450:

Met Phe Ser Cys Cys Ile Ser Val Cys Leu Cys Pro Cys Leu Asn Lys
-15 -10 -5

Gly Gln Ser Glu Asn Leu Ser Arg Asp Cys Gly His Trp Leu Asn Pro
1 5 10

His His Arg Arg Leu Trp Pro Phe Gly Arg Arg His Pro Gln Asp Cys
15 20 25

Gly Leu Phe Gln Asp Ser Gln Xaa Tyr Gly Glu Ser Lys Asp Trp Asn
30 35 40 45

Gly

(2) INFORMATION FOR SEQ ID NO: 451:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 88 amino acids
(B) TYPE: AMINO ACID
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Uterus

(ix) FEATURE:
(A) NAME/KEY: sig_peptide
(B) LOCATION: -29..-1
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 3.5
seq LTYLLLLSPIKYP/LD

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 451:

Met Arg Leu Cys Leu Ile Met Tyr Cys Ser Phe Gly Thr Leu Ser His
-25 -20 -15

Leu Thr Tyr Leu Leu Leu Leu Ser Pro Ile Lys Tyr Pro Leu Asp Leu
-10 -5 1

Asp Phe Leu Tyr Pro Ile Phe Ser Thr Val Tyr Lys Arg Tyr Ile Val
5 10 15

Thr Val Asn Phe Cys Ile Ser Cys Ser Glu Ser Phe Leu Leu Ser Asp
20 25 30 35

Leu Ile Ala Leu Phe Leu Ile Arg Glu Leu Gln Leu Leu Gln His Thr
40 45 50

Val Ser Val Val Gln Pro Pro Thr

55

(2) INFORMATION FOR SEQ ID NO: 452:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 47 amino acids
(B) TYPE: AMINO ACID
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Testis

(ix) FEATURE:
(A) NAME/KEY: sig_peptide
(B) LOCATION: -26..-1
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 10.5
seq LLLALLLPVQVSS/FV

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 452:

```
Met Gly Lys Gly Met Val Ala Met Leu Ile Leu Gly Leu Leu Leu Leu
    -25                 -20                 -15

Ala Leu Leu Leu Pro Val Gln Val Ser Ser Phe Val Pro Leu Thr Ser
-10                 -5                   1               5

Met Pro Glu Ala Thr Ala Ala Glu Thr Thr Lys Pro Ser Asn Gly
             10                  15                  20
```

(2) INFORMATION FOR SEQ ID NO: 453:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 55 amino acids
(B) TYPE: AMINO ACID
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Testis

(ix) FEATURE:
(A) NAME/KEY: sig_peptide
(B) LOCATION: -21..-1
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 9.5
seq LLVLFVLLANVQG/PG

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 453:

```
Met Gly Ser Ser Gly Leu Leu Ser Leu Leu Val Leu Phe Val Leu Leu
    -20                 -15                 -10

Ala Asn Val Gln Gly Pro Gly Leu Thr Asp Trp Leu Phe Pro Arg Arg
 -5                  1                   5                  10

Cys Pro Lys Ile Arg Glu Glu Cys Glu Phe Gln Glu Arg Asp Val Cys
             15                  20                  25

Thr Lys Asp Arg Gln Cys Arg
         30
```

(2) INFORMATION FOR SEQ ID NO: 454:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 78 amino acids
(B) TYPE: AMINO ACID
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Ovary

(ix) FEATURE:
(A) NAME/KEY: sig_peptide
(B) LOCATION: -35..-1
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 8.3
seq NLLLLHCVSRSHS/QN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 454:

```
Met Val Leu Gly Gly Cys Pro Val Ser Tyr Leu Leu Leu Cys Gly Gln
-35                 -30                 -25                 -20

Ala Ala Leu Leu Leu Gly Asn Leu Leu Leu Leu His Cys Val Ser Arg
                -15                 -10                  -5

Ser His Ser Gln Asn Ala Thr Ala Glu Pro Glu Leu Thr Ser Ala Gly
              1                   5                  10

Ala Pro Ser Arg Arg Ala Pro Gly Val Leu Arg Ala Gly Asn Met Ala
     15                  20                  25

Thr Pro Thr Leu Arg Ser Ser Ser Ala Leu Thr Tyr Leu Gly
 30                  35                  40
```

(2) INFORMATION FOR SEQ ID NO: 455:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 44 amino acids
(B) TYPE: AMINO ACID
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Testis

(ix) FEATURE:
(A) NAME/KEY: sig_peptide
(B) LOCATION: -18..-1
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 8.3
seq LLSLSSLPLVLLG/WE

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 455:

```
Met Glu Thr Gly Arg Leu Leu Ser Leu Ser Ser Leu Pro Leu Val Leu
        -15                 -10                 -5

Leu Gly Trp Glu Tyr Ser Ser Gln Thr Leu Asn Leu Val Pro Ser Thr
         1               5                  10

Ser Ile Leu Ser Phe Val Pro Phe Ile Pro Arg Val
 15                 20                  25
```

(2) INFORMATION FOR SEQ ID NO: 456:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 59 amino acids
(B) TYPE: AMINO ACID
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Ovary

(ix) FEATURE:
(A) NAME/KEY: sig_peptide
(B) LOCATION: -19..-1
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 8.2
seq QVLALVLVAALWG/GT

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 456:

```
Met Ala Ala Ser Leu Gly Gln Val Leu Ala Leu Val Leu Val Ala Ala
                -15                 -10                 -5

Leu Trp Gly Gly Thr Gln Pro Leu Leu Lys Arg Ala Ser Ala Gly Leu
             1               5                  10

Gln Arg Val His Glu Pro Thr Trp Ala Gln Gln Leu Leu Gln Glu Met
     15                 20                  25

Lys Thr Leu Phe Leu Asn Thr Glu Tyr Leu Met
 30                 35                  40
```

(2) INFORMATION FOR SEQ ID NO: 457:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 84 amino acids
(B) TYPE: AMINO ACID
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Spleen

(ix) FEATURE:
(A) NAME/KEY: sig_peptide
(B) LOCATION: -59..-1
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 8.1
seq FLLGISNLSQVRA/SN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 457:

```
Met His Ile Lys Ser Ile Ile Leu Glu Gly Phe Lys Ser Tyr Ala Gln
                -55                 -50                 -45

Arg Thr Glu Val Asn Gly Phe Asp Pro Leu Phe Asn Ala Ile Thr Gly
            -40                 -35                 -30

Leu Asn Gly Ser Gly Lys Ser Asn Ile Leu Asp Ser Ile Cys Phe Leu
        -25                 -20                 -15

Leu Gly Ile Ser Asn Leu Ser Gln Val Arg Ala Ser Asn Leu Gln Asp
    -10                 -5                   1               5

Leu Val Tyr Lys Asn Gly Gln Ala Gly Ile Thr Lys Ala Ser Val Ser
                10                  15                  20

Ile Xaa Phe Asp
            25
```

(2) INFORMATION FOR SEQ ID NO: 458:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 63 amino acids
(B) TYPE: AMINO ACID
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Testis

(ix) FEATURE:
(A) NAME/KEY: sig_peptide

(B) LOCATION: -19..-1
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 8
seq WGFLCVLFTAVHP/AP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 458:

```
Met Ser Pro Ser Pro Arg Trp Gly Phe Leu Cys Val Leu Phe Thr Ala
                -15                 -10                 -5

Val His Pro Ala Pro Ser Thr Ala Pro Val Gln Asp Lys Cys Pro Val
            1               5                   10

Asn Thr Trp Glu Ala Met Xaa Xaa Val Leu Pro Ala Ala Pro Ala Asn
    15                  20                  25

Arg Pro Pro Thr Gln Ala Phe Pro Ser Ala Ser Thr Ala Thr Gly
30                  35                  40
```

(2) INFORMATION FOR SEQ ID NO: 459:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 65 amino acids
(B) TYPE: AMINO ACID
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Testis

(ix) FEATURE:
(A) NAME/KEY: sig_peptide
(B) LOCATION: -24..-1
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 7.8
seq FLLCLCIAYWAST/AV

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 459:

```
Met Cys Ser Leu Leu Tyr Pro Leu Val Thr Phe Phe Leu Leu Cys Leu
                -20                 -15                 -10

Cys Ile Ala Tyr Trp Ala Ser Thr Ala Val Phe Leu Ser Thr Ser Asn
            -5                  1                   5

Glu Ala Val Tyr Lys Ile Phe Asp Asp Ser Pro Cys Pro Phe Thr Ala
    10                  15                  20

Lys Thr Cys Asn Pro Glu Thr Phe Pro Ser Ser Asn Glu Pro Arg His
25                  30                  35                  40

Gly
```

(2) INFORMATION FOR SEQ ID NO: 460:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 51 amino acids
(B) TYPE: AMINO ACID
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Spleen

(ix) FEATURE:
(A) NAME/KEY: sig_peptide
(B) LOCATION: -16..-1
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 7.6
seq FLFFSTLFSSIFT/EA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 460:

```
Met Leu Pro Phe Leu Phe Phe Ser Thr Leu Phe Ser Ser Ile Phe Thr
    -15                 -10                 -5

Glu Ala Gln Lys Gln Tyr Trp Val Cys Asn Ser Ser Asp Ala Ser Ile
  1               5                  10                  15

His Thr Pro Thr Val Ile Lys Cys Asn Thr Gln Phe Gln Leu Met Leu
            20                  25                  30

Thr Pro Gly
        35
```

(2) INFORMATION FOR SEQ ID NO: 461:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 86 amino acids
(B) TYPE: AMINO ACID
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Testis

(ix) FEATURE:
(A) NAME/KEY: sig_peptide
(B) LOCATION: -14..-1
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 7.5
seq VALNLILVPCCAA/WC

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 461:

```
Met Val Ala Leu Asn Leu Ile Leu Val Pro Cys Cys Ala Ala Trp Cys
```

```
            -10                      -5                      1

Asp Pro Arg Arg Ile His Ser Gln Asp Asp Val Leu Arg Ser Ser Ala
        5                   10                  15

Ala Asp Thr Gly Ser Ala Met Gln Arg Arg Glu Ala Trp Ala Gly Trp
    20                  25                  30

Arg Arg Ser Gln Pro Phe Ser Val Gly Leu Pro Ser Ala Glu Arg Leu
35                  40                  45                  50

Glu Asn Gln Pro Gly Lys Leu Ser Trp Arg Ser Leu Val Gly Glu Gly
                55                  60                  65

His Arg Ile Cys Asp Leu
            70
```

(2) INFORMATION FOR SEQ ID NO: 462:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 121 amino acids
(B) TYPE: AMINO ACID
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Testis

(ix) FEATURE:
(A) NAME/KEY: sig_peptide
(B) LOCATION: -53..-1
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 7.1
seq IAVGLGVAALAFA/GR

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 462:

```
Met Ala Ala Arg Gly Val Ile Ala Pro Val Gly Glu Ser Leu Arg Tyr
            -50                 -45                 -40

Ala Glu Tyr Leu Gln Pro Ser Ala Lys Arg Pro Asp Ala Asp Val Asp
        -35                 -30                 -25

Gln Gln Arg Leu Val Arg Ser Leu Ile Ala Val Gly Leu Gly Val Ala
    -20                 -15                 -10

Ala Leu Ala Phe Ala Gly Arg Tyr Ala Phe Arg Ile Trp Lys Pro Leu
-5                      1               5                   10

Glu Gln Val Ile Thr Glu Thr Ala Lys Lys Ile Ser Thr Pro Ser Phe
            15                  20                  25

Ser Ser Tyr Tyr Lys Gly Gly Phe Glu Gln Lys Met Ser Arg Arg Glu
        30                  35                  40

Ala Gly Leu Ile Leu Gly Val Ser Pro Ser Ala Gly Lys Ala Lys Ile
```

45 50 55

Arg Thr Ala His Arg Arg Val Met Ile
60 65

(2) INFORMATION FOR SEQ ID NO: 463:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 43 amino acids
(B) TYPE: AMINO ACID
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Testis

(ix) FEATURE:
(A) NAME/KEY: sig_peptide
(B) LOCATION: -15..-1
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 7.1
seq KLKLLSLLRPSLC/IP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 463:

Met Ile Lys Leu Lys Leu Leu Ser Leu Leu Arg Pro Ser Leu Cys Ile
-15 -10 -5 1

Pro Gln Leu Leu Arg Thr Asn Ala Thr Leu Leu Phe Thr Ile Ala Ser
5 10 15

Cys Asn Leu Gln Ile Pro Ala Ser Pro Arg Arg
20 25

(2) INFORMATION FOR SEQ ID NO: 464:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 42 amino acids
(B) TYPE: AMINO ACID
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Spleen

(ix) FEATURE:
(A) NAME/KEY: sig_peptide
(B) LOCATION: -20..-1
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 6.5
seq GLCVLQLTTAVTS/AF

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 464:

```
Met Pro Ser Val Asn Ser Ala Gly Leu Cys Val Leu Gln Leu Thr Thr
-20                 -15                 -10                  -5

Ala Val Thr Ser Ala Phe Leu Leu Ala Lys Val Asn Pro Phe Glu Xaa
                1               5                  10

Phe Leu Ser Arg Gly Phe Trp Leu Cys Ala
        15                  20
```

(2) INFORMATION FOR SEQ ID NO: 465:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 31 amino acids
(B) TYPE: AMINO ACID
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Ovary

(ix) FEATURE:
(A) NAME/KEY: sig_peptide
(B) LOCATION: -20..-1
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 6.4
seq ALFLLVSXYMIRS/GT

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 465:

```
Met Met Leu Gly Leu His Phe Ala Leu Phe Leu Leu Val Ser Xaa Tyr
-20                 -15                 -10                  -5

Met Ile Arg Ser Gly Thr Gly Asn Lys Ile Glu Glu Gly Gly Arg
                1               5                  10
```

(2) INFORMATION FOR SEQ ID NO: 466:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 48 amino acids
(B) TYPE: AMINO ACID
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Testis

(ix) FEATURE:
(A) NAME/KEY: sig_peptide
(B) LOCATION: -13..-1

(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 6.4
seq MALLLSVLRVLLG/GF

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 466:

```
Met Ala Leu Leu Leu Ser Val Leu Arg Val Leu Leu Gly Gly Phe Phe
        -10                 -5                   1

Ala Leu Val Gly Leu Ala Lys Leu Ser Glu Glu Ile Ser Ala Pro Val
    5                   10                  15

Ser Glu Arg Met Asn Ala Leu Phe Val Xaa Phe Ala Glu Val Leu Gly
 20                 25                  30                  35
```

(2) INFORMATION FOR SEQ ID NO: 467:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 41 amino acids
(B) TYPE: AMINO ACID
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Ovary

(ix) FEATURE:
(A) NAME/KEY: sig_peptide
(B) LOCATION: -17..-1
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 6.2
seq LWLSLVAWHWGEA/VL

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 467:

```
Met Leu Lys Ser Leu Trp Leu Ser Leu Val Ala Trp His Trp Gly Glu
    -15                 -10                 -5

Ala Val Leu Leu Ser Pro His Leu Pro Ala Ala Ala Glu Trp Pro Arg
    1                   5                   10                  15

Ala Ala Cys Asp Ser Gly Gly Glu Pro
                20
```

(2) INFORMATION FOR SEQ ID NO: 468:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 24 amino acids
(B) TYPE: AMINO ACID
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Ovary

(ix) FEATURE:
(A) NAME/KEY: sig_peptide
(B) LOCATION: -15..-1
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 6.1
seq IVTWLLXSFMSSA/EE

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 468:

```
Met Gly Ile Val Thr Trp Leu Leu Xaa Ser Phe Met Ser Ser Ala Glu
-15                 -10                 -5                   1

Glu Ser Val Ser Ala Arg Thr Arg
                5
```

(2) INFORMATION FOR SEQ ID NO: 469:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 37 amino acids
(B) TYPE: AMINO ACID
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Uterus

(ix) FEATURE:
(A) NAME/KEY: sig_peptide
(B) LOCATION: -28..-1
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 6
seq IGLMFLMLGCALP/IY

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 469:

```
Met Ala Gly Ile Lys Ala Leu Ile Ser Leu Ser Phe Gly Gly Ala Ile
            -25                 -20                 -15

Gly Leu Met Phe Leu Met Leu Gly Cys Ala Leu Pro Ile Tyr Asn Lys
        -10                 -5                   1

Tyr Trp Pro Pro Gly
  5
```

(2) INFORMATION FOR SEQ ID NO: 470:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 34 amino acids
(B) TYPE: AMINO ACID

(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Ovary

(ix) FEATURE:
(A) NAME/KEY: sig_peptide
(B) LOCATION: -26..-1
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 5.8
seq VKLVTLSVPTSLA/SS

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 470:

```
Met Lys Lys Gln Lys His Gln Lys Leu Trp Cys Ile Ser Val Lys Leu
    -25                 -20                 -15

Val Thr Leu Ser Val Pro Thr Ser Leu Ala Ser Ser Leu Thr Ser Pro
-10                 -5                  1               5

Thr Gly
```

(2) INFORMATION FOR SEQ ID NO: 471:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 78 amino acids
(B) TYPE: AMINO ACID
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Testis

(ix) FEATURE:
(A) NAME/KEY: sig_peptide
(B) LOCATION: -40..-1
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 5.8
seq VLFALFVAFLLRG/KL

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 471:

```
Met Asp Gly Ile Pro Met Ser Met Lys Asn Glu Met Pro Ile Ser Gln
-40                 -35                 -30                 -25

Leu Leu Met Ile Ile Ala Pro Ser Leu Gly Phe Val Leu Phe Ala Leu
                -20                 -15                 -10

Phe Val Ala Phe Leu Leu Arg Gly Lys Leu Met Glu Thr Tyr Cys Ser
            -5                  1               5

Gln Lys His Thr Arg Leu Asp Tyr Ile Gly Asp Ser Lys Asn Val Leu
```

10 15 20

Asn Asp Val Gln His Gly Arg Glu Asp Glu Asp Gly His Gly
25 30 35

(2) INFORMATION FOR SEQ ID NO: 472:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 91 amino acids
(B) TYPE: AMINO ACID
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Uterus

(ix) FEATURE:
(A) NAME/KEY: sig_peptide
(B) LOCATION: -57..-1
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 5.7
seq LAICSCLPGPGPA/LP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 472:

Met Gly Gly Phe Leu His Leu Pro Ala Leu Ser Ser Ser Cys Leu Trp
-55 -50 -45

Thr Phe Pro Pro Met Cys Val Arg Ile Phe Ser Tyr Val Pro Leu Pro
-40 -35 -30

Ile Leu Thr Pro Lys Thr Ile Asn Leu Ile Pro Val Leu Ala Ile Cys
-25 -20 -15 -10

Ser Cys Leu Pro Gly Pro Gly Pro Ala Leu Pro Leu Pro Ala Phe Pro
-5 1 5

Thr Leu Leu Val Ser Trp Tyr His Cys Pro Pro Gln Lys Lys Thr Gly
10 15 20

Met Met Asp Thr Asp Asp Phe Arg Ala Cys Pro
25 30

(2) INFORMATION FOR SEQ ID NO: 473:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 51 amino acids
(B) TYPE: AMINO ACID
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Homo Sapiens

(F) TISSUE TYPE: Testis

(ix) FEATURE:
(A) NAME/KEY: sig_peptide
(B) LOCATION: -19..-1
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 8
seq WGFLCVLFTAVHP/AP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 473:

```
Met Ser Pro Ser Pro Arg Trp Gly Phe Leu Cys Val Leu Phe Thr Ala
                -15                 -10                  -5

Val His Pro Ala Pro Ser Thr Ala Pro Val Gln Asp Lys Cys Pro Val
             1               5                  10

Asn Thr Trp Glu Ala Met Gln Ala Ser Ser Gln Gln Leu Leu Gln Thr
     15                  20                  25

Asp Pro Met
 30
```

(2) INFORMATION FOR SEQ ID NO: 474:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 93 amino acids
(B) TYPE: AMINO ACID
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Testis

(ix) FEATURE:
(A) NAME/KEY: sig_peptide
(B) LOCATION: -76..-1
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 5.3
seq IILASASFSPNFT/QV

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 474:

```
Met Thr Ser Gln Pro Val Pro Asn Glu Thr Ile Ile Val Leu Pro Ser
    -75                 -70                 -65

Asn Val Ile Asn Phe Ser Gln Ala Glu Lys Pro Glu Pro Thr Asn Gln
-60                 -55                 -50                 -45

Gly Gln Asp Ser Leu Lys Lys His Leu His Ala Glu Xaa Lys Val Ile
                -40                 -35                 -30

Gly Thr Ile Gln Ile Leu Cys Gly Met Met Val Leu Ser Leu Gly Ile
            -25                 -20                 -15
```

```
Ile Leu Ala Ser Ala Ser Phe Ser Pro Asn Phe Thr Gln Val Thr Ser
        -10                     -5                      1

Thr Leu Leu Asn Ser Ala Tyr Pro Phe Ile Gly Pro Gly
  5                 10                  15
```

(2) INFORMATION FOR SEQ ID NO: 475:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 127 amino acids
(B) TYPE: AMINO ACID
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Testis

(ix) FEATURE:
(A) NAME/KEY: sig_peptide
(B) LOCATION: -91..-1
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 4.8
seq IILRLPWLNRSQT/VV

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 475:

```
Met Arg Ala Leu Glu Asn Asp Phe Phe Asn Ser Pro Pro Arg Lys Thr
    -90                 -85                 -80

Val Arg Phe Gly Gly Thr Val Thr Glu Val Leu Leu Lys Tyr Lys Lys
-75                 -70                 -65                 -60

Gly Glu Thr Asn Asp Phe Glu Leu Leu Lys Asn Gln Leu Leu Asp Pro
                -55                 -50                 -45

Asp Ile Lys Asp Asp Gln Ile Ile Asn Trp Leu Leu Glu Phe Arg Ser
            -40                 -35                 -30

Ser Val Met Tyr Leu Thr Lys Asp Phe Glu Gln Leu Ile Ser Ile Ile
        -25                 -20                 -15

Leu Arg Leu Pro Trp Leu Asn Arg Ser Gln Thr Val Val Glu Glu Tyr
    -10                 -5                  1               5

Leu Ala Phe Leu Gly Asn Leu Val Ser Ala Glu Thr Val Phe Leu Arg
                10                  15                  20

Pro Cys Leu Ser Met Ile Ala Ser His Phe Xaa Pro Pro Glu Leu
            25                  30                  35
```

(2) INFORMATION FOR SEQ ID NO: 476:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 57 amino acids

(B) TYPE: AMINO ACID
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Spleen

(ix) FEATURE:
(A) NAME/KEY: sig_peptide
(B) LOCATION: -31..-1
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 4.8
seq WAFSCGTWLPSRA/EW

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 476:

```
Met Val Phe Pro Ala Lys Arg Phe Cys Leu Val Pro Ser Met Glu Gly
    -30                 -25                 -20

Val Arg Trp Ala Phe Ser Cys Gly Thr Trp Leu Pro Ser Arg Ala Glu
-15                 -10                 -5                    1

Trp Leu Leu Ala Val Arg Ser Ile Gln Pro Glu Glu Lys Glu Arg Ile
              5                  10                  15

Gly Gln Phe Val Phe Ala Arg Asp Gly
        20                  25
```

(2) INFORMATION FOR SEQ ID NO: 477:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 93 amino acids
(B) TYPE: AMINO ACID
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Testis

(ix) FEATURE:
(A) NAME/KEY: sig_peptide
(B) LOCATION: -82..-1
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 4.7
seq LTCLADLFHSIAT/XK

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 477:

```
Met Asn Cys Phe Gln Gly Thr Asn Ala Ser Ala Leu Glu Lys Asp Ile
        -80                 -75                 -70

Gly Pro Glu Gln Phe Pro Ile Asn Glu His Tyr Phe Gly Leu Val Asn
    -65                 -60                 -55
```

Phe Gly Asn Thr Cys Tyr Cys Asn Ser Val Leu Gln Ala Leu Tyr Ser
-50 -45 -40 -35

Cys Arg Pro Phe Arg Glu Asn Val Leu Ala Tyr Lys Ala Gln Gln Lys
-30 -25 -20

Lys Lys Glu Asn Leu Leu Thr Cys Leu Ala Asp Leu Phe His Ser Ile
-15 -10 -5

Ala Thr Xaa Lys Lys Lys Val Xaa Ser Ser His Leu Gly
1 5 10

(2) INFORMATION FOR SEQ ID NO: 478:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 55 amino acids
(B) TYPE: AMINO ACID
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Testis

(ix) FEATURE:
(A) NAME/KEY: sig_peptide
(B) LOCATION: -16..-1
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 4.6
seq ALRVRXXXFGTRA/CR

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 478:

Met Ala Ala Ala Leu Arg Val Arg Xaa Xaa Xaa Phe Gly Thr Arg Ala
-15 -10 -5

Cys Arg Arg His Gly Leu Pro His Arg Ala Xaa Trp Leu Arg Asn Arg
1 5 10 15

Val Xaa Asp Arg Tyr Phe Arg Ile Gln Glu Val Leu Lys Xaa Ala Arg
20 25 30

His Phe Arg Gly Arg Lys Arg
35

(2) INFORMATION FOR SEQ ID NO: 479:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 45 amino acids
(B) TYPE: AMINO ACID
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Testis

(ix) FEATURE:
(A) NAME/KEY: sig_peptide
(B) LOCATION: -15..-1
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 4.6
seq LLTHNLLSSHVRG/VG

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 479:

```
Met Lys Leu Leu Thr His Asn Leu Leu Ser Ser His Val Arg Gly Val
-15                 -10                     -5                1

Gly Ser Arg Gly Phe Pro Leu Arg Leu Gln Ala Thr Glu Val Arg Ile
            5                  10                  15

Cys Pro Val Glu Phe Asn Pro Asn Phe Val Ala Arg Arg
        20                  25                  30
```

(2) INFORMATION FOR SEQ ID NO: 480:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 61 amino acids
(B) TYPE: AMINO ACID
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Testis

(ix) FEATURE:
(A) NAME/KEY: sig_peptide
(B) LOCATION: -41..-1
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 4.6
seq VSAGSLLLPAPQA/EX

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 480:

```
Met Gly Xaa Phe Ser Arg Arg Thr Phe Cys Gly Arg Ser Gly Arg Ser
    -40                 -35                 -30

Cys Arg Gly Gln Leu Val Gln Val Ser Arg Pro Glu Val Ser Ala Gly
-25                 -20                 -15                 -10

Ser Leu Leu Leu Pro Ala Pro Gln Ala Glu Xaa His Ser Ser Xaa Xaa
                -5                  1                   5

Leu Tyr Pro Arg Pro Lys Ser Leu Leu Pro Lys Met Gly
        10                  15                  20
```

(2) INFORMATION FOR SEQ ID NO: 481:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 79 amino acids
(B) TYPE: AMINO ACID
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Ovary

(ix) FEATURE:
(A) NAME/KEY: sig_peptide
(B) LOCATION: -55..-1
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 4.6
seq CALSLPDAPGASG/GR

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 481:

```
Met Glu Gly Gly Val Arg Leu Asp Leu Ser Ala Cys Gly Glu Thr Ser
-55                 -50                 -45                 -40

Gly Val Ala Val Ser Glu Leu Pro Ala Ser Glu Thr Ala Ala Leu Val
                -35                 -30                 -25

Pro Glu Gly His Gly Pro Gly Leu Arg Ala Cys Ala Leu Ser Leu Pro
            -20                 -15                 -10

Asp Ala Pro Gly Ala Ser Gly Gly Arg His His Leu Ile Leu Val Pro
        -5                      1               5

Gly Gln Gln His Thr Gly Leu Pro Ala Ser His Val His Pro Gln
 10                 15                  20
```

(2) INFORMATION FOR SEQ ID NO: 482:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 18 amino acids
(B) TYPE: AMINO ACID
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Ovary

(ix) FEATURE:
(A) NAME/KEY: sig_peptide
(B) LOCATION: -14..-1
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 4.5
seq TLLSFAALTAAFS/VL

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 482:

Met Thr Leu Leu Ser Phe Ala Ala Leu Thr Ala Ala Phe Ser Val Leu
-10 -5 1

Pro Lys

(2) INFORMATION FOR SEQ ID NO: 483:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 78 amino acids
(B) TYPE: AMINO ACID
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Ovary

(ix) FEATURE:
(A) NAME/KEY: sig_peptide
(B) LOCATION: -21..-1
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 4.4
seq GLSKLQFAPFSSA/LD

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 483:

Met Ala Ala Ala Thr Gly Asp Pro Gly Leu Ser Lys Leu Gln Phe Ala
-20 -15 -10

Pro Phe Ser Ser Ala Leu Asp Val Gly Phe Trp His Glu Leu Thr Gln
-5 1 5 10

Lys Lys Leu Asn Glu Tyr Arg Leu Asp Glu Ala Pro Lys Asp Ile Lys
15 20 25

Gly Tyr Tyr Tyr Asn Gly Asp Ser Ala Gly Xaa Pro Ala Arg Leu Thr
30 35 40

Leu Glu Phe Ser Ala Phe Asp Met Ser Ala Pro Thr Pro Ser
45 50 55

(2) INFORMATION FOR SEQ ID NO: 484:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 32 amino acids
(B) TYPE: AMINO ACID
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Homo Sapiens

(F) TISSUE TYPE: Spleen

(ix) FEATURE:
(A) NAME/KEY: sig_peptide
(B) LOCATION: -27..-1
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 4.4
seq LSKSLLLVPSXLS/LL

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 484:

```
Met Phe Thr Ser Thr Gly Ser Ser Gly Leu Tyr Lys Ala Pro Leu Ser
        -25                 -20                 -15

Lys Ser Leu Leu Leu Val Pro Ser Xaa Leu Ser Leu Leu Xaa Ala Gln
    -10                 -5                  1               5
```

(2) INFORMATION FOR SEQ ID NO: 485:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 83 amino acids
(B) TYPE: AMINO ACID
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Testis

(ix) FEATURE:
(A) NAME/KEY: sig_peptide
(B) LOCATION: -40..-1
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 4.3
seq ITLVSAAPGKVIC/EM

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 485:

```
Met Thr Ser Met Thr Gln Ser Leu Arg Glu Val Ile Lys Ala Met Thr
-40                 -35                 -30                 -25

Lys Ala Arg Asn Phe Glu Arg Val Leu Gly Lys Ile Thr Leu Val Ser
                -20                 -15                 -10

Ala Ala Pro Gly Lys Val Ile Cys Glu Met Lys Val Glu Glu Glu His
            -5                      1               5

Thr Asn Ala Ile Gly Thr Leu His Gly Gly Leu Thr Ala Thr Leu Val
    10                  15                  20

Asp Asn Ile Ser Thr Met Ala Leu Leu Cys Thr Glu Arg Gly Ala Pro
25                  30                  35                  40

Gly Val Ser
```

(2) INFORMATION FOR SEQ ID NO: 486:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 86 amino acids
(B) TYPE: AMINO ACID
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Spleen

(ix) FEATURE:
(A) NAME/KEY: sig_peptide
(B) LOCATION: -73..-1
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 4.3
seq DIILSGLVPGSTT/LH

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 486:

```
Met Ala Asp Phe Gly Ile Ser Ala Gly Gln Phe Val Ala Val Val Trp
            -70                 -65                 -60

Asp Lys Ser Ser Pro Val Glu Ala Leu Lys Gly Leu Val Asp Lys Leu
        -55                 -50                 -45

Gln Ala Leu Thr Gly Asn Glu Gly Arg Val Ser Val Glu Asn Ile Lys
    -40                 -35                 -30

Gln Leu Leu Gln Ser Ala His Lys Glu Ser Ser Xaa Asp Ile Ile Leu
-25                 -20                 -15                 -10

Ser Gly Leu Val Pro Gly Ser Thr Thr Leu His Ser Ala Glu Ile Leu
                -5                  1                   5

Ala Glu Ile Ala Arg Val
        10
```

(2) INFORMATION FOR SEQ ID NO: 487:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 16 amino acids
(B) TYPE: AMINO ACID
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Ovary

(ix) FEATURE:
(A) NAME/KEY: sig_peptide
(B) LOCATION: -14..-1
(C) IDENTIFICATION METHOD: Von Heijne matrix

(D) OTHER INFORMATION: score 4.2
seq GILLGLLLLGHLT/VR

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 487:

```
Met Gly Ile Leu Leu Gly Leu Leu Leu Leu Gly His Leu Thr Val Arg
            -10                     -5                      1
```

(2) INFORMATION FOR SEQ ID NO: 488:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 144 amino acids
(B) TYPE: AMINO ACID
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Testis

(ix) FEATURE:
(A) NAME/KEY: sig_peptide
(B) LOCATION: -19..-1
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 4.1
seq LLLGQRCSLKVSG/QE

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 488:

```
Met Phe Leu Thr Val Lys Leu Leu Leu Gly Gln Arg Cys Ser Leu Lys
                -15                 -10                     -5

Val Ser Gly Gln Glu Ser Val Ala Thr Leu Lys Arg Leu Val Ser Arg
             1               5                  10

Arg Leu Lys Val Pro Glu Glu Gln Gln His Leu Leu Phe Arg Gly Gln
     15                  20                  25

Leu Leu Glu Asp Asp Lys His Leu Ser Asp Tyr Cys Ile Gly Pro Asn
 30                  35                  40                  45

Ala Ser Ile Asn Val Ile Met Gln Pro Leu Glu Lys Met Ala Leu Lys
                 50                  55                  60

Glu Ala His Gln Pro Gln Thr Gln Pro Leu Trp His Gln Leu Gly Leu
             65                  70                  75

Val Leu Ala Lys His Phe Glu Pro Gln Asp Ala Lys Ala Val Leu Gln
         80                  85                  90

Leu Leu Arg Gln Glu His Glu Glu Arg Leu Gln Lys Ile Ser Leu Glu
     95                 100                 105

His Leu Glu Gln Leu Ala Gln Tyr Leu Leu Ala Glu Glu Leu Thr Trp
110                 115                 120                 125
```

(2) INFORMATION FOR SEQ ID NO: 489:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 106 amino acids
(B) TYPE: AMINO ACID
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Testis

(ix) FEATURE:
(A) NAME/KEY: sig_peptide
(B) LOCATION: -32..-1
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 4.1
seq RLLSSLLLTMSNN/NP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 489:

```
Met Asn Val Ile Asp His Val Arg Asp Met Ala Ala Ala Gly Leu His
        -30                 -25                     -20

Ser Asn Val Arg Leu Leu Ser Ser Leu Leu Leu Thr Met Ser Asn Asn
    -15                 -10                     -5

Asn Pro Glu Leu Phe Ser Pro Pro Gln Lys Tyr Gln Leu Leu Val Tyr
  1               5                  10                  15

His Ala Asp Ser Leu Phe His Asp Lys Glu Tyr Arg Asn Ala Val Ser
            20                  25                  30

Lys Tyr Thr Met Ala Leu Gln Gln Lys Lys Ala Leu Ser Lys Thr Ser
        35                  40                  45

Lys Val Arg Pro Ser Thr Gly Asn Ser Ala Ser Thr Pro Gln Ser Gln
    50                  55                  60

Cys Leu Pro Ser Glu Ile Glu Val Lys Tyr
65                  70
```

(2) INFORMATION FOR SEQ ID NO: 490:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 59 amino acids
(B) TYPE: AMINO ACID
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Testis

(ix) FEATURE:
(A) NAME/KEY: sig_peptide
(B) LOCATION: -41..-1
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 4.1
seq RVLCPLLXAAAAP/KR

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 490:

```
Met Gly Thr Pro Ser Leu Ser Ile Leu Leu Ile Gly Ala Pro Glu Ser
    -40                 -35                 -30

Pro Ile Pro Tyr Phe Pro Tyr His Ser Gly Thr Gly Arg Val Leu Cys
-25                 -20                 -15                 -10

Pro Leu Leu Xaa Ala Ala Ala Ala Pro Lys Arg Asp Val Pro Glu Thr
                -5                  1               5

Gly Leu Thr Arg Gln Leu Lys Arg His Pro Gly
        10                  15
```

(2) INFORMATION FOR SEQ ID NO: 491:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 57 amino acids
(B) TYPE: AMINO ACID
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Testis

(ix) FEATURE:
(A) NAME/KEY: sig_peptide
(B) LOCATION: -26..-1
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 3.9
seq HALFVLCLLYAMS/HN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 491:

```
Met Val Tyr His Ala Leu Asp Ser Pro Asp Asp Asp Tyr His Ala Leu
    -25                 -20                 -15

Phe Val Leu Cys Leu Leu Tyr Ala Met Ser His Asn Lys Gly Met Asp
-10                 -5                  1               5

Pro Glu Lys Leu Glu Arg Ile Gln Leu Pro Val Pro Asn Ala Ala Glu
            10                  15                  20

Lys Thr Thr Tyr Asn His Pro His Gly
        25                  30
```

(2) INFORMATION FOR SEQ ID NO: 492:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 24 amino acids
(B) TYPE: AMINO ACID
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Spleen

(ix) FEATURE:
(A) NAME/KEY: sig_peptide
(B) LOCATION: -14..-1
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 3.8
seq FIVLSMWLCCGFE/IL

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 492:

```
Met Phe Ile Val Leu Ser Met Trp Leu Cys Cys Gly Phe Glu Ile Leu
                -10                  -5                    1

Gln Thr Lys Ser Trp Val Ala Gly
         5                   10
```

(2) INFORMATION FOR SEQ ID NO: 493:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 24 amino acids
(B) TYPE: AMINO ACID
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Spleen

(ix) FEATURE:
(A) NAME/KEY: sig_peptide
(B) LOCATION: -15..-1
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 3.8
seq VVILSSXVPLAAM/GV

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 493:

```
Met Val Val Val Ile Leu Ser Ser Xaa Val Pro Leu Ala Ala Met Gly
-15                 -10                 -5                     1

Val Met Gly Cys Val Arg Val Trp
            5
```

(2) INFORMATION FOR SEQ ID NO: 494:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 67 amino acids
(B) TYPE: AMINO ACID
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Ovary

(ix) FEATURE:
(A) NAME/KEY: sig_peptide
(B) LOCATION: -15..-1
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 3.8
seq AECSSLLHPSVRG/SI

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 494:

```
Met Leu Ala Glu Cys Ser Ser Leu Leu His Pro Ser Val Arg Gly Ser
-15                 -10                  -5                   1

Ile Pro Glu Ala Thr Cys Arg Val Leu Pro Cys Gly Pro Leu His Asn
              5                  10                  15

Met Ala Val Cys Ser Cys Lys Ala Ser Arg Ser Phe Tyr Cys Asn Phe
         20                  25                  30

Arg Ser Leu Arg Leu Ala Val Ser Asp Phe Leu Ile Leu Phe Gln Lys
     35                  40                  45

Gly Leu Gly
 50
```

(2) INFORMATION FOR SEQ ID NO: 495:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 31 amino acids
(B) TYPE: AMINO ACID
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Ovary

(ix) FEATURE:
(A) NAME/KEY: sig_peptide
(B) LOCATION: -15..-1
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 3.8
seq MARLLGLCAWARK/SV

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 495:

```
Met Gln Met Ala Arg Leu Leu Gly Leu Cys Ala Trp Ala Arg Lys Ser
-15                 -10                 -5                   1

Val Arg Met Ala Ser Ser Arg Met Thr Arg Arg Asp Pro Pro Arg
            5                   10                  15
```

(2) INFORMATION FOR SEQ ID NO: 496:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 47 amino acids
(B) TYPE: AMINO ACID
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Uterus

(ix) FEATURE:
(A) NAME/KEY: sig_peptide
(B) LOCATION: -43..-1
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 3.8
seq LISVLYLIPKTLT/TN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 496:

```
Met Thr Pro Gln Tyr Leu Pro His Gly Gly Lys Tyr Gln Val Leu Gly
            -40                 -35                 -30

Asp Tyr Ser Leu Ala Val Val Phe Pro Leu His Phe Ser Asp Leu Ile
        -25                 -20                 -15

Ser Val Leu Tyr Leu Ile Pro Lys Thr Leu Thr Thr Asn Ser Arg
    -10                 -5                   1
```

(2) INFORMATION FOR SEQ ID NO: 497:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 115 amino acids
(B) TYPE: AMINO ACID
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Spleen

(ix) FEATURE:
(A) NAME/KEY: sig_peptide
(B) LOCATION: -23..-1

(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 3.7
seq FLPPLXRAFACRG/CQ

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 497:

```
Met Val Val Leu Arg Ala Gly Lys Lys Thr Phe Leu Pro Pro Leu Xaa
            -20                 -15                 -10

Arg Ala Phe Ala Cys Arg Gly Cys Gln Leu Ala Pro Glu Arg Gly Ala
         -5                   1               5

Glu Arg Arg Asp Thr Ala Pro Ser Gly Val Ser Arg Phe Cys Pro Pro
 10                  15                  20                  25

Arg Lys Ser Cys His Asp Trp Ile Gly Pro Pro Asp Lys Tyr Ser Asn
                 30                  35                  40

Leu Arg Pro Val His Phe Tyr Ile Pro Glu Asn Glu Ser Pro Leu Glu
             45                  50                  55

Gln Lys Leu Arg Lys Leu Arg Gln Glu Thr Gln Glu Trp Asn Gln Gln
         60                  65                  70

Phe Trp Ala Asn Gln Asn Leu Thr Phe Ser Lys Glu Lys Glu Glu Phe
     75                  80                  85

Ile His Ser
 90
```

(2) INFORMATION FOR SEQ ID NO: 498:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 33 amino acids
(B) TYPE: AMINO ACID
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Testis

(ix) FEATURE:
(A) NAME/KEY: sig_peptide
(B) LOCATION: -20..-1
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 3.6
seq AHLCSDSLPESQQ/QD

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 498:

```
Met Lys Arg Glu Gly Gly Ala Ala His Leu Cys Ser Asp Ser Leu Pro
-20                 -15                 -10                  -5

Glu Ser Gln Gln Gln Asp Gly Asn His Ala Pro Asn Phe Ser Ser His
                  1                   5                  10
```

Gly

(2) INFORMATION FOR SEQ ID NO: 499:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 46 amino acids
(B) TYPE: AMINO ACID
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Testis

(ix) FEATURE:
(A) NAME/KEY: sig_peptide
(B) LOCATION: -41..-1
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 3.6
seq PYSLAACPCGSQG/GV

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 499:

```
Met Val Thr Cys Pro Gly Pro Ser Ser Gly Gln Pro Leu Ser Ser Met
    -40                 -35                 -30

Tyr Thr Ala Gly Asp Arg Arg Gly Ala Pro Ser Leu Pro Tyr Ser Leu
-25                 -20                 -15                 -10

Ala Ala Cys Pro Cys Gly Ser Gln Gly Gly Val Cys Met Arg
                -5                   1               5
```

(2) INFORMATION FOR SEQ ID NO: 500:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 104 amino acids
(B) TYPE: AMINO ACID
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Spleen

(ix) FEATURE:
(A) NAME/KEY: sig_peptide
(B) LOCATION: -18..-1
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 3.5
seq ALEVIVTLSETAA/AM

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 500:

```
Met Gln Arg Gln Leu Ala Leu Glu Val Ile Val Thr Leu Ser Glu Thr
        -15                     -10                 -5

Ala Ala Ala Met Leu Arg Lys His Thr Asn Ile Val Ala Gln Thr Ile
         1                   5                  10

Pro Gln Met Leu Ala Met Met Val Asp Leu Glu Glu Asp Glu Asp Trp
 15                  20                  25                  30

Ala Asn Ala Asp Glu Leu Glu Asp Asp Asp Phe Asp Ser Asn Ala Val
                 35                  40                  45

Ala Gly Glu Ser Ala Leu Asp Arg Met Ala Cys Gly Leu Gly Gly Lys
             50                  55                  60

Leu Val Leu Pro Met Ile Lys Glu His Ile Met Gln Met Leu Gln Asn
         65                  70                  75

Arg Lys Leu Cys Pro Ser Met Leu
     80                  85
```

(2) INFORMATION FOR SEQ ID NO: 501:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 82 amino acids
(B) TYPE: AMINO ACID
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Testis

(ix) FEATURE:
(A) NAME/KEY: sig_peptide
(B) LOCATION: -76..-1
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 3.5
seq LASASELPLGSRP/AP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 501:

```
Met Gly Asp Tyr Leu Leu Arg Gly Tyr Arg Met Leu Gly Glu Thr Cys
    -75                 -70                 -65

Ala Asp Cys Gly Thr Ile Leu Leu Gln Asp Lys Gln Arg Lys Ile Tyr
-60                 -55                 -50                 -45

Cys Val Ala Cys Gln Glu Leu Asp Ser Asp Val Asp Lys Asp Asn Pro
                -40                 -35                 -30

Ala Leu Asn Ala Gln Ala Ala Leu Ser Gln Ala Arg Glu His Gln Leu
            -25                 -20                 -15

Ala Ser Ala Ser Glu Leu Pro Leu Gly Ser Arg Pro Ala Pro Gln Pro
        -10                  -5                   1
```

His Gly
5

(2) INFORMATION FOR SEQ ID NO: 502:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 41 amino acids
(B) TYPE: AMINO ACID
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Ovary

(ix) FEATURE:
(A) NAME/KEY: sig_peptide
(B) LOCATION: -15..-1
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 8.1
seq LLYLLVPALFCRA/GG

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 502:

Met Trp Leu Leu Tyr Leu Leu Val Pro Ala Leu Phe Cys Arg Ala Gly
-15 -10 -5 1

Gly Ser Ile Pro Ile Pro Gln Lys Leu Phe Gly Glu Val Thr Ser Pro
5 10 15

Leu Phe Pro Lys Pro Tyr Pro Asn Thr
20 25

(2) INFORMATION FOR SEQ ID NO: 503:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 75 amino acids
(B) TYPE: AMINO ACID
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Testis

(ix) FEATURE:
(A) NAME/KEY: sig_peptide
(B) LOCATION: -58..-1
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 4
seq LAAVSPLVRSLIS/SN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 503:

```
          Met Lys Cys Gly Phe Leu Ala Tyr Leu Leu Ile Thr Leu Leu
                  -20                 -15                 -10

TAT GTT TGG CCA GTT ATT AAT GCT TGC CAG                                201
Tyr Val Trp Pro Val Ile Asn Ala Cys Gln
            -5                  1
```

(2) INFORMATION FOR SEQ ID NO: 60:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 128 base pairs
(B) TYPE: NUCLEIC ACID
(C) STRANDEDNESS: DOUBLE
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Testis

(ix) FEATURE:
(A) NAME/KEY: sig_peptide
(B) LOCATION: 21..95
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 8.5
seq LKVLLLPLAPAAA/QD

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 60:

```
AGGGCGGATC TTCTCCGGCC ATG AGG AAG CCA GCC GCT GGC TTC CTT CCC TCA   53
                      Met Arg Lys Pro Ala Ala Gly Phe Leu Pro Ser
                      -25                 -20                 -15

CTC CTG AAG GTG CTG CTC CTG CCT CTG GCA CCT GCC GCA GCC CAG GAT    101
Leu Leu Lys Val Leu Leu Leu Pro Leu Ala Pro Ala Ala Ala Gln Asp
                -10                 -5                  1

TCG ACT CAG GCC TCC ACT CCA GGC AGG                                128
Ser Thr Gln Ala Ser Thr Pro Gly Arg
        5                   10
```

(2) INFORMATION FOR SEQ ID NO: 61:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 313 base pairs
(B) TYPE: NUCLEIC ACID
(C) STRANDEDNESS: DOUBLE
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Spleen

```
Met Lys Leu Glu Phe Thr Glu Lys Asn Xaa Xaa Ser Phe Val Leu Gln
            -55                 -50                 -45

Asn Leu Asn Arg Gln Arg Lys Arg Lys Glu Tyr Trp Asp Met Ala Leu
        -40                 -35                 -30

Ser Val Asp Asn His Val Phe Phe Ala His Arg Asn Val Leu Ala Ala
    -25                 -20                 -15

Val Ser Pro Leu Val Arg Ser Leu Ile Ser Ser Asn Asp Met Lys Thr
-10                 -5                  1               5

Ala Asp Glu Leu Phe Ile Thr Ile Asp Thr Lys
            10                  15
```